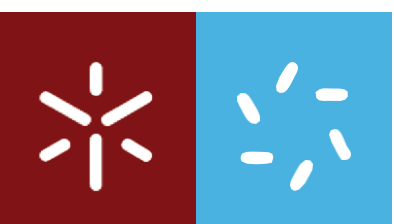


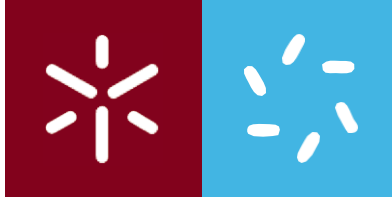


Eunice Conceição Lima da Costa

Post-fire restoration of soil microbial communities in a *Quercus suber* population

University of Minho
Science School





University of Minho

Science School

Eunice Conceição Lima da Costa

**Post-fire restoration of soil microbial
communities in a *Quercus suber*
population**

Master thesis

Master in Molecular Biology, Biotechnology and Bio-
entrepreneurship in Plants

This work was realized under the supervision
of:

**Doctor Maria Teresa Correia Guedes Lino
Neto**

And

Doctor Paula Cristina dos Santos Baptista

January of 2020

Direitos de autor e condições de utilização do trabalho por terceiros

Este é um trabalho académico que pode ser utilizado por terceiros desde que respeitadas as regras e boas práticas internacionalmente aceites, no que concerne aos direitos de autor e direitos conexos.

Assim, o presente trabalho pode ser utilizado nos termos previstos na licença abaixo indicada.

Caso o utilizador necessite de permissão para poder fazer um uso do trabalho em condições não previstas no licenciamento indicado, deverá contactar o autor, através do RepositóriUM da Universidade do Minho.



Atribuição-NãoComercial-SemDerivações

CC BY-NC-ND

<https://creativecommons.org/licenses/by-nc-nd/4.0/>

Acknowledgments

“No matter where I go, I know I’m not alone, I feel my saviour there beside me. He leads me through the night, he’s always been my guide. He promised He will never leave me” – Nik Day 2020

Portanto queria agradecer à Professora Teresa Lino Neto, minha orientadora, pela paciência que teve comigo na realização deste trabalho; pelo incentivo e encorajamento que me deu, por aumentar a minha fé e pelo precioso conhecimento que me transmitiu.

Agradeço também à Daniela pelo tempo dispendido comigo e por sempre se demonstrar disponível a ensinar-me e a ajudar-me em todas as coisas que eu precisava.

À Helena e à Juliana, na qualidade de amigas, que me ampararam nos momentos mais difíceis que encontrei ao longo deste trabalho experimental.

Ao Rómulo, o senhor Doutor e à Helena, que sabiam identificar as minhas fraquezas, quando mais ninguém as via.

Ao senhor Luis, pois fazia o impossível na aquisição de material necessário a este estudo.

Ao resto dos meus amigos, pelo apoio e carinho que me deram até agora e finalmente, e não menos importante, quero dedicar esta tese aos meus pais e à minha tia Chica, pelo amor e confiança que depositaram e depositam em mim. Pelo seu conforto ao longo deste tempo, pelas dificuldades que passamos e pelo exemplo de persistência e de força que eles foram e sempre serão para mim.

“Tenho-vos dito estas coisas para que em mim tenhais paz; no mundo teríeis aflições, mas tende bom animo, Eu venci o mundo” – João 16:33

Declaração de integridade

Declaro ter atuado com integridade na elaboração do presente trabalho académico e confirmo que não recorri à prática de plágio nem a qualquer forma de utilização indevida ou falsificação de informações ou resultados em nenhuma das etapas conducente à sua elaboração. Mais declaro que conheço e que respeitei o Código de Conduta Ética da Universidade do Minho.

Resumo

Os incêndios florestais causam distúrbios com enorme impacto nas florestas portuguesas de sobreiro. Devido à presença de cortiça, os sobreiros (*Quercus suber* L.) são reconhecidos como estando bem-adaptados à ocorrência de incêndios e a altas temperaturas. Contudo, a sustentabilidade das florestas de sobreiro também depende em grande parte das comunidades microbianas do solo, como seja a presença de fungos ectomicorrízicos ou rizobactérias. Neste trabalho, os efeitos da temperatura nas comunidades microbianas dos solos de sobreiro foram avaliados, bem como a restauração ecológica das florestas de *Quercus suber* após um episódio de incêndio florestal. A avaliação da taxa específica de morte microbiana foi realizada recorrendo a ensaios de temperatura (50°C a 125°C) efetuados com solos de sobreiro. A identificação das bactérias mais resistentes ao calor foi efetuada com auxílio a métodos de identificação molecular. Os resultados revelaram um aumento da taxa específica de morte microbiana com a temperatura, em que as comunidades bacterianas revelaram ser mais sensíveis ao calor que os fungos, provavelmente devido à produção de esporos. De acordo com este resultado, bactérias formadoras de esporos, tal como *Bacillus* spp foram identificadas como sendo as mais resistentes ao calor. Além disso, a análise da comunidade bacteriana por metabarcoding revelou uma elevada abundância de Firmicutes (*Bacillus*) em amostras de solo submetidas a 100°C por 15 e 30 min. Estes resultados fornecem assim uma previsão do que poderá acontecer às comunidades bacterianas após um incêndio nas florestas de sobreiro. Aproveitando a ocorrência natural de um incêndio em Santa Marta das Cortiças (Braga), as comunidades microbianas presentes em solos de sobreiro foram analisadas por metabarcoding. Colheram-se amostras de solo de nove árvores, diferenciadas pelos danos causados pelo fogo (queimadas, semi-queimadas e não-queimadas). A comunidade bacteriana foi comparada ao longo do tempo e os resultados revelaram que, de 5 a 18 meses após o incêndio, existiram diferenças na composição das comunidades bacterianas. Os solos de sobreiro apresentaram sempre uma elevada abundância de bactérias gram-negativas (Proteobacteria), seguidas de Acidobacteria, Actinobacteria e Chloroflexi. A variação do microbioma entre os solos afetados é explicada pelas diferenças na composição química do solo, intensidade com que o fogo atingiu os solos de sobreiro e fatores endofoclimáticos.

Palavras-chave: Comunidades Microbianas, Incêndios florestais, *Quercus suber*, Solo

Abstract

Wildfires cause disturbances with huge impact on Portuguese cork oak forests. Due to the production of cork, *Quercus suber* L. trees are recognized to be well-adapted to fires occurrence and to high temperatures. However, cork oak sustainability is also largely dependent on soil microbial communities, such as the presence of ectomycorrhizal fungi or rhizobacteria. In this work, the effects of temperature on cork oak soil microbial communities was studied, as well as the ecological restoration of *Quercus suber* forests after a wildfire episode. An evaluation of soil microbial specific death rate was performed using temperature assays (50°C to 125°C) on soils collected from cork oak trees. The most temperature resistant bacteria were identified by sequencing. Results revealed an increase of microbial death specific rate with temperature. Bacterial communities were more heat sensitive than fungi, as their survival is probably ensured by spore production. Accordingly, spore-forming bacteria such as *Bacillus* spp were identified as the most heat resistant bacteria. In addition bacterial community analysis by a metabarcoding approach revealed high abundance of Firmicutes (*Bacillus*) on soil samples subjected at 100°C for 15 and 30 min. Furthermore, these results provided a prediction of what could happen to bacterial communities after a wildfire in cork oak forests. Taking advantage from the natural occurrence of a natural wildfire in Santa Marta das Cortiças (Braga), cork oak soil microbial communities were surveyed using a metabarcoding approach. Soil samples from nine trees with three different types of fire damage (burnt, half-burnt and non-burnt) were collected, and bacterial community compared along time. Results revealed that from 5- to 18-months post-fire, there are differences on the composition of bacterial communities. A higher incidence of gram-negative bacteria (Proteobacteria), followed by Acidobacteria, Actinobacteria and Chloroflexi were always found for all cork oak soils. The variation on microbial communities among fire-affected soils is explained by differences on soil chemical composition, fire intensity and edaphoclimatic factors.

Key-words: *Quercus suber*, Microbial communities, Soil, Wildfires

Index

Resumo	viii
Abstract	ix
Table index	xii
Figure index	xiv
Chapter 1: General introduction	1
1.1. Importance and distribution of cork oak	2
1.2. The importance of associated forest microbial communities	5
1.3. Bibliography	11
Chapter 2: The effect of temperature increase in soil microbial communities	15
2.1. Thermal inactivation of soil microbial communities	16
2.2. Microbial thermal death described by mathematical models	17
2.3. Material and Methods	19
2.3.1. <i>Quercus suber</i> L. soil sampling	19
2.3.2. Experimental design	20
2.3.3. Temperature treatments and title determination	21
2.3.4. Determination of cell death kinetics	22
2.3.5. Analysis of colony biodiversity	22
2.3.6. Identification of the most heat resistant bacteria	22
2.3.7. Metabarcoding analysis of temperature treated soil	24
2.3.7.1. DNA sequence analysis and quality control	25
2.4. Results and Discussions	26
2.4.1. Soil chemical analysis	26
2.4.2. The effect of heat on soil microbial communities	27
2.4.3. Identification of heat resistant bacteria	32
2.4.4. Metabarcoding analysis of temperature treated soil	34
2.5. Conclusions	43
2.6. Bibliography	44
Chapter 3: Evaluation of soil microbial communities after a wildfire	47
3.1. Microorganism identification: a metabarcoding approach	48
3.2. Material and Methods	51
3.2.1. <i>Quercus suber</i> L. study population	51
3.2.2. Experimental design	54
3.2.3. Metabarcoding approach for soil microbial communities analysis	54
3.2.3.1. DNA sequence analysis and quality control	55
3.3. Results and discussion	56

3.3.1.	Chemical analysis of <i>Santa Marta das Cortiças</i> soils	56
3.3.2.	Amplification of soil DNA samples	58
3.3.3.	Data processing.....	60
3.3.4.	Bacterial taxonomic composition	61
3.3.4.1.	Bacterial diversity.....	68
3.4.	Conclusions	70
Chapter 4: Final conclusions and Future perspectives.....		74
Annex		76

Table index

Table 1 - Temperature treatments performed on cork oak soils to evaluate the influence of temperature on soil microbial communities. Temperature treatments were performed with distinct collected soils: 14 th March (a); 28 th May (b) and 24 th June of 2019 (c).....	21
Table 2 – PCR Components (25 µL) for the identification of the most heat resistant bacteria	23
Table 3 – PCR Components (25 µL) for 16S rRNA ITS region amplification, for bacteria and fungi respectively identification.....	25
Table 4 – Chemical analysis of studied soils taken from a Cork oak.	26
Table 5 - Death specific rates for soil bacterial and fungal communities. These values were determined by using a linearization of log ₁₀ (N/N ₀) vs time plots. Soil samples were collected on 14 th March – A; 28 th May – B and 24 th June of 2019.....	30
Table 6 - Analysis of microbial biodiversity after temperature application on soil microbial communities, as evaluated by the number of morphotypes present in those plates exhibiting well-separated colonies.	31
Table 7 - Identification of bacteria resistant to high temperatures, according to the sequencing of bacterial barcode 16S. The three best top-hits are displayed for each sequence (number in parenthesis reveal the number of hits for each species).	33
Table 8 – Quantification of soil DNA, extracted from samples subjected to 100°C of temperature, by nanodrop and Qubit method, for microbial communities' analysis by metabarcoding approach	36
Table 9 - Number of 16S rDNA V3-V4 reads of soil samples subjected to 100°C of temperature, after merging and quality filtering, as the number of obtained taxonomic classifications.....	36
Table 10 - Coefficients of similarity between bacterial communities present in different cork oak soil treated with 100°C for 0, 15 and 30 min. The Jaccard's index is displayed in the lower side of the table (blue) and the Sorenson's index in the upper side (green). The displayed indexes range between 0 - 1 (0: zero similarity; 1: maximum similarity). A gradient pattern of colours was applied according to the similarity's values (lighter colour - lower similarity value; darker colour - higher similarity value).	41
Table 11 – Diversity parameters for cork oak soil samples: untreated or treated with 15 or 30 min of heat (100°C). S – OTUs number.....	43
Table 12 – Sampled forest after 5-, 12- and 18-months after wildfire damage. Description of forest characteristics at the time of soil sampling.....	52
Table 13 - Fire damages and GPS coordinates of each sampled cork oak tree.....	52
Table 14 - PCR Components (25 µL) for 16S rRNA ITS region amplification, for bacteria and fungi respectively identification.....	55
Table 15 – Chemical analysis of soils collected on March 2018, 5-months post-fire occurrence, at Santa Marta das Cortiças (Braga).....	57
Table 16 – Chemical analysis of soils collected on April 2019, 18-months post-fire occurrence, at Santa Marta das Cortiças (Braga).....	58
Table 17 – Data processing of reads obtained by Illumina MiSeq metabarcoding using 16S barcode in DNA samples obtained from soils of different damaged cork oak trees. Raw dataset was processed as described in Materials	

and Methods and clustered into OTUs (results without singletons and unclassified reads). Number of OTUs correspond to results after dataset subsampling and removing OTUs with less than 5 reads.	60
Table 18 - Diversity parameters for cork oak soil samples harvested 5-, 12- and 18-months post-fire at Santa Marta das Cortiças. S – OTUs number.....	70

Figure index

Figure 1 – Cork oak (<i>Quercus suber</i>) tree.....	2
Figure 2 – Cork oaks that were recently stripped, displaying their living tissues exposed to environmental stressors..	4
Figure 3 – <i>Quercus suber</i> L. world distribution, APCOR. Portugal, north of Africa and southwestern of Spain are the areas where cork oak tree predominates, followed by France and Italy.....	4
Figure 4 – Common microbial survival curves. Linear survival curve(a); Non-linear: survival tailed curve (b); survival shoulder-tailed curve (c); survival shoulder curve (d); N/N ₀ - microbial cell survivors; adapted (Toure et al., 2017).	19
Figure 5 - Cork oak tree used on the study of temperature influence on soil microbial communities. GPS coordinates at University of Minho are 41 33'45.76"N; 8 23'40.87"O (photo taken on 14-05-2019).....	20
Figure 6 - Soil sampling method for analysis of temperature influence on soil microbial communities. A mix of three cores was created in order to form several samples for more and complemented information see Table 1. ...	20
Figure 7 - Preparation of soil microbial suspensions and corresponding 10-fold dilutions	22
Figure 8 – DNeasy Power Soil Kit protocol for extracting DNA form Cork oak soil samples. Changes to supplier's protocol are highlighted in bold and underlined.	24
Figure 9 – Bacterial survival curves of soil communities after temperature imposition. The curves were obtained considering the proportion of surviving cells (A – C) and the corresponding semilogarithmic relationship (D – F) along time. Different graphs represent assays performed with distinct collected soils (A, D – 14 th March; B, E – 28 th May; C, F – 24 th June of 2019).	28
Figure 10 – Fungal survival curves of soil communities after temperature imposition. The curves were obtained considering the proportion of surviving cells (A – C) at the corresponding semilogarithmic relationship (D – F). Different graphs represent assays performed with distinct collected soils (A, D – 14 th March; B, E – 28 th May; C, F – 24 th June of 2019).	29
Figure 11 - Influence of temperature on the inactivation on soil microbial communities, as described by Arrhenius plots. A – Temperature influence on bacterial communities; B – Temperature influence on fungal communities. K - Death specific rate; T – Temperature	31
Figure 12 – Electrophoresis of 16S region from the 14 selected bacterial isolates (taken from the 125°C treated soil samples). DNA was extracted and used to amplify 16S region by using the 799F and 1492R primer pair. M – 100bp plus ready-to-use DNA Ladder bioron	32
Figure 13 - Phylogenetic tree from sequence alignment of bacteria resistant to high temperatures.....	34
Figure 14 – Electrophoresis of 16S V3V4 region from soil samples treated with 100°C of temperature. DNA was extracted and used to amplify 16S V3V4 region by using the 16S V3V4FW and 16S V3V4 RV primer pair. Legend: bp – 100bp plus ready-to-use DNA Ladder Bioron; Heat treatment samples: B collection (1 – 0 min; 2 – 15 min; 3 – 30 min; 4 – 60 min; 5 – 90 min ; 6 – 120 min); A collection (7– 0 min; 8 – 15 min; 9 – 30 min; 10 – 50 min; 11 – 80 min; 12 – 120 min; C collection (13 – 0 min; 14 – 15 min; 15 – 30 min; 16 – 60 min; 17 – 90 min; 18 – 120 min;.....	35
Figure 15 – Electrophoresis of ITS region from soil samples treated with 100°C of temperature. DNA was extracted and used to amplify ITS region by using the ITS1F and ITS2 primer pair. Legend: bp – 100bp plus ready-to-use	

DNA Ladder Bioron; Heat treatment samples: B collection (1 – 0 min; 2 – 15 min; 3 – 30 min; 4 – 60 min; 5 – 90 min ; 6 – 120 min); A collection (7– 0 min; 8 – 15 min; 9 – 30 min; 10 – 50 min; 11 – 80 min; 12 – 120 min; C collection (13 – 0 min; 14 – 15 min; 15 – 30 min; 16 – 60 min; 17 – 90 min; 18 – 120 min; 35	
Figure 16 – Representation of bacterial taxonomic abundance obtained from sampled cork oak soil (without heat treatment) application. In this krona graph (Ondov et al., 2011), OTUs are identified until family level (97% identity)..... 37	
Figure 17 – Representation of bacterial taxonomic abundance obtained from cork oak soil treated at 100°C for 15 min. In this krona graph (Ondov et al., 2011), OTUs are identified until family level (97% identity). 38	
Figure 18 – Representation of bacterial taxonomic abundance obtained from cork oak soil for 30 min of 100°C application. OTUs identified until genus level (97 % identity)..... 39	
Figure 19 – Abundance and richness of bacterial phyla detected in untreated cork oak soils or treated with 100°C for 15 and 30 min, as revealed by Illumina MiSeq 16S amplicon sequencing (A) Phylum abundance (identified at 97 %); (B) Phylum richness (identified at 97. Phylum abundance and richness higher than 5 % are represented as “Others”. 39	
Figure 20 – Bacterial class revealed by Illumina MiSeq 16S amplicon sequencing (A) Class abundance (identified at 97 %) present on cork oak soil treated with 100°C for 0, 15 and 30 min; (B) Class richness (identified at 97 %) present on cork oak soil treated with 100°C for 0, 15 and 30 min. Class abundance and richness higher than 5 % are represented in the colour legend..... 40	
Figure 21 – Venn diagram of shared bacterial OTUs between untreated, and heat (100°C) treated soils for 15 and 30 min. The OTUs were classified up to genus level (97 % identity) and represent total of 634 genus. OTUs number identified in each sample are in parentheses..... 41	
Figure 22 – Rarefaction curves for bacterial community (number of OTUs) at 97 % identity. Treatments included 0, 15 and 30 min of heat application (100°C). Rarefaction curves were obtained at Past3 software v3.26 (Hammer, 2019).and plotted in GraphPad Prism 7.04 software. 42	
Figure 23 – rDNA region used in fungal identification. It is divided into SSU (18S and 5.8S) and LSU (28S). ITS regions are located between 18S subunit and 28S subunit and include 5.8S subunit. Primer for ITS region amplification are represented in black arrows 49	
Figure 24 – 16S rDNA gene used on bacteria identification. It is divided into conserved regions (blue) and hypervariable regions (red). Primer for hypervariable region amplification is also presented (green arrow), as the sequence methodologies used on metagenomic approach 49	
Figure 25 – Region map of the sampled cork oak forest (Stª Marta das Cortiças, Braga) used for the study of soil microbial communities by metabarcoding approach. Photo from 06-09-2017, Google earth Pro. Sampled trees are highlighted by a red sign. 51	
Figure 26 – <i>Quercus suber</i> tree selection according to tree damage status. a) 100% damaged cork oak; b) 50% damaged cork oak; c) cork oak without fire damage 53	
Figure 27 - Soil sampling method for metabarcoding approach on soil microbial communities..... 54	
Figure 28 – Optimization of PCR for amplifying ITS region. An annealing temperature gradient (50°-53°) PCR was used to optimize PCR. DNA was extracted and used to amplify ITS region by using the ITSF1 and ITS2 primer pair Legend: (bp) 100bp plus ready-to-use DNA Ladder Bioron; (c-) negative control; (1) [DNA] 3ng/ µL; (2) [DNA] 4	

ng/ μ L (3) [DNA] 6 ng/ μ L; (ci) [DNA] 53,6 ng/ μ L.. The most adequate temperature to perform PCR and amplify ITS region was 53°C (highlighted by a red rectangle).....	59
Figure 29 – Optimization of PCR for amplifying 16S region. An annealing temperature gradient (52°-56°) PCR was used to optimize PCR. DNA was extracted and used to amplify 16S V3V4 region by using the 16S V3V4FW and 16S V3V4 RV primer pairs. Legend: (bp) 100bp plus ready-to-use DNA Ladder Bioron; (c-) negative control; (1) [DNA] 3ng/ μ L; (2) [DNA] 4 ng/ μ L (3) [DNA] 6 ng/ μ L; (ci) [DNA] 53,6 ng/ μ L. The most adequate temperature to perform PCR and amplify 16S V3V4 region was 54°C (highlighted by a red rectangle).....	59
Figure 30 – Abundance and richness of bacterial phyla detected on Stª Marta das Cortiças soil as revealed by Illumina MiSeq 16S amplicon sequencing. Phylum abundance: A – 5 months post-fire (March 2018); C – 12 months post-fire (October 2018) and E – 18 months post-fire (April 2019) identified at 97%; Phylum richness: B – 5 months post-fire (March 2018); D – 12 months post-fire (October 2018) and F - 18 months post-fire (April 2019), identified at 97%.....	63
Figure 31 – Abundance and richness of bacterial class detected on Stª Marta das Cortiças soil as revealed by Illumina MiSeq 16S amplicon sequencing. Class abundance: A – 5 months post-fire (March 2018); C – 12 months post-fire (October 2018) and E – 18 months post-fire (April 2019) identified at 97%; Class richness: B – 5 months post-fire (March 2018); D – 12 months post-fire (October 2018) and F - 18 months post-fire (April 2019), identified at 97%.....	64
Figure 32 – Venn diagram of shared bacterial OTUs 5 months post-fire (A); 12 months post-fire (B) and 18 months post-fire (C). And bacterial OTUs shared between non-burnt cork oak soil (D); half-burnt cork oak soil (E) and between burnt cork oak soils (F) is also provided. The OTUs were classified up to genus level (97 % identity) and represent total of 3354 genus. OTUs number identified in each sample are in parentheses.	67
Figure 33 – Rarefaction curves for bacterial community (number of OTUs) at 97 % identity. Samples came from A – 5 months post-fire; B – 12 months post-fire and 18 months post-fire (C). Rarefaction curves were obtained at Past3 software v3.26 (Hammer, 2019) and plotted in GraphPad Prism 7.04.....	69

Chapter 1: General introduction

1.1. Importance and distribution of cork oak

Cork oak (*Quercus suber* L.) (Figure 1) belong to the *Cerris* sub-genus (*Cerris* section) of *Quercus* genus, according to the new classification (Denk *et al.*, 2017). This genus is a member of the Fagaceae family, which includes other genera such as *Castanea* and *Fagus* (Toribio *et al.*, 2005). Cork oaks are low spreading trees with short stems and thick branches (Aronson *et al.*, 2009). This perennial trees are monoecious with a flowering period from April to June that can be extended until autumn (Pereira & Tomé, 2004). Cork oak flowering begins at 15 to 20 years of age, with fruit production (acorns) fluctuating over the years. For example, *Quercus suber* can have a high yield of acorns for 2 to 3 years and a yield, followed by a reduced yield for 10 years (Pereira & Tomé, 2004). Male flowers are pendulous, long and come from the auxiliary buds of the previous year's branches, and female flowers appear in the new under vigorous growth (Gil & Varela, 2008). The leaves of cork oaks are green, dark, and denticular, where 5 to 8 pairs of secondary veins diverge from its central vein. Leaves usually measure between 2.5 to 10 cm x 1.2 to 6.5 cm (Amorim, 2014). This *Quercus* species is characterized by the presence of a bark with a continuous layer of thick and grooved cork on the outside (Pereira, 2007a).



Figure 1 – Cork oak (*Quercus suber*) tree.

Cork grow is promoted during spring and early summer, being highly controlled by annual climatic variations, such as winter precipitation and spring temperatures (Pereira & Tomé, 2004). The first cork is removed at 25-30 years of age and take places every 9 years (Leal *et al.*, 2008). The cork is the suberous parenchyma originated by the cork meristem, which gives to this material characteristic features. This lightweight, elastic material is a good thermal and electrical insulator, acoustic and vibration absorber and has also the ability to be compressed without lateral expansion (Gil, 2007). This last trait is due to the elasticity conferred by the cells present in this material, which promote an elastic recovery due to the action of the compressed gas inside them (Gil, 2007). Cork is also a material that dissipates creep energy, has low thermal conductivity, chemical and biological stability (Gil, 2007). Due to these characteristics, cork has a high economic value (Pereira, 2007a), for the production of wine bottling stoppers (alimentary industry), paving, wall and ceiling cladding (construction industry), thermal insulation (aerospace industry), badminton shuttlecocks and baseball balls (sports), shoe soles (footwear industry) and other applications (Leal *et al.*, 2008; Direito, 2011)

Cork removal is done manually and the first stripping, from which virgin cork is produced, is performed when the tree has a trunk perimeter of 70 cm at breast height (Pereira, 2007b). This is a value is specified by Portuguese legislation. This perimeter occurs when the tree is between 18 and 25 years old. The second stripping occurs between the ages of 27 and 35 and the remaining ones are performed when cork oak has 45 years of age (Pereira & Tomé, 2004; Costa *et al.*, 2010). From the third stripping, every 9 years. The cork undergoes morphological changes (Pereira & Tomé, 2004). Virgin cork is characterized by many severe fractures, due to the intense radial growth and tangential stress. In the remaining stripings, cork presents smoother fractures, derived from the decrease in stem growth stresses (Pereira, 2007b; Oliveira & Costa, 2012). The phenotypic and morphological biodiversity that exists among cork oaks is due to the hybridization that existed in the past (Pereira, 2007a). For this reason, today we can find different qualities of cork from distinct cork oaks.

Cork removal contributes to an increase of trees vulnerability to external biotic and abiotic agents (Catry *et al.*, 2012). After stripping (Figure 2), the exposure of the living tissue causes an immediate loss of water and plant responds by closing their stomata interrupting plant nutrition (Leal *et al.*, 2008). Cork oaks tree start their recovering after 24-30 days after the regeneration of phloem.



Figure 2 – Cork oaks that were recently stripped, displaying their living tissues exposed to environmental stressors.

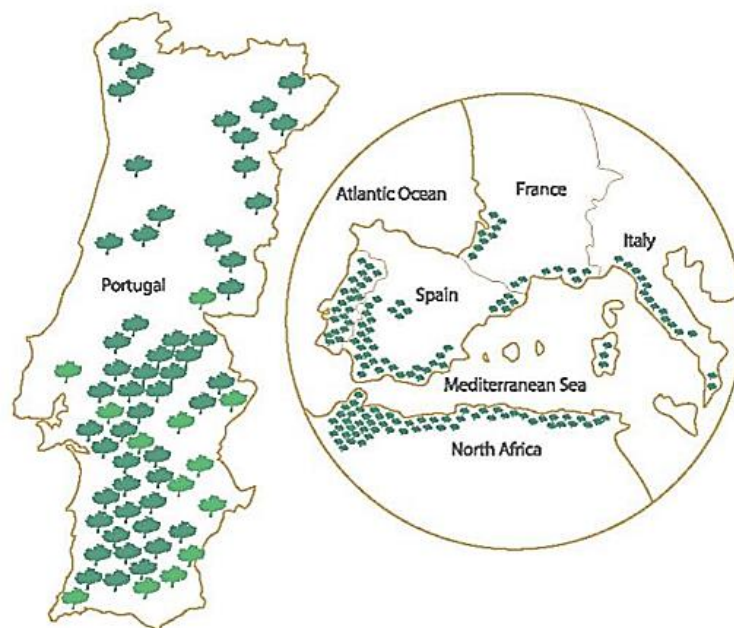


Figure 3 – *Quercus suber* L. world distribution, APCOR. Portugal, north of Africa and southwestern of Spain are the areas where cork oak tree predominates, followed by France and Italy.

Quercus suber is one of the most important evergreen tree of the western Mediterranean region, being a common species of oak from the Iberian Peninsula (Pereira & Tomé, 2004; Costa *et al.*, 2010). From Morocco and Iberian Peninsula to the western edge of the Italian Peninsula,

cork oak forest covers over 1.5 million hectares in Europe and 700 000 hectares in North Africa (Figure 3) (Pereira & Tomé, 2004; Aronson *et al.*, 2009; Mauri, 2016). Accordingly, *Quercus suber* is well adapted to hot and dry temperatures being considered as a very tolerant specie (Pereira, 2007a).

1.2. The importance of associated forest microbial communities

Plants shelter a large diversity of microbial communities, and the dynamics of plant-microorganism interaction are known to be crucial for maintaining the ecosystem functioning (Parasuraman *et al.*, 2019). Indeed, microbial communities have existed together with plants for millions of years and play important roles in host growth and health (Singh *et al.*, 2019). For example, plant associated microorganisms can provide nutrients (including water), as well as higher resistance to abiotic and biotic factor. Soil microorganisms can also play an important role on the maintenance of forest ecosystems by producing organic and inorganic compounds through the decomposition of litter, death microbial biomass and death wood (Baldrian, 2017).

Studies performed over the past decade have identified microorganisms associated with different plant hosts and specific plant organs. Plant microbiota or microbiome, comprises all active microorganisms that interact with plants (Orozco-Mosqueda *et al.*, 2018), also including the functional genetic pool of viruses and prokaryotes (Compant *et al.*, 2019; Singh *et al.*, 2019). Plant microbiota live in different habitats, which comprises the whole plant or their organs, such as leaves, roots, shoots, seeds and flowers (Singh *et al.*, 2019). Accordingly, different microbiotas could be found associated with a plant, such as the phyllosphere, endosphere, episphere, rhizosphere, rhizoplane, anthosphere, spermosphere, carposphere microbiotas (Shade *et al.*, 2017; Ciafardini & Zullo, 2018), soil microbiome (Al-Dagal & Fung, 1990; Levy *et al.*, 2018; Compant *et al.*, 2019). The phyllosphere comprises all the aboveground plant organs, such as leaves, stems and flowers (Remus-Emsermann & Schlechter, 2018).

Several studies over the past decade found that in the phyllosphere there is a great microbial diversity, which is specific for each plant species (Lindow & Brandl, 2003; Esser *et al.*, 2015). Indeed, bacteria (mainly *Pseudomonas syringae* and *Erwinia (Pantoea)* spp, are predominant microorganisms on leaf surfaces (Lindow & Brandl, 2003) and are capable of reaching populations with densities greater than 10^4 to 10^5 bacteria per mm^2 leaf surface, [10^8 bacteria per g^{-1} leaf in extreme cases (Remus-Emsermann *et al.*, 2014)]. Furthermore, different authors revealed that phyllospheric bacteria are more prevalent in areas closer to trichomes and

stomata (Remus-Emsermann & Schlechter, 2018). A better knowledge on epi- and endophyte fungal communities that thrive in the phyllosphere would be useful for getting a better understanding of the factors that influence fungal composition and structure, in order to predict their response to climate change (Gomes *et al.*, 2018).

Two different habitats can be distinguished. The surface of plant tissues are inhabited by microorganisms called epiphytes (Faeth *et al.*, 2002; Backman & Sikora, 2008; Turner *et al.*, 2013). Other microorganisms (known as endophytes) are able to colonize the internal tissues of the plant (Orozco-Mosqueda *et al.*, 2018). The specific location of endophytes in cell tissues are not well described, although these microorganisms were found in xylem vessels, intracellular apoplast, dead or dying cells (Turner *et al.*, 2013). Symbiotic systemic endophytes are well known for increasing plant fitness reducing herbivory by alkaloids production and increasing the nutrient uptake in poor soils. In return the host plant gives refuge and photosynthates to the endophyte (Faeth *et al.*, 2002). Both endophyte and epiphyte display relationships with plants which are characterized for being neutral, beneficial or detrimental (Faeth *et al.*, 2002; Backman & Sikora, 2008; Turner *et al.*, 2013).

The area of soil that contains the plant root system is called rhizosphere and is composed, not only by the plant roots, but also by rhizodeposited adhesives, peeled root cells and exudates. Rhizosphere is highly influenced by the physiological processes that occur within the plant (Clairmont *et al.*, 2019), being also considered as a site of high soil microbial activity, thus representing one of the most complex ecosystems (Compant *et al.*, 2019). Indeed, the rhizospheric soil has been described as “the most complicated biomaterial on the planet”, since comprises two components: abiotic structure and biological diversity. Associated to the root, the rhizoplane is the community of microorganisms on the root surface (microbial biofilms) (Clairmont *et al.*, 2019). Relationships between microbial communities in rhizosphere and rhizoplane are not yet known or have been poorly studied. The root microbiota is mainly composed by *Acidobacteria*, *Verrucomicrobia*, *Bacteroidetes*, *Proteobacteria*, *Planctomycetes* and *Actinobacteria* (Compant *et al.*, 2019), which are known to establish relationships with roots (Singh *et al.*, 2019). The community of microorganisms present in rhizosphere can provide substances that drive plant growth and development by producing phytohormones that stimulate root growth. In certain cases, microorganisms can even stimulate uncontrolled cell growth (as the case of *Agrobacterium tumefaciens* or *Ustilago maydis*). This morphological modification may result in an increase in

water uptake by plants. For example, the fungi of *Tricoderma* sp. grows and develops in association with plant roots, contributing for their development (Singh *et al.*, 2019).

Plant microbiomes perform functions for the plant growth and health. Thus, the understanding of interactions between plants and the microbial world, as well as the factors inherent to the formation of microbial communities, lead to a better understanding of plants as meta-organisms (Compant *et al.*, 2019). Also, a better knowledge of the benefits taken by microorganisms through this association are being achieved (Compant *et al.*, 2019). For example, a wide variety of compounds secreted by plants, such as organic acids, vitamins, sugars, among others, are currently known to be used by microbial communities as signals (Singh *et al.*, 2019). On the other hand, volatile substances and other compounds, are secreted by microorganisms in order to directly or indirectly activate plant immunity, control plant development or plant morphogenesis (Singh *et al.*, 2019). For example, cytokinins and auxins are transferred by microorganisms to areas around the roots, in order to promote the growth of the root system (Singh *et al.*, 2019). There are also volatile compounds produced by PGPR – Plant Growth Promoter Rhizobacteria - such as acetoin and 2,3-butanediol that are used as signalling compounds for plant growth (Singh *et al.*, 2019). Plant associated microbiomes are also important on promoting plant growth and on defence to biotic factors (Orozco-Mosqueda *et al.*, 2018). Soils have a huge microbiological diversity (Zheng *et al.*, 2019), which are essential for virtually all biogeochemical cycle processes (Prosser *et al.*, 2007), such as nitrogen, phosphorus (Sergaki *et al.*, 2018) and carbon cycles (Crowther *et al.*, 2016). Also, these microorganisms can provide protection against abiotic and biotic stress (Sergaki *et al.*, 2018) and regulate decomposition of organic matter (Zheng *et al.*, 2019), being also fundamental in mineralization and immobilization processes (Pizarro-Tobías *et al.*, 2015). All of these functions are possible due to the metabolic versatility of these microbial communities (Prosser *et al.*, 2007).

Soil microbes can resist to significant variations in soil physical parameters occurring during the day and seasons, such as temperature and moisture, which are crucial for the microbial activity (Maier *et al.*, 2009). Many microorganisms are also resistant to the soil texture itself, which varies from soil to soil, according to other environmental factors (Maier *et al.*, 2009). Furthermore, the presence of certain organisms could result in biotic stressors for others, as microbial communities from different soils are frequently in competition (Maier *et al.*, 2009). Indeed, certain microorganisms can segregate inhibitory substances, which may influence the emergence of new microbial communities, by inhibiting their appearance or reducing the number of existing

microorganisms in that community, in order to maintain a biotic balance in the soil (Maier *et al.*, 2009). Besides these, many factors are known to disturb forest ecosystems, such as anthropogenic factors, environmental pollution and fires (Mataix-Solera *et al.*, 2011; Baldrian, 2017). Accordingly, human behaviour can influence the fire frequency and changes in the vegetation patterns, which have led to environmental problems in some locations over the past five decades (Mataix-Solera *et al.*, 2011). Indeed, forest fires are a major cause of changes in forest ecosystems, increasing the risk of soil erosion and desertification (Granged *et al.*, 2011). Despite that, forest fires can provide diverse benefits to the ecosystems, such as the consumption of superfluous vegetation (organic matter) and release of nutrients into the soil (inorganic matter) (Cowan *et al.*, 2016). Among others, the negative impacts of forest fires comprise the heat that directly affects soil microbial communities, the alteration of the physical structure, the sudden acidification of soil, decrease of moisture and/or electrical conductivity (Pérez-Valera *et al.*, 2017). Forest fires generally have more negative than positive impacts on the physical, chemical and biological soil properties (Mataix-Solera *et al.*, 2011), which also depend on the intensity of the fire occurrence (Pérez-Valera *et al.*, 2017).

Many authors have suggested definitions and indicators of forest fire severity, by the assessment of physical, chemical and ecological changes observed after fires (Cowan *et al.*, 2016). In addition, the intensity of forest fires can be rated based on the rate of thermal energy production and forest fire duration (Certini, 2005). This assessment should take into account, not only the impacts of above ground fire, but also the spread of heat belowground, which affects the soil forest ecosystem (Mataix-Solera *et al.*, 2011). Low intensity fires typically include those that are applied in controlled conditions, during specific weather conditions and which serve to reduce the amount of fuel (*e.g.* dry leaves, twigs). In contrast, a severe fire is usually responsible for leaving a trail of negative effects on the soil: reducing the organic matter by combustion, the decrease of nutrients through volatilization, soil erosion, changes on aggregate stability that weakens the soil structure and changes on microbial communities (Mataix-Solera *et al.*, 2011). Therefore, although low severity fires do not significantly affect soils, severe burning can affect a wide range of soil properties and in some cases those impacts are irreversible (Granged *et al.*, 2011). Thus, soil properties may have a permanent, long-term or short-term alteration induced by fire, depending on severity and frequency of fires and post-fire weather conditions.

After a wildfire episode, soils suffer important biological, chemical and physical changes (Granged *et al.*, 2011). Among these, changes in the chemical properties of soils are one of the

most important, due to the defragmentation of clay minerals and increase of inorganic compounds. Wildfires provide ashes from the burning soil, which are rich in magnesium, potassium and calcium. The amount of ash (micro and macronutrients), soil nutrients, organic matter content are all factors that contribute for pH variation in the soil after a fire (Altun *et al.*, 2004). High amounts of ashes are known to promote an acidification of acidic and neutral soils (basic soils are not greatly affected) (Altun *et al.*, 2004). As the soil pH is related to the functioning of terrestrial ecosystems, soil fertility and biogeochemical processes, the acidification of soils will affect different ecosystem functions. Therefore, some authors argue that soil pH is negatively correlated with temperature, also suggesting that this phenomenon may be caused by increased accumulation of soil organic matter and increased organic acids (Hong *et al.*, 2019).

Depending on the fire severity, the impact on organic matter can be the volatilization of the micronutrients, carbonization or complete oxidation. The combustion of organic matter is consistent with a decrease of soil pH and increase of electrical conductivity (Granged *et al.*, 2011). While forest fires can cause depletion of organic material on the soil surface, nutrients as phosphorous, potassium, calcium, magnesium, among others, can change in their quantity and spatial distribution after this forest disturbance, moving to deeper areas of the soil after rainfall (Altun *et al.*, 2004). Furthermore, certain compounds suffer specific modifications. For example, soil organic nitrogen compounds can remain after low-intensity fires, but proteins suffer specific modifications on their peptide form. This progressive modification occurs at two stages: first some NH_2 groups, together with an amino acid are removed, without changing the peptide structure; then the N-amide group is converted to heterocyclic compounds (Certini, 2005). During severe fires, organic nitrogen is converted to its inorganic forms, ammonium (NH_4^+) and nitrate (NO_3^-). Ammonium is a direct product of combustion, while nitrate forms ammonium a few weeks or months after fire, as a result of nitrification reactions. Forest fires do not necessarily have the same impact on phosphorus (P), as on available soil nitrogen, because P losses through volatilization or leaching are small. However, fires result in an enrichment of available P for a short period time. Indeed, in acidic soils, orthophosphate binds to Al, Fe and Mn oxides through chemical adsorption, while in neutral or alkaline soils P binds to Ca minerals and precipitates as calcium phosphate. The time at which the positive effect of fire on P availability is short and is highly variable, depending on several factors (Certini, 2005).

Forest fires also negatively influence the biological properties of soil (Ekinci, 2006).

The temperatures reached by forest fires tend to promote the death of living beings present in the soil and in extreme cases can completely sterilize the soil. During a wildfire episode, soil surface temperatures can reach between 200 °C to 300 °C, making nearly impossible a microbial colonization after forest fire, being the exception fungal spores that can withstand severe temperatures (Buscardo *et al.*, 2010; Mataix-Solera *et al.*, 2011).

The ability of certain microbial species, communities or ecosystems to recover after a disturbance without significantly altering their structure, function or productivity is called resilience. This term can be used to assess the ability of a specific species, community or ecosystem to return to its original state after the end of the disturbance (Granged *et al.*, 2011). Soil microbial communities are highly dependent on the environment. Some microbial groups can benefit from those altered circumstances while other became harmed (Pérez-Valera *et al.*, 2017), due to the previously described factors or by the absence of water (Cowan *et al.*, 2016). Therefore, mechanisms such as competition between microorganisms can limit the similarity between microbial communities before and after wildfire episode (Pérez-Valera *et al.*, 2017).

Ectomycorrhizal fungi are sensitive to forest fires because mortality of this fungi usually occurs at temperatures around 60°C and above (Cowan *et al.*, 2016). Although high intensity fires affect the function of ectomycorrhizal fungal communities, leading to their total extinction (Buscardo *et al.*, 2010), some ectomycorrhizal fungi can produce spores able to survive at high temperatures (Cowan *et al.*, 2016). Such resistance structures contribute to the similarities in composition of ectomycorrhizal communities before and following forest fires (Buscardo *et al.*, 2010). In any case, fire is known to promote significant loss of fungal biomass, according to the abundance of mycorrhizae, even though there is a "protection" of these microorganisms that develop in deeper soils (Mataix-Solera *et al.*, 2011). In contrast to fungi, Smith *et al.* (2008) analysed the bacterial community of burnt and unburnt soil and concluded that the composition of microbial communities was significantly different in both conditions. The presence of *Alphaproteobacteria* and *Gammaproteobacteria* was characteristic of unburned soils, while *Betaproteobacteria* and *Bacillus* were the most common in burnt soils (Smith *et al.*, 2008). Therefore, changes in soil microbial communities can lead in many ways to soil degradation and consequently to ecosystem disturbance. For this reason, soil microbes can be important indicators of soil quality and consequently indicators of the health status of the plant (Barreiro *et al.*, 2010; Pizarro-Tobías *et al.*, 2015).

In conclusion, there are many environmental factors, the combustion process, temperature, air humidity, wind speed, among others, are important in the extent of forest damage and recovery (Certini, 2005). After forest fires, soil recovery takes a long time. The recovery of soil organic matter in burned areas only begins with the natural or artificial reintroduction of vegetation, usually of those species characterized by rapid growth after wildfire (Certini, 2005).

The aim of this work is to determine the impact of high temperatures (wildfire) on soil microbial communities. One of the main concerns of cork oaks producers is the raising in the frequency/severity of wildfires, due to a combination of increasing mean temperatures and drought (Acácio *et al.*, 2009). This climate change is predicted to be particularly serious for the Mediterranean area (Lionello & Scarascia, 2018). For studying the impact on microbial communities, which will have a role on cork oak forests recovery, two specific objectives were considered: i) to evaluate the effect of temperature increasing (application of heat) on bacterial communities, and ii) to evaluate the recovery of microbial communities after a forest wildfire. For this, **Chapter 2** focuses on the evaluation of microbial viability before and after application of increasing temperatures (50°C to 150°C) and a long time. In this chapter, the microbial biodiversity is also evaluated by cultural methods and the most resistant bacteria to high temperatures are identified. Finally, using a metabarcoding analysis, the effect of temperature on whole soil bacterial community present on cork oak soil is studied. In **Chapter 3**, a metabarcoding analysis of soil samples taken from a cork oak forest (Santa Marta das Cortiças, Braga, Portugal) presenting cork oaks differently damaged is performed. For this, soil harvest was performed 5, 12 and 18 months after the forest fire. Evaluations on microbial abundance, richness, biodiversity and comparisons between all soil samples are discussed.

1.3. Bibliography

- Acácio V, Holmgren M, Rego F, Moreira F, Mohren GMJ. 2009. Are drought and wildfires turning Mediterranean cork oak forests into persistent shrublands? *Agroforestry Systems* **76**: 389–400.
- Al-Dagal M, Fung DY. 1990. Aeromicrobiology — A Review. *Critical Reviews in Food Science and Nutrition* **29**: 333–340.
- Altun L, Bilgili E, Sağlam B, Küçük Ö, Yılmaz M, Tüfekçioğlu A. 2004. Soil organic matter, soil pH and soil nutrient dynamics in forest stands after fire. In: Natural Resource Management for Sustainable Development. International Soil Conference, 10.
- Amorim. 2014. A Arte da Cortiça. *Amorim*: 96.
- Aronson J, Pereira JS, Pausas JUG. 2009. *Cork Oak Woodlands on the Edge Society for ecological restoration international the Science and Practice of ecological reStoration Advance praise for Cork Oak Woodlands on the Edge*. Island Press.
- Backman PA, Sikora RA. 2008. Endophytes: An emerging tool for biological control. *Biological*

Control **46**: 1–3.

Baldrian P. 2017. Forest microbiome: Diversity, complexity and dynamics. *FEMS Microbiology Reviews* **41**: 109–130.

Barreiro A, Martín A, Carballas T, Díaz-Raviña M. 2010. Response of soil microbial communities to fire and fire-fighting chemicals. *Science of the Total Environment* **408**: 6172–6178.

Buscardo E, Rodríguez-Echeverría S, Martín MP, De Angelis P, Pereira JS, Freitas H. 2010. Impact of wildfire return interval on the ectomycorrhizal resistant propagules communities of a Mediterranean open forest. *Fungal Biology* **114**: 628–636.

Catry FX, Moreira F, Pausas JG, Fernandes PM, Rego F, Cardillo E, Curt T. 2012. Cork oak vulnerability to fire: The role of bark harvesting, tree characteristics and abiotic factors. *PLoS ONE* **7**: 1–9.

Certini G. 2005. Effects of fire on properties of forest soils: A review. *Oecologia* **143**: 1–10.

Ciafardini G, Zullo BA. 2018. Virgin olive oil yeasts: A review. *Food Microbiology* **70**: 245–253.

Clairmont LK, Stevens KJ, Slawson RM. 2019. Site-specific differences in microbial community structure and function within the rhizosphere and rhizoplane of wetland plants is plant species dependent. *Rhizosphere* **9**: 56–68.

Compant S, Samad A, Faist H, Sessitsch A. 2019. A review on the plant microbiome: Ecology, functions, and emerging trends in microbial application. *Journal of Advanced Research* **19**: 29–37.

Costa A, Pereira H, Madeira M. 2010. Analysis of spatial patterns of oak decline in cork oak woodlands in Mediterranean conditions. *Annals of Forest Science* **67**: 204–204.

Cowan AD, Smith JE, Fitzgerald SA. 2016. Recovering lost ground: Effects of soil burn intensity on nutrients and ectomycorrhiza communities of ponderosa pine seedlings. *Forest Ecology and Management* **378**: 160–172.

Crowther TW, Todd-Brown KEO, Rowe CW, Wieder WR, Carey JC, MacHmuller MB, Snoek BL, Fang S, Zhou G, Allison SD, *et al.* 2016. Quantifying global soil carbon losses in response to warming. *Nature* **540**: 104–108.

Denk T, Grimm GW, Manos PS, Deng M, Hipp AL. 2017. An Updated Infrageneric Classification of the Oaks: Review of Previous Taxonomic Schemes and Synthesis of Evolutionary Patterns. In: 13–38.

Direito DG. 2011. A industria da cortiça e o seu potencial de inovação.

Ekinci H. 2006. Effect of Forest Fire on Some Physical , Chemical and Biological Properties of Soil in Çanakkale , Turkey. *International Journal of Agriculture & Biology* **8**: 102–106.

Esser DS, Leveau JHJ, Meyer KM, Wiegand K. 2015. Spatial scales of interactions among bacteria and between bacteria and the leaf surface. *FEMS Microbiology Ecology* **91**: 1–13.

Faeth SH, Haase SM, Sackett SS, Sullivan T, Remington RK, Hamilton CE. 2002. Does Fire Maintain Symbiotic, Fungal Endophyte Infections in Native Grasses? *Symbiosis* **32**: 211–248.

Gil L. 2007. *A cortiça como material de construção*. Santa Maria de Lamas - Portugal: APCOR – Associação Portuguesa de Cortiça Av.

Gil L, Varela MC. 2008. EUFORGEN Technical guidelines for genetic conservation and use - Cork oak. *International Plant Genetic Resources Institute*: 6 p.

Gomes T, Pereira JA, Benhadi J, Lino-Neto T, Baptista P. 2018. Endophytic and Epiphytic Phyllosphere Fungal Communities Are Shaped by Different Environmental Factors in a Mediterranean Ecosystem. *Microbial Ecology* **76**: 668–679.

Granged AJP, Zavala LM, Jordán A, Bárcenas-Moreno G. 2011. Post-fire evolution of soil properties and vegetation cover in a Mediterranean heathland after experimental burning: A 3-year study. *Geoderma* **164**: 85–94.

Hong S, Gan P, Chen A. 2019. Environmental controls on soil pH in planted forest and its response

to nitrogen deposition. *Environmental Research* **172**: 159–165.

Leal S, Nunes AEE, Pereira AEH. 2008. Cork oak (*Quercus suber* L .) wood growth and vessel characteristics variations in relation to climate and cork harvesting Cork oak (*Quercus suber* L .) wood growth and vessel characteristics variations in relation to climate and cork harvesting.

Levy A, Conway JM, Dangl JL, Woyke T. 2018. Elucidating Bacterial Gene Functions in the Plant Microbiome. *Cell Host and Microbe* **24**: 475–485.

Lindow SE, Brandl MT. 2003. Microbiology of the Phyllosphere MINIREVIEW Microbiology of the Phyllosphere. *Applied and Environmental Microbiology* **69**: 1875–1883.

Lionello P, Scarascia L. 2018. The relation between climate change in the Mediterranean region and global warming. *Regional Environmental Change* **18**: 1481–1493.

Maier RM, Pepper IL, Gerba CP. 2009. Introduction to Environmental Microbiology. In: Environmental Microbiology. Elsevier Inc.

Mataix-Solera J, Cerdà A, Arcenegui V, Jordán A, Zavala LM. 2011. Fire effects on soil aggregation: A review. *Earth-Science Reviews* **109**: 44–60.

Mauri JS-M-AD de RGCTHDA. 2016. *European Atlas of Forest Tree Species*. Luxembourg: Publication Office of the European Union.

Oliveira G, Costa A. 2012. How resilient is *Quercus suber* L. to cork harvesting? A review and identification of knowledge gaps. *Forest Ecology and Management* **270**: 257–272.

Orozco-Mosqueda M del C, Rocha-Granados M del C, Glick BR, Santoyo G. 2018. Microbiome engineering to improve biocontrol and plant growth-promoting mechanisms. *Microbiological Research* **208**: 25–31.

Parasuraman P, Pattnaik S, Busi S. 2019. Plant-Microbe Interactions in Ecosystems Functioning and Sustainability. In: New and Future Developments in Microbial Biotechnology and Bioengineering. Elsevier B.V., 255–266.

Pereira H. 2007a. The cork oak. In: Cork. 241–249.

Pereira H. 2007b. The extraction of cork. In: Cork. Elsevier, 127–144.

Pereira H, Tomé M. 2004. Non-Wood products | Cork Oak. In: Encyclopedia of forest sciences. Oxford: Elsevier, 613–620.

Pérez-Valera E, Goberna M, Faust K, Raes J, García C, Verdú M, Gomes T, Pereira JAJS, Benhadi J, Lino-Neto T, et al. 2017. Fire modifies the phylogenetic structure of soil bacterial co-occurrence networks. *Environmental Microbiology* **19**: 317–327.

Pizarro-Tobías P, Fernández M, Niqui JL, Solano J, Duque E, Ramos JL, Roca A. 2015. Restoration of a Mediterranean forest after a fire: Bioremediation and rhizoremediation field-scale trial. *Microbial Biotechnology* **8**: 77–92.

Prosser JI, Bohannon BJM, Curtis TP, Ellis RJ, Firestone MK, Freckleton RP, Green JL, Green LE, Killham K, Lennon JJ, et al. 2007. The role of ecological theory in microbial ecology. *Nature Reviews Microbiology* **5**: 384–392.

Remus-Emsermann MNP, Lückner S, Müller DB, Potthoff E, Daims H, Vorholt JA. 2014. Spatial distribution analyses of natural phyllosphere-colonizing bacteria on *Arabidopsis thaliana* revealed by fluorescence in situ hybridization. *Environmental Microbiology* **16**: 2329–2340.

Remus-Emsermann MNP, Schlechter RO. 2018. Phyllosphere microbiology: At the interface between microbial individuals and the plant host. *New Phytologist* **218**: 1327–1333.

Sergaki C, Lagunas B, Lidbury I, Gifford ML, Schäfer P. 2018. Challenges and approaches in microbiome research: from fundamental to applied. *Frontiers in Plant Science* **9**: 1–12.

Shade A, Jacques MA, Barret M. 2017. Ecological patterns of seed microbiome diversity, transmission, and assembly. *Current Opinion in Microbiology* **37**: 15–22.

Singh D, Raina TK, Kumar A, Singh J, Prasad R. 2019. Plant microbiome: A reservoir of novel genes and metabolites. *Plant Gene* **18**: 100177.

- Smith NR, Kishchuk BE, Mohn WW. 2008. Effects of wildfire and harvest disturbances on forest soil bacterial communities. *Applied and Environmental Microbiology* **74**: 216–224.
- Toribio M, Celestino C, Molinas M. 2005. Cork oak, *Quercus suber* L. In: Protocol for Somatic Embryogenesis in Woody Plants. Netherlands: Springer, 445–457.
- Turner TR, Jmanes EK, Poole PS. 2013. The Plant Microbiome. *Genome Biology* **14**: 1–10.
- Zheng Q, Hu Y, Zhang S, Noll L, Böckle T, Dietrich M, Herbold CW, Eichorst SA, Woebken D, Richter A, *et al.* 2019. Soil multifunctionality is affected by the soil environment and by microbial community composition and diversity. *Soil Biology and Biochemistry* **136**: 107521.

Chapter 2: The effect of temperature increase in soil microbial communities

In Microbiology, a microbial cell is considered viable when under favourable environmental conditions can divide into one or more living daughter cells also viable. To be considered dead or unviable, the microorganism has to lose this ability, which commonly comes from the disruption of environmental conditions by the presence of lethal agents (e.g. temperature, pH, radiation, chemicals in lethal doses) (Casolari, 1988). Whenever the lethal agent is temperature, death is described as thermal death. Thermal death under controlled situations helps to find solutions for hospital problems, food preserving and to determine the behaviour of soil microbial communities when subjected to a wildfire. Temperature lethal effects are consequences of the thermal energy (Pepper & Dowd, 2009) on bacterial and fungal communities (Hugo, 1971).

2.1. Thermal inactivation of soil microbial communities

Microbial thermal inactivation (thermal death) can be isothermal or non-isothermal. In thermodynamics, an isothermal process is a thermodynamic transformation that leads to a variation in the state of a physical system without the changing of system temperature over time. In contrast, a non-isothermal thermodynamic transformation involves a variation of temperature during time. The induction of temperature (heat) to a system that is thermodynamically at equilibrium (thus causing a disturbance) leads to the loss of energy that will not only affect the cell as a whole, but also all molecules and biochemical reactions within the system (Hugo, 1971).

The increase of thermal energy is due to the increase of kinetic energy of all molecules in the system (in the case of thermal death within microbial cells) (Mazur, 2006). When there is an increase of thermal energy, microbes begin to dehydrate, enzymes to denature and microbial cells began to die by oxidation. This happens due to the breakdown of hydrogen bonds and covalent bonds between amino acid chains, affecting their three-dimensional structures needed for functional proteins (Xie *et al.*, 2003; Mazur, 2006; Pepper & Dowd, 2009). Some microorganisms are more sensitive to humid heat than to dry heat. The difference between these two types of disturbance is observed by the fact that wet heat is more effective in killing soil microorganisms than dry heat. Certain microbial communities have thermal amplitudes ranging from 50°C to 210°C, but these temperatures can be more lethal in the presence of moisture (Mataix-Solera *et al.*, 2011). The moist heat is deadliest than dry heat, because is more effective on denaturing enzymes leading to higher microbial death. During the moist heat imposition thermal energy is directly transferred to cells due to the presence of water (Xie *et al.*, 2003).

There are certain microbes more resistant to temperature than others (Mataix-Solera *et al.*, 2011). For example, some nitrifying bacteria, protozoa and fungi cannot resist temperatures higher than 70°C. Arbuscular fungi suffer cell death at temperatures ranging from 80°C to 90°C, while most microbial communities do not live above 115°C. However, spore-forming strains can maintain their communities at higher temperatures due to late spore burst (Mataix-Solera *et al.*, 2011). The maximum heat treatment by which microorganisms maintain their viability defines their maximal heat tolerance (Hugo, 1971).

Most soil microbial communities are resistant to large thermal ranges on soil. The optimal temperature range for growth of each community and temperature resistance makes their distinction (Hugo, 1971). While psychrophilic microorganisms are characterized by preferring temperatures of 20°C, the mesophilic prefer 20-45°C, thermophilic (45-90°C) and hyperthermophile (>90°C). The differentiation between such microorganisms provides a pattern of temperature-induced mortality in their natural habitats (Hugo, 1971). The temperatures suitable for the growth of thermophilic microorganisms are consequently inhibiting the growth of mesophilic microorganisms and the optimal temperature for growth of these later microorganisms are growth inhibitors for psychrophilic microorganisms (Maier *et al.*, 2009). Although there is a wide variety of microorganisms in the soil, most of them are mesophilic due to the buffering effect of the soil temperature (Maier *et al.*, 2009).

2.2. Microbial thermal death described by mathematical models

Microbiology uses mathematical modelling to describe the response of microbial populations to environmental conditions, as well as to discriminate the parameters that influence those responses (Klotz *et al.*, 2007; Ferrer *et al.*, 2009; Huang, 2014; Garre *et al.*, 2018). Predictive microbiology follows a few steps on data analysis. First, samples must be subjected to different environmental conditions and plotted into survival or growth curves. Then, each survival or growth curve must be analysed using a suitable primary model to determine kinetic parameters, such as growth or death rates. Finally, analysis on parameter effects such as temperature is performed using secondary models (Huang, 2017). Primary models describe changes in the number of microorganisms, or other microbial responses, as a function of time and secondary models describe how the primary models vary depending on other parameters, such as temperature, acidity, water activity, salt content, among others (Zimmermann, 2012; Huang, 2014). But on predictive microbiology, mathematical models can also be classified as tertiary models (Ferrer *et al.*, 2009). Tertiary models

are software applications generated by primary and secondary models, usually used by non-modellers (Ferrer *et al.*, 2009). Mathematical primary models can translate thermal death of microorganisms by plotting the Log_{10} of survival fraction vs time or plotting the percentage of survival fraction vs time (Klotz *et al.*, 2007; Toure *et al.*, 2017). These graphical representations (survival curves) are a cumulative form of the temporal distribution of lethal/deadly events on microorganisms (Klotz *et al.*, 2007; Toure *et al.*, 2017).

The behaviour of microorganisms can be interpreted in different ways. The inactivation process resembles the first order of reaction. The lethal events can occur randomly over time in a population of cells that are similar in their susceptibility to the agent, but differences in sensitivity to lethal agents can occur between individual cells (Klotz *et al.*, 2007). For many decades, mathematical prediction of microbial death used the first order of kinetics – survival fraction vs time used to follow a linear relationship (Corradini *et al.*, 2007; Huang, 2014, 2019). However, the majority of environmental survival curves are not linear (Corradini *et al.*, 2007; Huang, 2014). According to different environmental conditions, survival curves (Figure 4) can have several shapes (Moats, 1971; Peled *et al.*, 1977; Casolari, 1988) and inactivation kinetics depends on the conditions applied to microbial cells (Klotz *et al.*, 2007). Survival curves may be linear - the microbial survival rate is proportional to the number of surviving cells over time - or nonlinear. Nonlinear survival curves are subdivided into tailed curves, shoulder-tailed curves (sigmoid), shoulder curves, and logarithmic curves. Survival shoulder curves are characterized by the appearance of a lag phase on the first minutes of heat treatment. This indicates a non-instantaneous thermal death, due to the presence of agglomerated microbial communities. Tail curves (biphasic) are usually interpreted by the presence of intrinsically more resistant microorganisms than others, normally two subpopulations where one microbial community is more heat resistant than the other. Sigmoid curves are a combination of survival biphasic curves with survival shoulder curves. Finally, logarithmic curves express heterogeneous communities of microorganisms that differ on heat sensitivity (Moats, 1971; Peleg & Cole, 1998b; Xiong *et al.*, 1999).

Microbial rates elucidate the time required to reach a microbial event or condition (Smelt & Brul, 2014). Therefore, microbial death rates indicate the rate at which microbial inactivation occurs over time (Moats, 1971) and describes the behaviour of microbial communities during heat treatment (Smelt & Brul, 2014). Microbial death rates cannot be directly determined as they depend on the number of surviving cells over time.

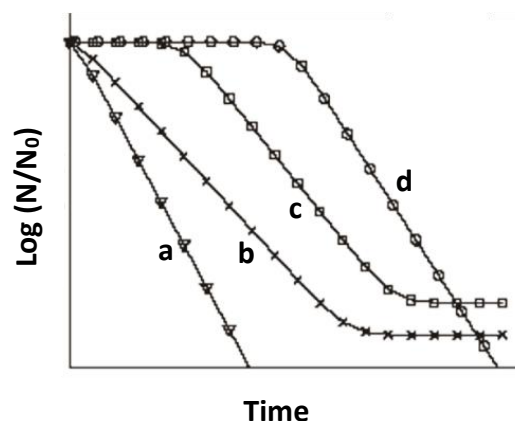


Figure 4 – Common microbial survival curves. Linear survival curve(a); Non-linear: survival tailed curve (b); survival shoulder-tailed curve (c); survival shoulder curve (d); N/N_0 - microbial cell survivors; adapted (Toure et al., 2017).

The objective of this chapter is to evaluate the influence of temperature on soil microbial communities by evaluating the title of microbial suspensions from cork oak soil samples, to which temperatures of 50°C to 150°C were applied. With the help of survival graphs [(N/N_0) vs time and $\text{Log } (N/N_0)$ vs time], the decrease of microbial load over time was evaluated and specific rates calculated. The decrease in biodiversity was tested by counting the bacterial morphotypes found in different samples and the most resistant bacteria to 125°C were identified by molecular methods. In this chapter, differences on microbial communities present in soil samples subjected to heat treatment were also evaluated along time, by using a barcoding approach.

2.3. Material and Methods

2.3.1. *Quercus suber* L. soil sampling

A cork oak tree located at University of Minho (Braga, Portugal) was chosen for evaluating the response of its soil microbial community to heat (Figure 5). The sampled cork oak was apparently healthy with no signs of defoliation or other diseases signs, being near to other healthy cork oak trees.

Soil samples were collected in three dates (14th March, 28th May and 24th June of 2019). After removing the uppermost layer of soil that consisted of plant litter and other organic material, three independent soil cores (5 cm in diameter and 10 cm in depth) were collected. Soil sampling was performed under the middle of cork oak canopy, in the three tree trunk directions. In total, 9 soil cores (3 cores $\times$ 3 sampling dates) were collected, which were kept at 4°C until processing (Figure 6). The three soil samples (cores) from each collection date were thoroughly mixed.



Figure 5 - Cork oak tree used on the study of temperature influence on soil microbial communities. GPS coordinates at University of Minho are 41°33'45.76"N; 8°23'40.87"E (photo taken on 14-05-2019).

A soil sample was sent for chemical analysis performed by *A2-Análises Químicas*TM (Guimarães, Portugal). The chemical soil analysis included gravimetry, pH (H₂O), pH (CaCl₂), electrical conductivity, organic matter, organic carbon, total nitrogen; carbon: nitrogen ratio; phosphorus (P₂O₅), potassium (K₂O), calcium (CaO), magnesium (MgO), sodium; boron, sulphur, iron and manganese.

2.3.2. Experimental design

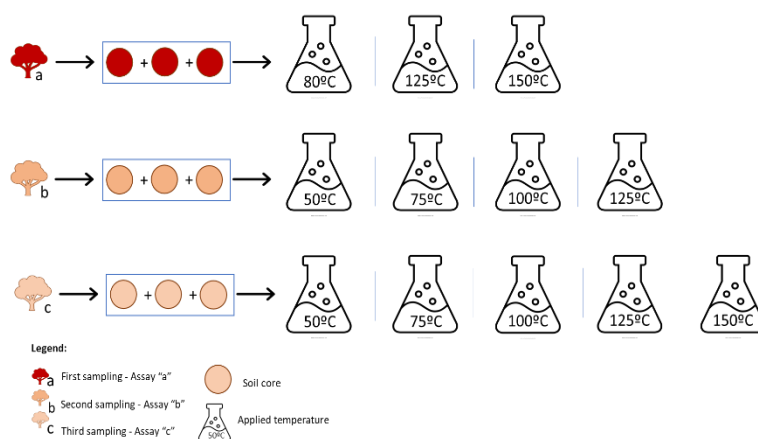


Figure 6 - Soil sampling method for analysis of temperature influence on soil microbial communities. A mix of three cores was created in order to form several samples for more and complemented information see Table 1.

For evaluating the effect of temperature on soil microbial community, soil samples from distinct collection dates were used in different temperature assays (Figure 6). For each temperature treatment, different periods were applied to allow the construction of survival curves (Table 1).

Table 1 - Temperature treatments performed on cork oak soils to evaluate the influence of temperature on soil microbial communities. Temperature treatments were performed with distinct collected soils: 14th March (a); 28th May (b) and 24th June of 2019 (c).

Time (min)	Temperature (°C)																	
	50			75			80			100			125			150		
	a	b	c	a	b	c	a	b	c	a	b	c	a	b	c	a	b	c
0	-	✓	✓	-	✓	✓	✓	-	-	-	✓	✓	✓	✓	✓	✓	-	✓
15	-	✓	✓	-	✓	✓	✓	-	-	-	✓	✓	✓	✓	✓	✓	-	✓
30	-	✓	✓	-	✓	✓	✓	-	-	-	✓	✓	✓	✓	✓	✓	-	✓
50	-	-	-	-	-	-	✓	-	-	-	-	-	✓	-	-	✓	-	-
60	-	✓	✓	-	✓	✓	-	-	-	-	✓	✓	-	✓	✓	-	-	✓
80	-	-	-	-	-	-	✓	-	-	-	-	-	✓	-	-	✓	-	-
90	-	✓	✓	-	✓	✓	-	-	-	-	✓	✓	-	✓	✓	-	-	✓
120	-	✓	✓	-	✓	✓	✓	-	-	-	✓	✓	✓	✓	✓	✓	-	✓
150	-	-	-	-	-	-	✓	-	-	-	-	-	✓	-	-	✓	-	-
180	-	-	-	-	-	-	✓	-	-	-	-	-	✓	-	-	✓	-	-

2.3.3. Temperature treatments and title determination

Each soil mixture (2g) was subjected to different temperature treatments (Table 1), using a *Memmert Model 700* incubator (*Memmert GmbH, Germany*). Temperatures were certified by using a data logger *Thermocouple USB EL-USB-TC-LCD* from *Lascar Eletronics*.

After temperature treatment a microbial solution was prepared by using 1g of treated soil and sterilized water (5mL for temperature treatments of 125°C and 150°C and 10mL for the remaining treatments). This difference was due to the predicted reduction in the number of microorganisms present in soil samples treated at 150°C or 125°C, in comparison to the remaining temperature treatments. After a thoroughly mixing by vortexing, serial 10-fold dilutions (1mL of final volume) were prepared, in order to enable the title determination (Figure 7). From all dilutions, 100µL were spread onto PCA (Plate Count Agar) medium (*VWR Prolabo Chemicals*) for bacterial forming units count and PDA (Potato Dextrose Agar) medium (*Liofilchem srl, Italy*) for fungal forming units counts. Tree technical replicates were performed for each experiment. Incubation proceeded at 30°C for 48h before colonies counting. For determining the title as colony forming unit (CFU) per g of soil, the equation 1 was used.

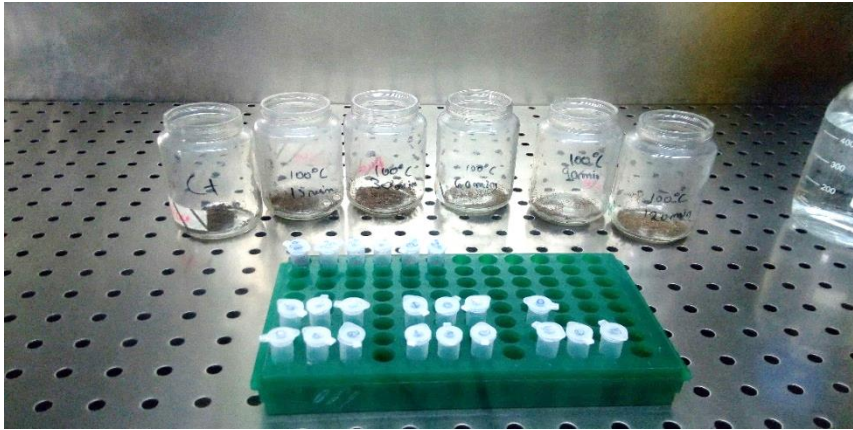


Figure 7 - Preparation of soil microbial suspensions and corresponding 10-fold dilutions

Equation 1:

$$Title (CFU/g \text{ of soil}) = Colonies \text{ count} * \left(\frac{1}{10^{-n}} \right) * \frac{1}{inoculated \text{ volume (mL)}} * fold \text{ dilution of soil}$$

where n corresponds to the dilution.

2.3.4. Determination of cell death kinetics

The survival curves were obtained by plotting the percentage of surviving cells ($N/N_0 * 100$), where N is the microbial title at time t and N_0 is the title at $t=0$. Microbial survival curves were also plotted on a log-linear scale, using the $\log_{10} (N/N_0)$ on the y-axis and time on x-axis. Graphical representations were performed using a *nonfit curve One phase decay* provided by *GraphPad prism 7.04* software. The effect of temperature on microbial community death was evaluated by a graph representing the specific death rate as a function of temperature.

2.3.5. Analysis of colony biodiversity

For evaluating the microbial community biodiversity after application of different temperatures, the morphological characterization of obtained colonies was performed. For this evaluation, plates containing well separated colonies were used. The criteria used to distinguish colonies were based on morphological characteristics, such as colony shape, border, colour and elevation. The number of morphotypes found in each temperature/time point was compared.

2.3.6. Identification of the most heat resistant bacteria

The molecular identification of the most resistant bacteria to temperature was performed using the 16S ribosomal RNA as a barcode. DNA extractions were performed using a *Quick-DNA™*

Fungal/Bacterial Miniprep Kit (Zymo Research, USA) following the supplier conditions. A PCR amplification was performed using the pair of primers *799F* and *1492R* for the 16S rRNA region in a PCR reaction of 25 µL of final volume (Table 2). Amplification occurred on a *Bio-Rad T100 Thermal Cycler* using the following programme: 3 min at 94°C for initial denaturation, followed by 35 cycles of 30s at 94°C for denaturation, 1min at 55°C for annealing temperature and 30s at 72°C for the extension. PCR was ended with a final extension of 10 min at 72°C.

PCR products were evaluated by electrophoresis on an agarose gel (1% w/w) prepared in 0.5x TAE buffer (0.01M Tris; pH 8.0; 47.5mM acetic acid; 25mM EDTA). For allowing the visualization of DNA, *green safe buffer* (nzytech) was added to the agarose gel (100 µL of *green safe buffer*/100mL gel). A mix of 8µL of DNA plus 2µL of green dye (nzytech) was loaded into the agarose gel, as well as the molecular marker (*100 bp plus ready-to-use DNA Ladder*, bioron). Electrophoresis ran at 109V for 30min. The agarose gel was observed with an *UV transilluminator (VWR Genosmart)* and pictures were taken with an image acquisition system (*VWR Genosmart*).

Table 2 – PCR Components (25 µL) for the identification of the most heat resistant bacteria

PCR components	Amount (µL)
ddH ₂ O	19.3
Complete KCl reaction Buffer (10x) bioron	2.5
dNTPs (10mM)	0.5
Primer <i>799F</i> * (10 mM)	0.5
Primer <i>1492R</i> * (10 mM)	0.5
DSF- <i>Taq</i> DNA polymerase bioron	0.2
DNA template	1
Total	25

* *799F* – AACMGGATTAGATACCKG; *1492R* – GGTTACCTTGTTACGACTT; using these primers a 693bp PCR product is expected

The PCR product was purified by adding isopropanol (40 µL of 75% v/v) to 10 µL of PCR product. After an incubation of 15 min at room temperature, a centrifugation of 4500 rpm for 30 min, at 4°C, was performed. The supernatant was discarded and another centrifugation at 300 rpm for 1 min at 4°C was performed. The supernatant was again discarded and the precipitated DNA was washed by adding 150 µL of isopropanol 75% (v/v). Centrifugation was repeated at 300rpm for 7 min at 4°C and final supernatant was discarded. The obtained pellet was dried in a horizontal flow chamber for at least 30 min. DNA was resuspended in 10 µL of ultrapure sterilized H₂O. Obtained samples were sent for sequencing at STABVIDA (Caparica,

Portugal). Sequences were blasted against NCBI (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>). The best blast hits were considered based on higher similarity identity and e-value.

2.3.7. Metabarcoding analysis of temperature treated soil

Soil samples from the second collection, subjected to 100°C for 0, 15 and 30min, were selected for metabarcoding sequencing. Soil DNA was extracted from 1g using the *DNeasy Power Soil Kit* (*Qiagen, The Netherlands*) with some changes (Figure 8).

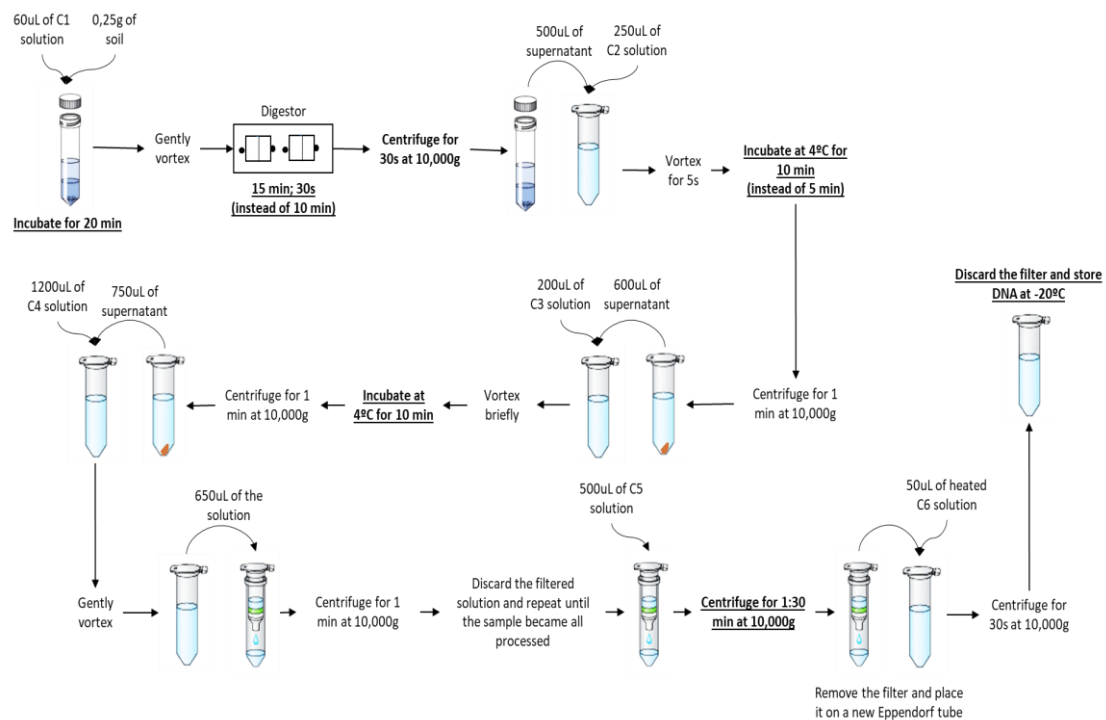


Figure 8 – DNeasy Power Soil Kit protocol for extracting DNA from Cork oak soil samples. Changes to supplier's protocol are highlighted in bold and underlined.

The quantity and quality of obtained DNA were accessed using a *Nanodrop spectrometer ND-1000 3.8.1*, (Thermo Fisher Scientific) using $A_{260\text{ nm}}/A_{280\text{ nm}}$ and $A_{260\text{ nm}}/A_{230\text{ nm}}$ values. For accurately quantify the DNA before sending to sequencing services, a fluorescent DNA quantification assay was performed with the *Qubit dsDNA HS Assay Kit* (Thermo Fisher Scientific, Waltham, MA, USA), using *Qubit 4 fluorometer*.

To ensure DNA quality for *Illumina Miseq sequencing*, a PCR amplification was performed using the pair of primers *16S V3V4 FW* and *16S V3V4 RV* for the 16S rRNA region and *ITS1F* and *ITS2* for ITS region in a 25µL PCR reaction (Table 3). Amplification occurred on a *Bio-Rad T100 Thermal Cycles* using the following programme: 4 min at 94°C for initial denaturation, followed by

35 cycles of 30s at 94°C for denaturation, 30s at variable temperatures (53°C to 55°C) for annealing temperature and 30s at 72°C for the extension. PCR was ended with a final extension of 10 min at 72°C. Amplified products were separated in an agarose gel electrophoresis, as described in the previous section.

Table 3 – PCR Components (25 μ L) for 16S rRNA ITS region amplification, for bacteria and fungi respectively identification.

PCR components	Amount (μ L)
ddH ₂ O	20.15
Complete NH ₄ reaction Buffer (10x): pH 8.8, 0.1% Tween 20, 25mM M _g Cl ₂ Bioron	2.5
dNTPs (10 mM)	0.25
Primer 16S V3V4 FW* or ITS1F** (10 mM)	0.5
Primer 16S V3V4 RV* or ITS2** (10 mM)	0.5
DSF- <i>Taq</i> DNA polymerase Bioron (5U/ μ L)	0.1
DNA template	1
Total	25

* 16S V3V4 FW – TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCTA; 16S V3V4 RV – GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAC; using these primers a 400 bp PCR product is expected.

** ITS1F – CTTGGTCATTAGAGGAAGTAA; ITS2 – GCTGCGTTCCTCATCGATGC; using these primers a 230 bp PCR product is expected

2.3.7.1. DNA sequence analysis and quality control

Raw reads were extracted from *Illumina MiSeq®System* in *fastq* format and quality-filtered with *PRINSEQ version 0.20.4* (Schmieder & Edwards, 2011) to remove sequencing adapters, reads with less than 100 bases and trim bases with an average quality lower than Q25 in a window of 5 bases. The quality report of each library sequencing was viewed in *FastQC v0.11.8* (Andrews, 2010). The sequence trimming was performed in *Sickle* (Joshi & Fass, 2011). Additional quality filtering and overlapping paired-end reads merge was performed using *BayesHammer module of Spades 3.12.0 software* (Nikolenko *et al.*, 2013). Using *Usearch v11.0.667*, read pair were merged (Edgar & Flyvbjerg, 2015). Detection and removal of sequencing adapters and primers, as well as the clipping of limited skewing and poor quality read ends was performed by *Ea-utils (fastq-mcf) v 1.04.636* (Aronesty, 2013).

Sequence results organization into Operational Taxonomic Units (OTUs) at 97% of identity (which represent bacterial species) was performed using *micca 1.7.0 software* (Albanese *et al.*, 2015). At the same time, taxonomy was assigned by using the SILVA database (Silva release 132) (Quast *et al.*, 2013; Yilmaz *et al.*, 2014; Glöckner *et al.*, 2017), in order to classify each bacterial

OTU sequence and convert data into a *biom format*. This final analysis was achieved using *Qiime 1.9.1* (Caporaso *et al.*, 2010). Unknown classifications, OTUs identified as chloroplasts or mitochondria were removed from OTU table, as well as those low abundance OTUs (with less than 5 reads).

Analysis of α -diversity data was calculated using the *Past3 software v3.26* (Hammer, 2019). Rarefaction curves were constructed using *GraphPad Prism 7.04 software* and diversity indices determined. Venn diagram was obtained by *Excel software*. β -diversity was computed in *Community Analysis Package (CAP) version 6.2.4*, where Jaccard and Sorenson's similarity coefficients were determined using *ANOSIM* analysis (Beals, 1984).

2.4. Results and Discussions

2.4.1. Soil chemical analysis

For evaluating the effect of heat on the microbial community associated to cork oak, the soil was sampled from a specific tree (Figure 5).

Table 4 – Chemical analysis of studied soils taken from a Cork oak.

Analysed parameter	Cork oak soil		Reference value
	Results	Interpretation	
Granulometry	Sandy Sand (78.1% Sand; 9.1% Clay; 12.8% Lime)		-
pH (H ₂ O)	5.85 ± 0.01	Acid	3.4 – 7.8
pH (CaCl ₂)	5.19 ± 0.01	Slightly acid	-
Electrical conductivity	112 ± 2 μ S/cm	Non saline	-
Organic matter	9.38 ± 0.01 %	Very high	-
Organic carbon	5.44 ± 0.04 %	-	-
Total nitrogen	0.39 ± 0.02 %	In excess	-
Carbon: nitrogen	13.9	Normal	-
Phosphorus (P ₂ O ₅)	156.8 ± 0.4 mg/kg	High	98 – 162 mg/kg
Potassium (K ₂ O)	281.9 ± 1.3 mg/kg	In excess	74 – 140 mg/kg
Calcium (CaO)	1603.1 ± 0.9 mg/kg	In excess	819 – 1047 mg/kg
Magnesium (MgO)	270.0 ± 0.4 mg/kg	In excess	100 – 205 mg/kg
Sulphur	12.4 ± 0.1 mg/kg	High	>10 mg/kg
Iron	130.6 ± 0.1 mg/kg	In excess	50 – 100 mg/kg
Manganese	186.1 ± 0.0 MnAl	In excess	25 – 100 MnAl
Boron	0.77 ± 0.00 mg/kg	Low	0.5 – 5 mg/kg
Sodium	28.7.0 ± 0.1 mg/kg	-	-

The chemical analysis of sampled soil revealed a sandy acid soil, rich in organic matter and in several nutrients (Table 4).

The soil pH (H₂O) was indeed acid (5.85 ± 0.01) but within the range of 3.4 - 7.8 found by Torres 2008. However, these values are considered acidic when compared to pH values obtained for other *Q. suber* forests. In Hinojo forest (Huelva, southwest of Spain) the pH values are between 4.9 - 6.0 (Andivia *et al.*, 2010), and northern Sardinia (Italy) cork oak soils have pH values of 5.8. However very acid soils have also been found in southern Sardinia (Italy) cork oak forests (pH 2.7) (Rossetti *et al.*, 2015). The low values of pH found in cork forest could be due to the high amount of clay minerals, iron and aluminium (Torres, 2008). Phosphorous, potassium, calcium, magnesium, iron and manganese were the nutrients present in higher amounts, and the poorest nutrients were sulphur, boron and sodium (Table 4). When compared to Hinojo cork oak forest (Spain), where the organic matter content ranges from 0.3% - 1.5% (Andivia *et al.*, 2010), the studied soil revealed to have a high organic matter content ($9.38 \pm 0.01\%$).

2.4.2. The effect of heat on soil microbial communities

The survival of soil microbial communities was evaluated by determining the title of microbial suspensions, prepared from soil samples subjected to heat along time. Cell survival curves were prepared for describing the number (proportion) of surviving cells along time. Using two different media, the same assay was performed for bacteria (Figure 9) and fungi (Figure 10). For studying fresh soil, the assay was repeated with soil samples collected in different periods (A – collected on 14th March; B – collected on 28th May and C – collected on 24th June of 2019).

As expected, the microbial survival percentage (N/N_0) decreases logarithmically with the treatment time, due to the reduction of microorganisms after the application of increased temperatures (Klotz *et al.*, 2007). The effect of temperature is most visible at the first 15 min of heat treatment on bacterial communities and at the first 25 min on fungal communities. This result reveals that bacteria communities are most heat sensitive than fungal communities, although some authors refer that bacterial spores are most heat resistant than fungi and yeast spores (Smelt & Brul, 2014).

According to cell death kinetics, the $\log_{10}(N/N_0)$ vs time plot should give a straight line (first order of kinetics) when all cells in a population have identical sensitivity to heat (Moats, 1971; Klotz *et al.*, 2007).

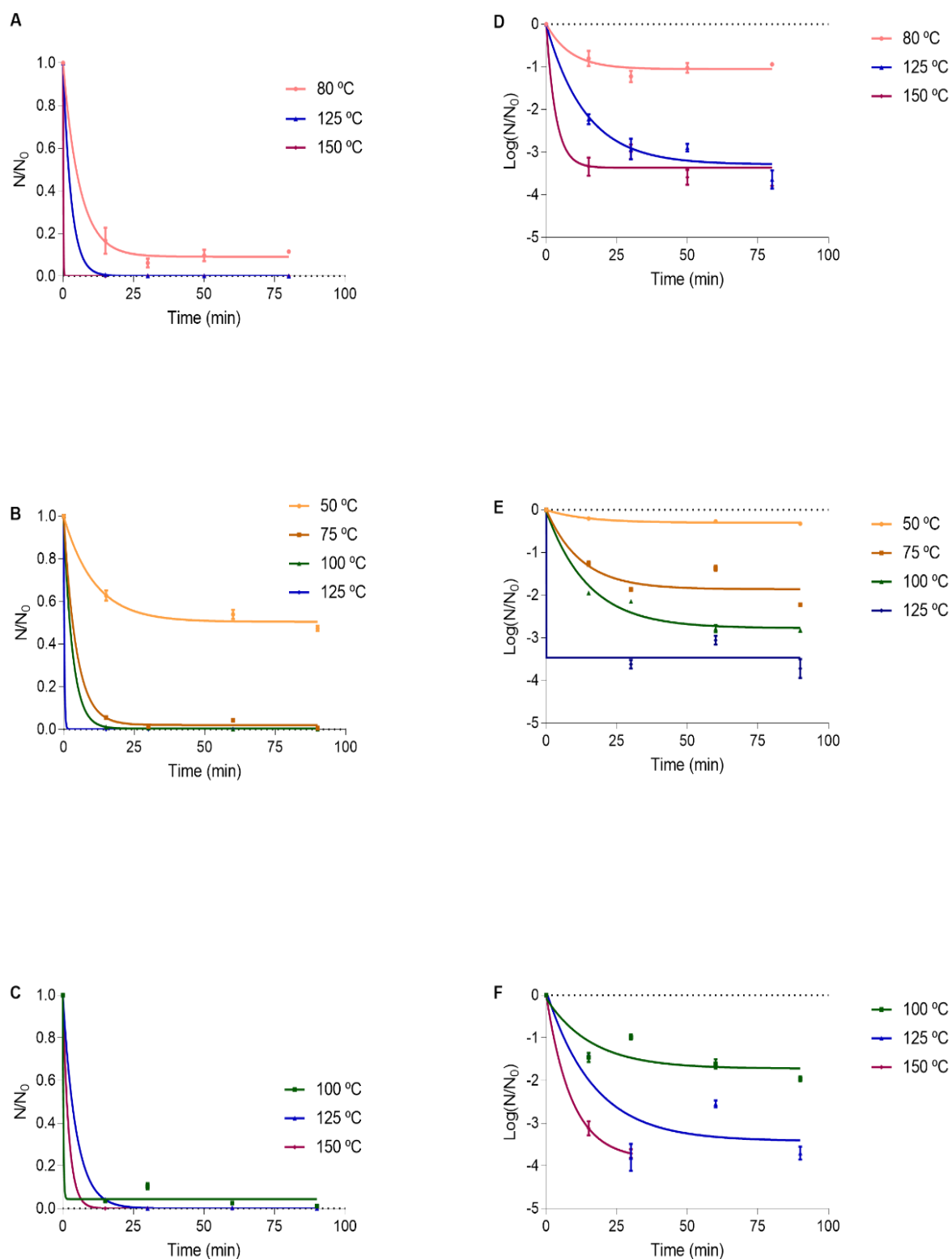


Figure 9 – Bacterial survival curves of soil communities after temperature imposition. The curves were obtained considering the proportion of surviving cells (A – C) and the corresponding semilogarithmic relationship (D – F) along time. Different graphs represent assays performed with distinct collected soils (A, D – 14th March; B, E – 28th May; C, F – 24th June of 2019).

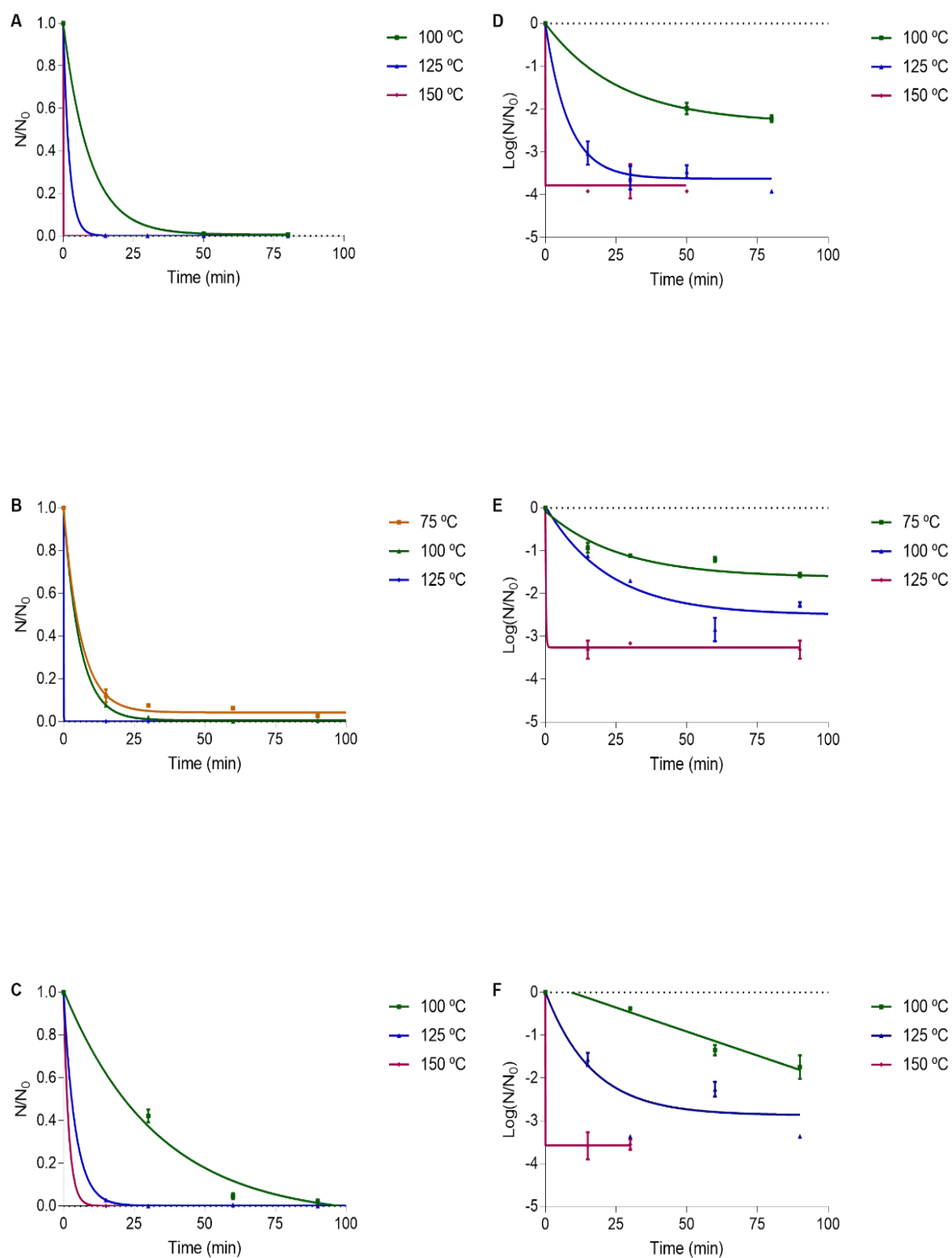


Figure 10 – Fungal survival curves of soil communities after temperature imposition. The curves were obtained considering the proportion of surviving cells (A – C) at the corresponding semilogarithmic relationship (D – F). Different graphs represent assays performed with distinct collected soils (A, D – 14th March; B, E – 28th May; C, F – 24th June of 2019).

However, mixed communities typically present concave curves when plotting $\log_{10}(N/N_0)$ as a function of time. Such curves are due to the presence of a large spectrum of microorganisms displaying distinct heat resistance in the population. Some organisms or spores are more easily destroyed than others (Moats, 1971; Peleg & Cole, 1998b). The obtained nonlinear curves for $\log_{10}(N/N_0)$ vs. time for bacterial (Figure 9) and fungal (Figure 10) communities, which do not follow a first order kinetics, thus reveal the presence of a complex microbial community in sampled soils. This behaviour was also detected in other complex microbial mixtures (Moats, 1971; Peleg & Cole, 1998b; Xiong *et al.*, 1999 or for single ones (Peleg & Cole, 1998a).

To understand the behaviour of soil microbial communities when heated, death specific rates (K) were calculated using the obtained surviving curves. In a simple population (using a single microbial species), the first order kinetics dictates that the slope of $\log_{10}(N/N_0)$ vs time straight line corresponds to the death specific rate. In spite of working with complex microbial mixtures, death specific rates were determined from all $\log_{10}(N/N_0)$ vs time plots using a linearization method, as done for simple populations (Table 5).

Table 5 - Death specific rates for soil bacterial and fungal communities. These values were determined by using a linearization of $\log_{10}(N/N_0)$ vs time plots. Soil samples were collected on 14th March – A; 28th May – B and 24th June of 2019.

T (°C)	Bacteria			Fungi		
	A	B	C	A	B	C
50	-	0.0030	-	-	-	-
75	-	0.0182	-	-	0.0120	-
80	0.0090	-	-	0.0290	-	-
100	-	0.0261	0.0172	-	0.0173	0.0224
125	0.0380	0.0353	0.0335	0.0670	0.0240	0.0290
150	0.0366	-	0.1237	-	-	0.1185

The obtained death specific rates (K) increase with temperature increase. This reveals that microbial death is higher at higher temperatures. But there are differences between thermal inactivation of bacterial and fungal communities. The influence of temperature on the inactivation of microbial communities are often described by Arrhenius plots ($\log_{10}K$ vs $1/T$), which usually gives a straight line. The steeper the slope, the most sensitive is the community to heat changes. For each soil collection, straight lines with distinct slopes were obtained both for bacteria (Figure 9) and fungi (Figure 10), which could be the result of using different microbial communities. Soil microbial communities are very dynamic and change according to the season and other

environmental conditions (Waldrop & Firestone, 2006). Therefore, in each soil sampling, different complex microbial communities were taken, displaying distinct heat resistance abilities. This would result in dissimilar Arrhenius plots as observed for each sampling (Figure 11). Furthermore, Arrhenius plot slopes were closer when similar environmental conditions occurred during soil harvesting [March (a) and May (b) – spring], in relation to summer collection [June (c)], possibly indicating more similar communities. Surprisingly, summer microbial communities seemed to be more heat sensitive (steeper slopes) than communities from spring collections, which could be due to the differential representation of active cells/spores in each sample. However, such conclusions should be taken with care, as first order kinetics were followed in such complex communities.

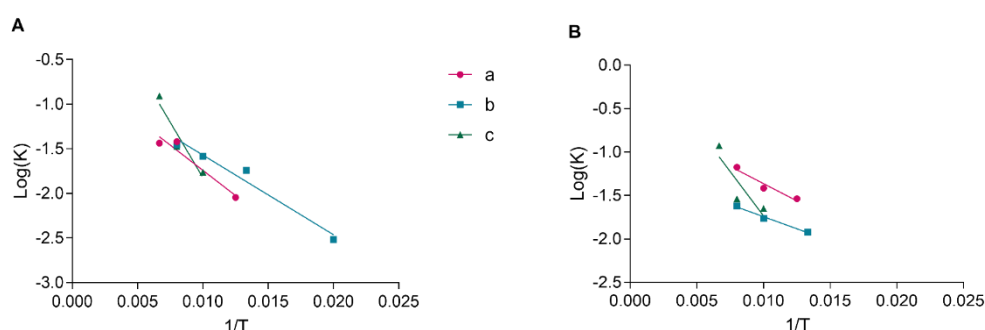


Figure 11 - Influence of temperature on the inactivation on soil microbial communities, as described by Arrhenius plots. A – Temperature influence on bacterial communities; B – Temperature influence on fungal communities. K - Death specific rate; T – Temperature

Therefore the presented Arrhenius graphs, only serve to predict the behaviour of such complex populations of microorganisms and evaluate the sensitivity of soil microbial communities as a whole and not as single and individual communities, as reported by Ross *et al.* (Ross *et al.*, 2014).

Table 6 - Analysis of microbial biodiversity after temperature application on soil microbial communities, as evaluated by the number of morphotypes present in those plates exhibiting well-separated colonies.

Bacterial morphotypes							Fungal morphotypes						
Time (min)	Temperature (°C)						Time (min)	Temperature (°C)					
	0	50	75	100	125	150		0	50	75	100	125	150
15	14	7	4	4	2	1	15	4	4	4	4	1	0
30	14	5	4	5	3	0	30	4	3	4	4	2	0
60	14	5	4	4	4	0	60	4	3	3	3	3	0
90	14	3	5	4	3	0	90	4	3	2	2	1	0
120	14	4	3	4	3	0	120	4	5	3	4	2	0

In order to evaluate the heat effect on the soil microbial biodiversity, the number of bacterial and fungal morphotypes was evaluated (Table 6). The number of distinct morphotypes decreased with temperature and time of heat exposure, although this is more evident for bacteria than for fungi. This result suggests that besides a reduction on the number of surviving bacteria/fungi, also the diversity of soil communities is greatly decreased after heat treatment.

2.4.3. Identification of heat resistant bacteria

From soils treated at 125°C, 14 bacterial morphotypes (colonies that appeared 15 and 30 min at 125°C) were selected to be identified. Identification was performed by 16S barcoding. To accomplish that, DNA was extracted (Annex 1) and used to amplify 16S regions with *799F* and *1492R* primers (Figure 12). PCR products were amplified using the same primers.

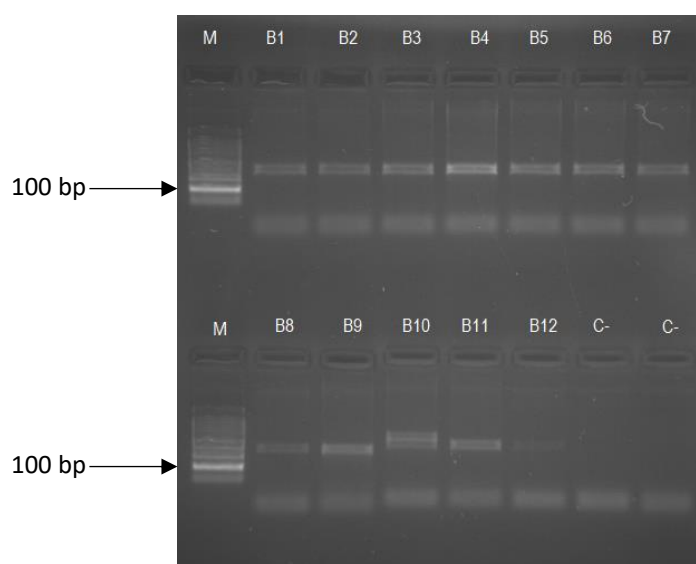


Figure 12 – Electrophoresis of 16S region from the 14 selected bacterial isolates (taken from the 125°C treated soil samples). DNA was extracted and used to amplify 16S region by using the *799F* and *1492R* primer pair. M – 100bp plus ready-to-use DNA Ladder bioron

The obtained sequences (Annex 2) were blasted against available sequences (NCBI), using the BLAST algorithm. For OTUs (operational taxonomic units) with identity >98% species was accepted, for sequences between 98% and 95% only genus was accepted and for less than 95% were considered as unknown. Bacterial sequences were blasted and sorted according to the identity score and lowest E-values (Table 7). For each sequence, the three top-hits are displayed.

Table 7 - Identification of bacteria resistant to high temperatures, according to the sequencing of bacterial barcode 16S. The three best top-hits are displayed for each sequence (number in parenthesis reveal the number of hits for each species).

Isolate	Top-Hit	E-value	Identity percentage (%)	Sample size (bp)
B2	<i>Bacillus thuringiensis</i> (18)	2e-159 – 7e-158	100 – 99.36	312
	<i>Bacillus cereus</i> (56)	5e-159 – 3e-157	100 – 99.36	
	<i>Bacillus anthracis</i> (3)	5e-159 – 3e-157	100 – 99.36	
B3	<i>Hyphomonas jannaschiana</i>	7e-19	93.06	329
B4	<i>Bacillus megaterium</i> (36)	2e-154 – 4e-155	99.04 – 98.14	324
	<i>Bacillus aryabhattai</i> (25)	2e-154 – 9e-157	99.04 – 98.14	
	<i>Bacillus subtilis</i> (8)	1e-155 – 3e-156	98.44 – 98.14	
B5	<i>Bacillus cereus</i> (25)	2e-159 – 4e-160	99.37 – 98.75	322
	<i>Bacillus anthracis</i> (2)	4e-160	99.37	
	<i>Bacillus thuringiensis</i> (23)	4e-160	99.37 – 98.75	
B6	<i>Bacillus cereus</i> (25)	3e-156 – 9e-157	98.75 – 98.44	323
	<i>Bacillus anthracis</i> (2)	3e-157	98.75	
	<i>Bacillus thuringiensis</i> (21)	3e-156 – 3e-157	98.75 – 98.44	
B7	<i>Bacillus cereus</i> (25)	2e-163 – 9e-162	100 – 99.37	320
	<i>Bacillus anthracis</i> (9)	2e-163 – 9e-162	100	
	<i>Bacillus thuringiensis</i> (13)	2e-163 – 9e-162	100 – 99.68	
B8	<i>Bacillus thuringiensis</i>	3e-122	93.46	311
B9	<i>Bacillus cereus</i> (26)	1e-160 – 5e-159	99.07 – 98.76	325
	<i>Bacillus anthracis</i> (9)	3e-161 – 5e-159	99.07 – 98.76	
	<i>Bacillus thuringiensis</i> (12)	1e-160 – 5e-159	99.07 – 98.76	
B10	<i>Bacillus velezensis</i>	1e-46	93.33	467
B11	<i>Bacillus subtilis</i> (44)	2e-163 – 9e-162	100 – 99.69	320
	<i>Bacillus amyloliquefaciens</i> (10)	2e-163 – 9e-162	100 – 99.69	
B12	<i>Bacillus spp</i>	4e-135	97.55	288
B13	No similarity found	-	-	368
B14	<i>Bacillus spp</i>	1e-140	95.94	355

As most samples were blasted as *Bacillus*, a sequence alignment was performed to verify similarities between sequences (Annex 3). A phylogenetic tree was prepared to relate sequences (Figure 13). A clear cluster was performed by the complex *Bacillus thuringiensis/cereus/anthracis* (B2, B5, B6, B7 and B9), which have been all described as members of the *Bacillus cereus* group and considered as belonging to one and the same species ((Helgason *et al.*, 2000)). In addition, other detected bacteria included *B. megaterium* (or *B. aryabhattai* based on their sequence homology, (Freedman *et al.*, 2018)), and *B. amyloliquefaciens* (or its sister species *B. subtilis*, (Freedman *et al.*, 2018)). From all bacteria, *B. cereus* isolates were the most frequently detected, possibly revealing their higher abundance. The higher abundance of *Bacillus* as heat resistant bacteria could be related with their ability to form resistance spores as they are known to be spore-forming bacteria (Kort *et al.*, 2005). *Bacillus* spores are widely studied due to easy genetic manipulation (Setlow, 2006). The use of High Pressurized Carbon Dioxide (HPCD) indicated that bacterial spores can be destroyed with high temperatures ($\geq 60^{\circ}\text{C}$) (Rao *et al.*, 2015). Accordingly,

the application of moist heat (87°C - 90°C) on *Bacillus subtilis* spores resulted in spore destruction (Rao *et al.*, 2015). Similarly, *Bacillus cereus* spores can be eliminated at 70°C using 600MPa (Evelyn & Silva, 2015). Comparing heat inactivation between cells and spores, spore destruction requires longer time periods than bacterial cells (Rao *et al.*, 2015).



Figure 13 - Phylogenetic tree from sequence alignment of bacteria resistant to high temperatures

Phylogenetic tree (Figure 13) presents a *unknown sequence* (B10) and *Bacillus subtilis* (B14) as the most divergent sequences found on the studied bacterial morphotypes. *Bacillus subtilis* (B11) seems to be an ancestor of *Bacillus megaterium* (B4) and sequences obtained from B2, B5, B6, B7 and B9 morphotypes are genetically similar (wich were identified as *Bacillus cereus*). These results may be explained by the often exchange of genetic material between some *Bacillus* species in natural environments (Helgason *et al.*, 2000; Donnarumma *et al.*, 2010).

2.4.4. Metabarcoding analysis of temperature treated soil

In order to evaluate microbial communities in detail after temperature application, molecular identification of heat-treated soil communities was performed by using 16S and ITS barcoding. DNA was extracted from soil samples subjected to temperatures of 100°C for several periods of time (Table 8) and amplified. PCR amplification reaction occurred using the primer pair for 16S V3V4 region (*V3V4FW* and 16S *V3V4 RV*) for bacteria identification and using the primer pair for the ITS region (*ITS1F* and *ITS2*) for fungi identification (Figure 14 and Figure 15 respectively). Due to the low amounts of DNA extracted (Table 8) and funding limitations, only one soil sample was sequenced for bacterial barcode (B – 28th May) using the initial treatment times (100°C for 0, 15 and 30 min).

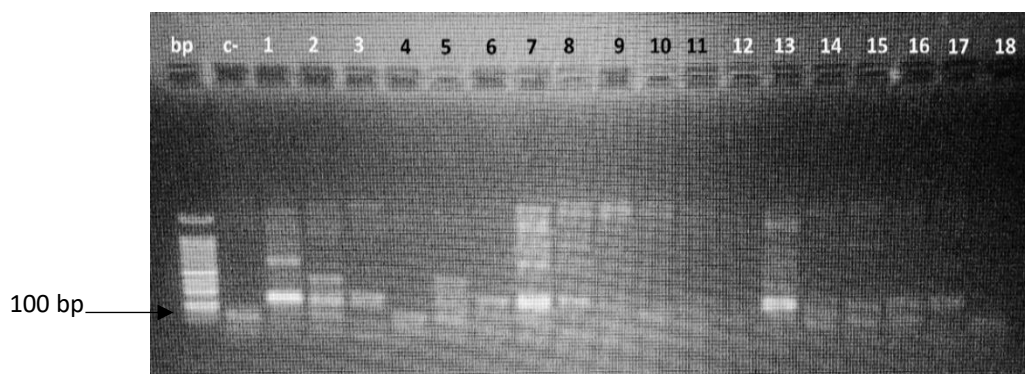


Figure 14 – Electrophoresis of 16S V3V4 region from soil samples treated with 100°C of temperature. DNA was extracted and used to amplify 16S V3V4 region by using the 16S V3V4FW and 16S V3V4 RV primer pair. Legend: bp – 100bp plus ready-to-use DNA Ladder Bioron; Heat treatment samples: B collection (1 – 0 min; 2 – 15 min; 3 – 30 min; 4 – 60 min; 5 – 90 min ; 6 – 120 min); A collection (7– 0 min; 8 – 15 min; 9 – 30 min; 10 – 50 min; 11 – 80 min; 12 – 120 min; C collection (13 – 0 min; 14 – 15 min; 15 – 30 min; 16 – 60 min; 17 – 90 min; 18 – 120 min;

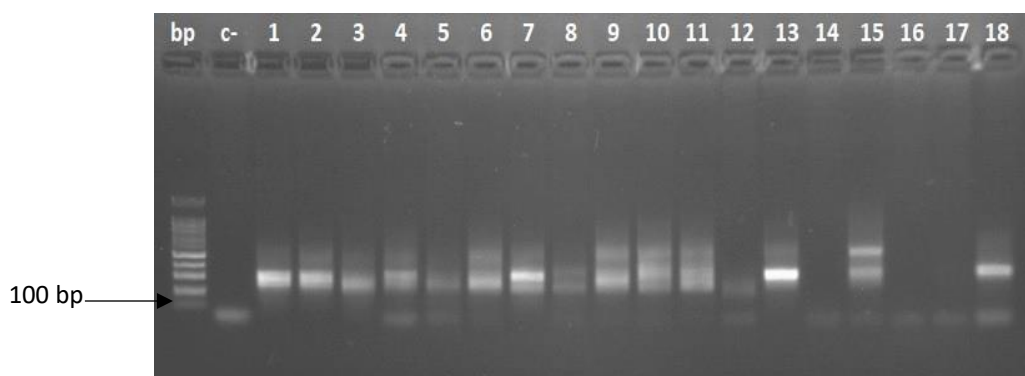


Figure 15 – Electrophoresis of ITS region from soil samples treated with 100°C of temperature. DNA was extracted and used to amplify ITS region by using the *ITS1F* and *ITS2* primer pair. Legend: bp – 100bp plus ready-to-use DNA Ladder Bioron; Heat treatment samples: B collection (1 – 0 min; 2 – 15 min; 3 – 30 min; 4 – 60 min; 5 – 90 min ; 6 – 120 min); A collection (7– 0 min; 8 – 15 min; 9 – 30 min; 10 – 50 min; 11 – 80 min; 12 – 120 min; C collection (13 – 0 min; 14 – 15 min; 15 – 30 min; 16 – 60 min; 17 – 90 min; 18 – 120 min;

The results will be then evaluated and a decision regarding subsequent sequencing of other samples will be taken. As no other samples were jointly sent for fungal barcode sequencing, samples are still awaiting to be sequenced. Sequence data analysis from 16S region amplification was performed based on Pylro et al., (2014) pipeline and other authors (Soh *et al.*, 2013; Pylro *et al.*, 2014; Mataragas *et al.*, 2018; Sadaippan *et al.*, 2020).

Table 8 – Quantification of soil DNA, extracted from samples subjected to 100°C of temperature, by nanodrop and Qubit method, for microbial communities' analysis by metabarcoding approach

Assay	Samples	nanodrop ng/μL	Qubit ng/μL	A _{260/280}	A _{260/230}
A (March 2019)	0 min	61.20	1.07	1.94	2.11
	15 min	15.70	11.30	1.85	1.67
	30 min	7.20	0.44	1.73	1.51
	50 min	2.90	Out of range	1.56	0.96
	80 min	3.00	1.06	1.34	0.62
	120 min	2.50	1.18	0.84	0.44
B (May 2019)	0 min	75.00	28.80	1.84	2.44
	15 min	19.10	8.80	1.48	1.71
	30 min	5.30	0.63	1.54	1.71
	60 min	2.20	0.70	1.21	0.64
	90 min	2.40	1.14	1.17	0.75
	120 min	5.40	0.16	1.05	0.58
C (June 2019)	0 min	57.40	43.40	1.90	1.85
	15 min	16.00	6.40	1.71	1.28
	30 min	4.60	0.31	1.56	0.93
	60 min	7.70	0.16	1.52	0.66
	90 min	4.70	0.94	1.53	0.82
	120 min	13.50	0.37	1.30	0.74

A total of 207.272 raw reads were obtained from the three soil samples subjected at 100°C for 0, 15 and 30 min (Table 9). The trimming process resulted in 206.524 reads and merged pair-end reads resulted in 89.540 reads. Detection and removal of sequencing adapters and primers, and clipping of limited skewing and poor quality at read's resulted in 64.069 sequences (Aronesty, 2013). After sequence analysis, 218 OTUs were allocated as unclassified, 3 classified as chloroplasts, 3 as mitochondria and 1 as non-identified bacteria. At the end, 634 identified OTUs were classified.

Table 9 - Number of 16S rDNA V3-V4 reads of soil samples subjected to 100°C of temperature, after merging and quality filtering, as the number of obtained taxonomic classifications.

Name	Reads processing				Taxonomic classification of OTUs					
	Initial read pairs	After trimming	Merged reads	Unclassified reads	OTUs	Phylum	Class	Order	Family	Genus
0 min	50.576	50.362	21.747	12.358	458	8	12	76	83	134
15 min	67.826	67.598	29.054	20.544	418	10	13	73	74	108
30 min	88.870	88.564	38.739	31.167	359	9	13	65	63	108
total	207.272	206.524	89.540	64.069	634	20	44	53	129	217

2.4.4.1. Bacterial community analysis

Data analysis on bacterial abundance revealed differences on soil bacterial communities with time of heat exposure. Without heat treatment, the most abundant phyla were *Proteobacteria* (comprising 41% of total number of reads), followed by *Actinobacteria* (35%), *Acidobacteria* (7%), and *Bacteroidetes* (6%) (Figure 16).

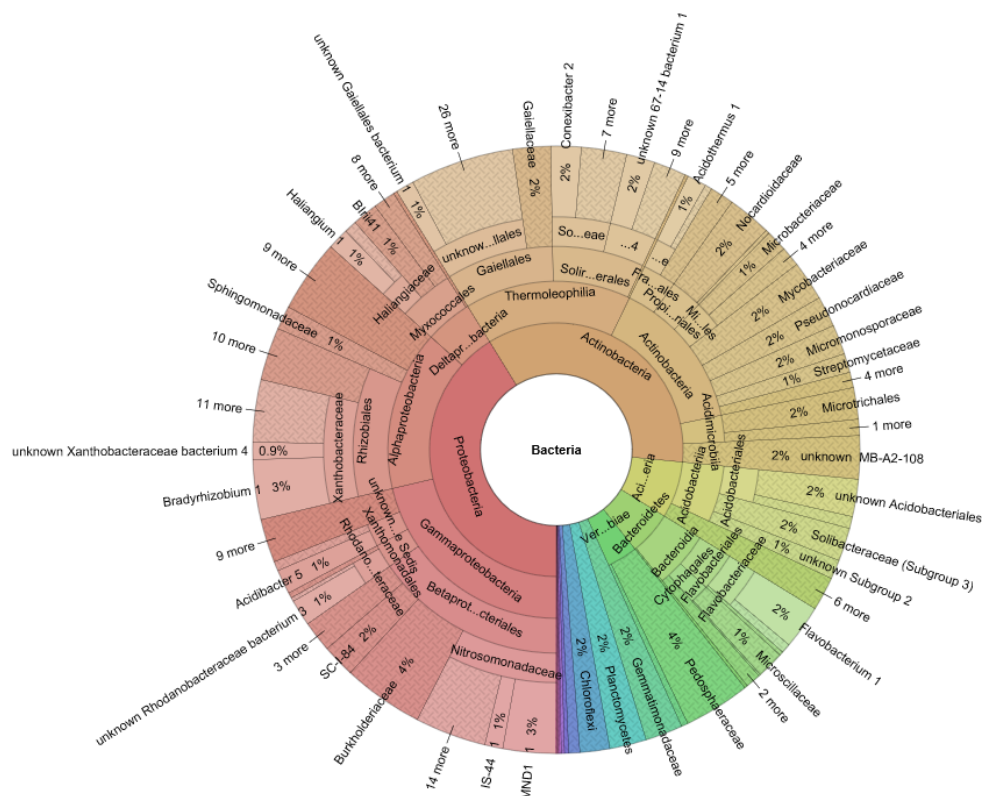


Figure 16 – Representation of bacterial taxonomic abundance obtained from sampled cork oak soil (without heat treatment) application. In this krona graph (Ondov et al., 2011), OTUs are identified until family level (97% identity).

Several authors report the presence of *Proteobacteria*, *Acidobacteria* and *Actinobacteria* as being the most abundant phyla in the soil. In addition, they all report the low presence of the genus *Firmicutes*. Within *Proteobacteria*, the most abundant class was *Gammaproteobacteria* (21%), followed by *Alphaproteobacteria* (15%), and *Deltaproteobacteria* (5%). From *Actinobacteria* the most abundant class was *Thermoleophila* (16%), followed by *Actinobacteria* (15%); and from *Bacteroidetes*, the most abundant was *Bacteroidia* (5%). The most abundant genus belongs to *Gaiellales* family (*Thermoleophila*, *Actinobacteria*) with 6% of the total number of reads and classified as *unknown Gaiellales* genus. For further reference, it is notable that *Firmicutes* phylum (0.6%) is represented as “other” phylum.

After the application of heat (100°C) for 15 min, there was a clear alteration on the bacterial community. In this sample, the most abundant phyla were *Firmicutes* (55%), followed by *Actinobacteria* (21%), *Proteobacteria* (15%), and *Bacteroidetes* (3%) (Figure 17).

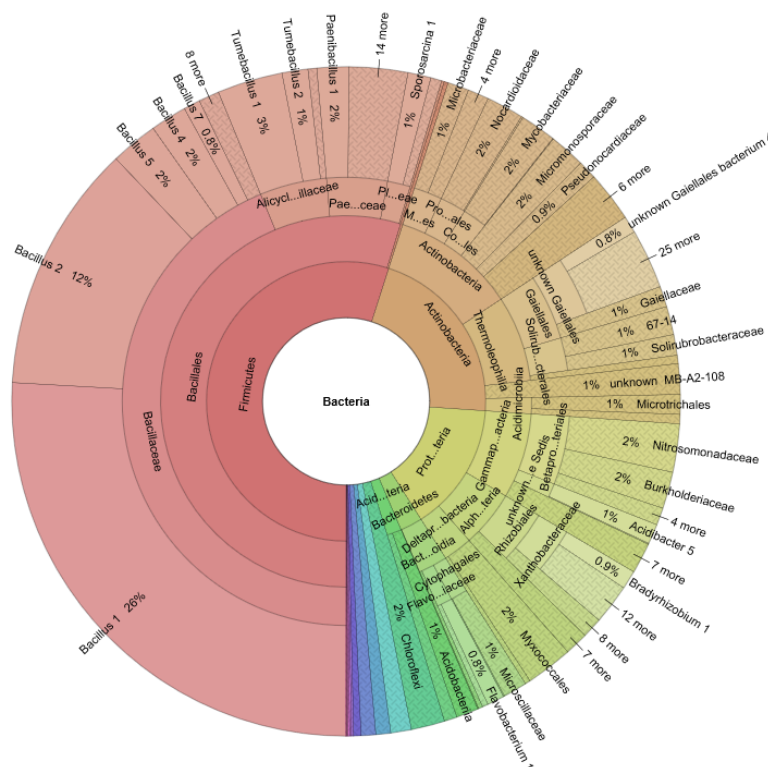


Figure 17 – Representation of bacterial taxonomic abundance obtained from cork oak soil treated at 100°C for 15 min. In this krona graph (Ondov et al., 2011), OTUs are identified until family level (97% identity).

The most significant change was the relative increase on *Firmicutes* reads, almost all belonging to *Bacillales* order, that increased from a relative abundance of 0.6% (non-treated soils) to 55% (in heat treated soils for 15 min). In contrast, *Actinobacteria* and *Proteobacteria* decreased their abundance from 41% to 15%, and 35% to 21%, respectively. The most abundant *Actinobacteria* classes were *Actinobacteria* (11%) and *Thermoleophilum* (7%); and those from *Proteobacteria* were *Gammaproteobacteria* (7%) and *Alphaproteobacteria* (5%). The most predominant family in this sample was *Bacillaceae* (44%), being *Bacillus spp* the most predominant genus (42% of the total number of reads).

After 30 min of heat (100°C) application, the increase in *Firmicutes* (*Bacillales*) even higher (81% of total number of reads), which was accompanied by a decrease on *Actinobacteria* (from 15% to 10%) and *Proteobacteria* (from 21% to 7%) phyla (Figure 18).

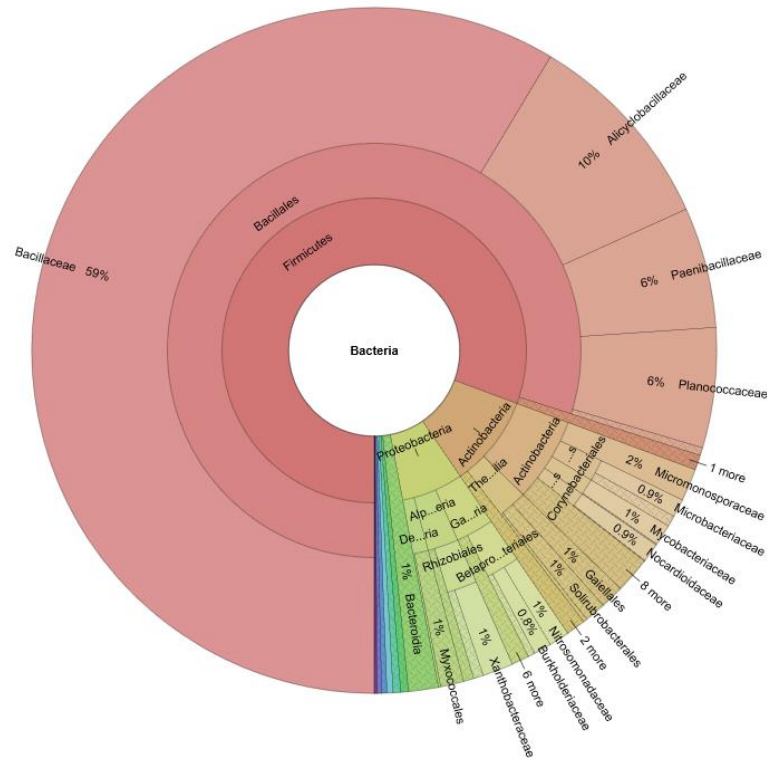


Figure 18 – Representation of bacterial taxonomic abundance obtained from cork oak soil for 30 min of 100°C application. OTUs identified until genus level (97 % identity).

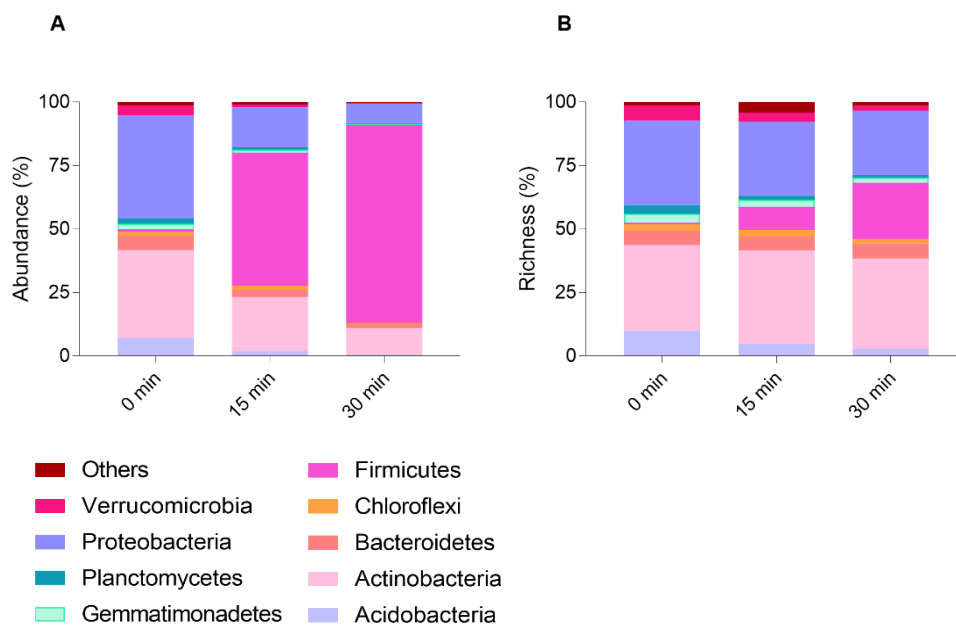


Figure 19 – Abundance and richness of bacterial phyla detected in untreated cork oak soils or treated with 100°C for 15 and 30 min, as revealed by *Illumina MiSeq 16S* amplicon sequencing (A) Phylum abundance (identified at 97 %); (B) Phylum richness (identified at 97. Phylum abundance and richness higher than 5 % are represented as “Others”.

Within *Firmicutes*, the most abundant order was *Bacillaceae* (59%), comprising almost 55% of the total number of reads from the *Bacillus* genus. These changes on bacterial community with temperature are better described on bar graphs displaying the relative abundance of phyla (Figure 19A) or classes (Figure 20A).

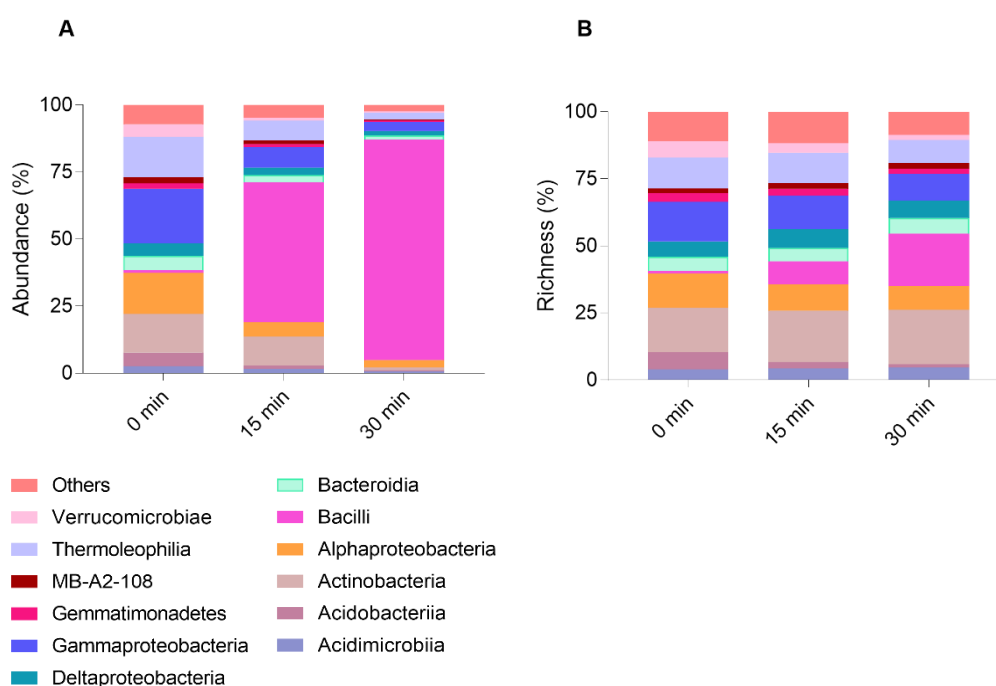


Figure 20 – Bacterial class revealed by *Illumina MiSeq 16S* amplicon sequencing (A) Class abundance (identified at 97 %) present on cork oak soil treated with 100°C for 0, 15 and 30 min; (B) Class richness (identified at 97 %) present on cork oak soil treated with 100°C for 0, 15 and 30 min. Class abundance and richness higher than 5 % are represented in the colour legend.

However, not only relative taxa abundance changes with temperature, but also their richness. The total number of detected genus decreased with temperature: 458 bacterial genera detected in non-treated soils, followed by 418 and 359 genera found in soils heat-treated 15 min and 30 min, respectively (Figure 21, Annex 3). Also, the relative number of *Firmicutes* (*Bacilli*) taxa increased with heat, while there was a decrease on *Proteobacteria* (*Alphaproteobacteria* and *Gammaproteobacteria*) (Figures 19B and 20B).

These results show that the time period of heat exposure is translated into a significant modification of bacterial communities. The similarity between samples, as evaluated by Jaccard's or Sorenson indexes, revealed that there is a decrease in similarity with heat (Table 10).

Table 10 - Coefficients of similarity between bacterial communities present in different cork oak soil treated with 100°C for 0, 15 and 30 min. The Jaccard's index is displayed in the lower side of the table (blue) and the Sorenson's index in the upper side (green). The displayed indexes range between 0 - 1 (0: zero similarity; 1: maximum similarity). A gradient pattern of colours was applied according to the similarity's values (lighter colour - lower similarity value; darker colour - higher similarity value).

	0 min	15 min	30 min
0 min	1	0,914	0,892
15 min	0,841	1	0,92
30 min	0,805	0,852	1

The results also reveal that there are microorganisms such as *Bacillus spp* are better adapted to heat situations than other microorganisms (*Proteobacteria* members). For example, the presence of *Proteobacteria* in greater abundance in natural and recovering environments has been reported to be higher than in situations of environmental stress, such as those with increased temperature (Hernández *et al.*, 2020) . On the other hand, gram-positive bacteria (such as *Bacillus spp*) have been reported to be more resistant to heat due to the presence of a thicker cell wall than gram-negative bacteria (eg, *Burkholderia* genus from *Burkholderiaceae* family - *Proteobacteria*) (Jing *et al.*, 2019). In addition, the high presence of *Bacillus spp* on soil may interfere with the abundance of other microorganisms as this genus has the ability to produce antimicrobial proteins (Grutsh *et al.*, 2018).

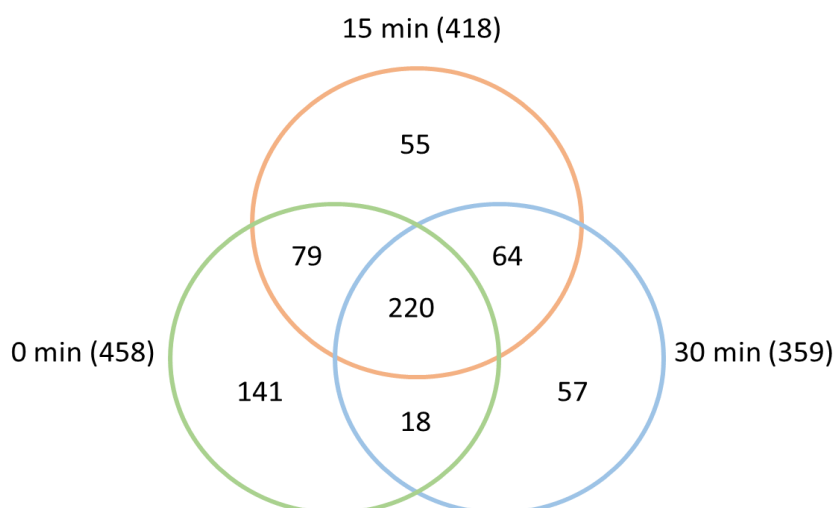


Figure 21 – Venn diagram of shared bacterial OTUs between untreated, and heat (100°C) treated soils for 15 and 30 min. The OTUs were classified up to genus level (97 % identity) and represent total of 634 genus. OTUs number identified in each sample are in parentheses.

Also, *Bacillus* genus, have “the Quorum sensing” throughout they can govern cell density and regulate gene expression that can enhance this genus survival (Grutsh *et al.*, 2018). This mechanism consists in the production and release of self-inducers (signalling molecules) in order to increase cell concentration, in response to fluctuations in population density at the cellular level (Miller & Bassler, 2001; Grutsh *et al.*, 2018).

The number of shared OTUs among cork oak samples revealed that about 34% of bacterial genera (220) are present in all cork oak samples.

2.4.4.2. Bacterial diversity

Microbiome diversity is an important indicator of healthy or degraded ecosystems. A large diversity of microbes is generally associated with good ecosystem conditions (Calle, 2019). Various ecological indices can be used to assess diversity, which are subdivided into alpha and beta diversity. Alpha diversity measures the variability of species within a sample, while beta diversity accounts for differences in composition between samples (Gotelli & Coldwell, 2001). In alpha diversity, the most common measure is richness - number of different species present in a specific environment (Gotelli & Coldwell, 2011; Calle, 2019). For this reason, bacterial diversity was assessed by plotting rarefaction curves (Figure 22) and by determining different diversity parameters.

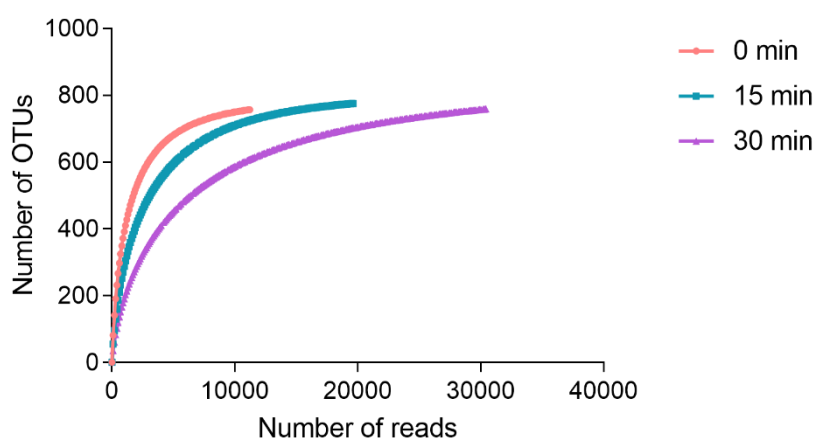


Figure 22 – Rarefaction curves for bacterial community (number of OTUs) at 97 % identity. Treatments included 0, 15 and 30 min of heat application (100°C). Rarefaction curves were obtained at *Past3 software v3.26* (Hammer, 2019).and plotted in *GraphPad Prism 7.04 software*.

Rarefaction curves revealed greater microbial diversity in non-treated soils than in heat stressed soils (100°C). Statistical analysis (*ANOVA*) proved that among the three samples, the

bacterial diversity presented is different ($p < 0.0001$). Furthermore, as a plateau was reached in all curves, we can infer that the analysed bacterial communities are well represented. *Richness* (S) was estimated by the number of different species observed in the sample. However, this parameter may underestimate the real richness of a certain environment as few species may not be detected (Gotelli & Coldwell, 2011; Calle, 2019). Therefore, different diversity indices were used for depicting diversity of microbial communities, such as *Simpson* ($1-D$), *Shannon* (H'), or *Fisher_alpha* (Table 11).

Table 11 – Diversity parameters for cork oak soil samples: untreated or treated with 15 or 30 min of heat (100°C). S – OTUs number.

	0 min	15 min	30 min
S	758	776	760
<i>Simpson_1-D</i>	0.9946	0.9238	0.8019
<i>Shannon_H</i>	5.902	4.538	3.323
<i>Equitability_J</i>	0.8902	0.682	0.501
<i>Fisher_alpha</i>	182.9	161.1	141.2

According to previous results, both the rarefaction curves and all diversity parameters indicate a decrease in microbial diversity with heat treatment. Furthermore, the homogeneity of communities, as evaluated by *Equitability index* (J), decreases with treatment extension, indicating the high dominance of a few species within the community in relation to others.

2.5. Conclusions

The environmental temperatures may have an influence on the survival ability of microbial communities. This work revealed that microbial communities taken when higher temperatures occur (June – summer) seemed to be more sensitive to heat than communities obtained with milder temperatures (March – spring).

Soil microbial communities are composed by a complex mixture of microbes with different heat sensitivities. Therefore, during the first minutes after temperature application, most heat sensitive microorganisms are destroyed, while heat-resistant (such as spore-forming microorganisms) are able to survive. Metabarcoding results of non-treated and heat (100°C) treated soils have revealed that a large spore-forming group largely prevails after 30 min at 100°C. Furthermore, the evaluation of the most heat resistant bacterial isolates present in cork oak soils allowed the detection of multiple *Bacillus* spp. (*Bacillus cereus*, *Bacillus megaterium*, and *Bacillus subtilis*). These results could be largely due to the ability of *Bacillus* species to produce spores.

Fluctuations on the abundance of such resistant bacteria could contribute for the detected differences on microbial community response to heat. For example, at the environment. This could be due to the percentage of active cells present in the microbial community, in relation to the corresponding spores.

2.6. Bibliography

- Albanese D, Fontana P, De Filippo C, Cavalieri D, Donati C. 2015. MICCA: A complete and accurate software for taxonomic profiling of metagenomic data. *Scientific Reports* **5**: 1–7.
- Andivia E, Fernández M, Vázquez-Piqué J, González-Pérez A, Tapias R. 2010. Nutrients return from leaves and litterfall in a mediterranean cork oak (*Quercus suber* L.) forest in southwestern Spain. *European Journal of Forest Research* **129**: 5–12.
- Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. *Babraham Institute*.
- Aronesty E. 2013. Comparison of Sequencing Utility Programs. *The Open Bioinformatics Journal* **7**: 1–8.
- Beals EW. 1984. Bray-curtis ordination: An effective strategy for analysis of multivariate ecological data. *Advances in Ecological Research* **14**: 1–55.
- Calle ML. 2019. Statistical Analysis of Metagenomics Data. *Genomics & Informatics* **17**: e6.
- Caporaso JG, Kuczynski J, Stombaugh J, Bittinger K, Bushman FD, Costello EK, Fierer N, Peña AG, Goodrich JK, Gordon JI, *et al.* 2010. QIIME allows analysis of high-throughput community sequencing data. *Nature methods* **7**: 335–6.
- Casolari A. 1988. Microbial death. In: Bazim MJ, Prosser JL, eds. *Physiological Models in Microbiology*. CRC Press, Inc, 1–44.
- Corradini MG, Normand MD, Peleg M. 2007. Modeling non-isothermal heat inactivation of microorganisms having biphasic isothermal survival curves. *International Journal of Food Microbiology* **116**: 391–399.
- Donnarumma F, Paffetti D, Stotzy G, Giannini R, Vettori C. 2010. Potential gene exchange between *Bacillus thuringiensis* subsp. *kurstaki* and *Bacillus* spp. in soil in situ. *Soil Biology and Biochemistry* **42**: 1329–1337.
- Edgar RC, Flyvbjerg H. 2015. Error filtering, pair assembly and error correction for next-generation sequencing reads. *Bioinformatics* **31**: 3476–3482.
- Evelyn, Silva FVM. 2015. High pressure processing of milk: Modeling the inactivation of psychrotrophic *Bacillus cereus* spores at 38–70 °C. *Journal of Food Engineering* **165**: 141–148.
- Ferrer J, Prats C, López D, Vives-Rego J. 2009. Mathematical modelling methodologies in predictive food microbiology: A SWOT analysis. *International Journal of Food Microbiology* **134**: 2–8.
- Freedman AJE, Peet KC, Boock JT, Penn K, Prather KLJ, Thompson JR. 2018. Isolation, Development, and Genomic Analysis of *Bacillus megaterium* SR7 for Growth and Metabolite Production Under Supercritical Carbon Dioxide. *Frontiers in Microbiology* **9**: 1–21.
- Garre A, González-Tejedor G, Peñalver-Soto JL, Fernández PS, Egea JA. 2018. Optimal characterization of thermal microbial inactivation simulating non-isothermal processes. *Food Research International* **107**: 267–274.
- Glöckner FO, Yilmaz P, Quast C, Gerken J, Beccati A, Ciuprina A, Bruns G, Yarza P, Peplies J, Westram R, *et al.* 2017. 25 years of serving the community with ribosomal RNA gene reference databases and tools. *Journal of Biotechnology* **261**: 169–176.
- Gotelli NJ, Coldwell RK. 2001. Quantifying biodiversity: procedures and pitfalls in the measurement and comparison of species richness. *Ecology letters* **4**: 379–391.
- Gotelli NJ, Coldwell RK. 2011. Estimating species richness. In: *Biological diversity: frontiers in measurement and assessment*. 39–54.
- Grutsh AA, Nimmer PS, Pittsley RH, Mckillip JL. 2018. *Bacillus* spp. as pathogens in the dairy industry. In: *Foodborne Diseases*. Elsevier Inc., 193–211.
- Hammer Ø. 2019. *Manual Past* 3.25.
- Helgason E, Økstad OA, Caugant DA, Johansen HA, Fouet A, Mock M, Hegna I, Kolstø AB. 2000. *Bacillus anthracis*, *Bacillus cereus*, and *Bacillus thuringiensis* - One species on the basis of genetic evidence. *Applied*

and *Environmental Microbiology* **66**: 2627–2630.

Hernández M, Calabi Ma, Conrad R, Dumont MG. 2020. Analysis of the microbial communities in soils of different ages following volcanic eruptions. *Pedosphere* **30**: 126–134.

Huang L. 2014. IPMP 2013 - A comprehensive data analysis tool for predictive microbiology. *International Journal of Food Microbiology* **171**: 100–107.

Huang L. 2017. IPMP Global Fit – A one-step direct data analysis tool for predictive microbiology. *International Journal of Food Microbiology* **262**: 38–48.

Huang L. 2019. Reconciliation of the D/z model and the Arrhenius model: The effect of temperature on inactivation rates of chemical compounds and microorganisms. *Food Chemistry* **295**: 499–504.

Hugo WB. 1971. *Inhibition and Destruction of the Microbial Cell*. London: Academic Press Inc.

Jing Y, Wang Y, Liu S, Zhang X, Wang Q, Liu K, Yin Y, Deng J. 2019. Interactive effects of soil warming, throughfall reduction, and root exclusion on soil microbial community and residues in warm-temperate oak forests. *Applied Soil Ecology* **142**: 52–58.

Joshi NA, Fass JN. 2011. Sickie: A sliding-window, adaptive, quality-based trimming tool for FastQ files. (Version 1.33) [Software]. Available at <https://github.com/najoshi/sickle>.

Klotz B, Pyle DL, Mackey BM. 2007. New mathematical modeling approach for predicting microbial inactivation by high hydrostatic pressure. *Applied and Environmental Microbiology* **73**: 2468–2478.

Kort R, O'Brien AC, Van Stokkum IHM, Oomes SJCM, Crielaard W, Hellingwerf KJ, Brul S. 2005. Assessment of heat resistance of bacterial spores from food product isolates by fluorescence monitoring of dipicolinic acid release. *Applied and Environmental Microbiology* **71**: 3556–3564.

Maier RM, Pepper IL, Gerba CP. 2009. Introduction to Environmental Microbiology. In: Environmental Microbiology. Elsevier Inc.

Mataix-Solera J, Cerdà A, Arcenegui V, Jordán A, Zavala LM. 2011. Fire effects on soil aggregation: A review. *Earth-Science Reviews* **109**: 44–60.

Mataragas M, Alessandria V, Ferrocino I, Rantsiou K, Cocolin L. 2018. A bioinformatics pipeline integrating predictive metagenomics profiling for the analysis of 16S rDNA/rRNA sequencing data originated from foods. *Food Microbiology* **76**: 279–286.

Mazur P. 2006. Physical factors implicated in the death of microorganisms at subzero temperatures. *Annals of the New York Academy of Sciences* **85**: 610–629.

Miller MB, Bassler BL. 2001. Quorum Sensing in Bacteria. *Annual Review of Microbiology* **55**: 165–199.

Moats WA. 1971. Kinetics of thermal death of bacteria. *Journal of bacteriology* **105**: 165–171.

Nikolenko SI, Korobeynikov AI, Alekseyev MA. 2013. BayesHammer: Bayesian clustering for error correction in single-cell sequencing. *BMC Genomics* **14**.

Peled ON, Salvadori A, Peled UN, Kidby DK. 1977. Death of microbial cells: rate constant calculations. *Journal of Bacteriology* **129**: 1648–1650.

Peleg M, Cole MB. 1998a. Reinterpretation of microbial survival curves. *Critical Reviews in Food Science and Nutrition* **38**: 353–380.

Peleg M, Cole MB. 1998b. Reinterpretation of Microbial Survival Curves. *Critical Reviews in Food Science and Nutrition* **38**: 353–380.

Pepper IL, Dowd SE. 2009. Aeromicrobiology. In: Environmental Microbiology: Second Edition. Academic Press Inc, 83–103.

Pylro VS, Roesch LFW, Morais DK, Clark IM, Hirsch PR, Tótola MR. 2014. Data analysis for 16S microbial profiling from different benchtop sequencing platforms. *Journal of Microbiological Methods* **107**: 30–37.

Quast C, Pruesse E, Yilmaz P, Gerken J, Schweer T, Yarza P, Peplies J, Glöckner FO. 2013. The SILVA ribosomal RNA gene database project: Improved data processing and web-based tools. *Nucleic Acids Research* **41**: 590–596.

Rao L, Xu Z, Wang Y, Zhao F, Hu X, Liao X. 2015. Inactivation of *Bacillus subtilis* spores by high pressure CO₂ with high temperature. *International Journal of Food Microbiology* **205**: 73–80.

Ross T, McMeekin TA, Baranyi J. 2014. *Predictive Microbiology and Food Safety*. Elsevier.

Rossetti I, Bagella S, Cappai C, Caria MC, Lai R, Roggero PP, Martins da Silva P, Sousa JP, Querner P, Seddaiu G. 2015. Isolated cork oak trees affect soil properties and biodiversity in a Mediterranean wooded grassland. *Agriculture, Ecosystems and Environment* **202**: 203–216.

Sadaiappan B, Kannan S, Palaniappan S, Manikkam R, Ramasamy B, Anilkumar N, Subramanian M. 2020.

Metagenomic 16S rDNA amplicon data of microbial diversity and its predicted metabolic functions in the Southern Ocean (Antarctic). *Data in Brief* **28**: 104876.

Schmieder R, Edwards R. 2011. Quality control and preprocessing of metagenomic datasets. *Bioinformatics* **27**: 863–864.

Setlow P. 2006. Spores of *Bacillus subtilis*: Their resistance to and killing by radiation, heat and chemicals. *Journal of Applied Microbiology* **101**: 514–525.

Smelt JPPM, Brul S. 2014. Thermal Inactivation of Microorganisms. *Critical Reviews in Food Science and Nutrition* **54**: 1371–1385.

Soh J, Dong X, Caffrey SM, Voordouw G, Sensen CW. 2013. Phoenix 2: A locally installable large-scale 16S rRNA gene sequence analysis pipeline with Web interface. *Journal of Biotechnology* **167**: 393–403.

Torres E. 2008. Cork Oak Woodlands on the Edge: Ecology, Adaptive Management, and Restoration. *Restoration Ecology* **18**: 615–617.

Toure A, Quattara K, Bahi C, Djaman AJ, Coulibaly A. 2017. Development and antimicrobial potencial of soap based on aqueous extract of leaves of morinda morindiodes (Morinda, rubiaceae) against cutaneous pathogens. *Eurrpean Journal of Pharmaceutical and Medica Research* **4**: 183–187.

Waldrop MP, Firestone MK. 2006. Seasonal Dynamics of Microbial Community Composition and Function in Oak Canopy and Open Grassland Soils. *Microbial Ecology* **52**: 470–479.

Xie C, Li YQ, Tang W, Newton RJ. 2003. Study of dynamical process of heat denaturation in optically trapped single microorganisms by near-infrared Raman spectroscopy. *Journal of Applied Physics* **94**: 6138–6142.

Xiong R, Xie G, Edmondson AE, Sheard MA. 1999. A mathematical model for bacterial inactivation. *International Journal of Food Microbiology* **46**: 45–55.

Yilmaz P, Parfrey LW, Yarza P, Gerken J, Priesse E, Quast C, Schweer T, Peplies J, Ludwig W, Glöckner FO. 2014. The SILVA and ‘all-species Living Tree Project (LTP)’ taxonomic frameworks. *Nucleic Acids Research* **42**: 643–648.

Zimmeramann M. 2012. Resistência de esporos de *Byssoschlamys fulva* e *Bacillus coagulans* em polpa de tomate sob condições isotérmicas, não isotérmicas e de altas pressões hidrostáticas.

Chapter 3: Evaluation of soil microbial communities after a wildfire

Determination of the microbial community composition is important because it provides identification and knowledge about those communities, their relationships with plants and with ecosystem (Kirk *et al.*, 2004; Pylro *et al.*, 2014). Traditionally, several methods [Community Level Physiological Profiling (CLPP) and Fatty Acid Methyl Ester analysis (FAME)] are used to identify microorganism due to its simplicity and low cost (Kirk *et al.*, 2004; Strickland & Rousk, 2010). However, the acquired time to perform all tests, discrimination of non-culturable microorganisms and the appearance of cross contaminations (Rocha *et al.*, 2015), lead to the development of molecular methods (Pulsed-Field Gel Electrophoresis (PFGE), DNA array hybridization, Terminal Restriction Fragment Length polymorphism (T-RFLP), Denaturing Gradient Gel Electrophoresis (DGGE), DNA sequencing etc) for microorganism identification (Naidoo *et al.*, 2013; Fajarningsih, 2016).

3.1. Microorganism identification: a metabarcoding approach

Metagenomic approaches revolutionized the analysis of microbial communities (Pylro *et al.*, 2014). It allows the study of all genomes of sampled microorganisms and provides knowledge about microbial community diversity and abundance (Matallana-Surget *et al.*, 2018). Metabarcoding is a method of biodiversity evaluation that comprises the amplification of barcodes on the extracted environmental DNA (Degnan & Ochman, 2012). Usually, it involves environmental DNA extraction from different tissues, different sources or different strains; and a polymerase chain reaction (PCR) that amplifies the barcode region for subsequent sequencing (Edgar, 2013; Kowalska *et al.*, 2019). DNA barcode is a genetic sequence that mark a genome as a code bar (Tresbach *et al.*, 2015; Kowalska *et al.*, 2019; Wilson *et al.*, 2019). This sequence must be hypervariable among species, but amplifiable between different taxa (Das *et al.*, 2014; Kowalska *et al.*, 2019). Thus, the use of ribosomal RNA (rDNA) genes is frequently used in microbial ecology, either in population structure descriptions or in the assessment of microbial diversity (Soh *et al.*, 2013; Kim & Chun, 2014; Kowalska *et al.*, 2019). Therefore, Internal Transcribed Spacer (ITS) and 16S rDNA genes are used on fungal and bacterial molecular identification as DNA barcode sequences, respectively (Woo *et al.*, 2008). Internal Transcribed Spacer (ITS, Figure 23), is a non-coding domain located in RNA, between the 18S [Small Subunit (SSU)] and 28S [Large Subunit (LSU)] and covers the 5.8S subunit (Schoch *et al.*, 2012). ITS region is widely used for the analysis of fungal diversity in environmental samples as DNA barcode (Fajarningsih, 2016; Ghosh *et al.*, 2019), because it fulfil the requirements for a DNA barcode (Fajarningsih, 2016).

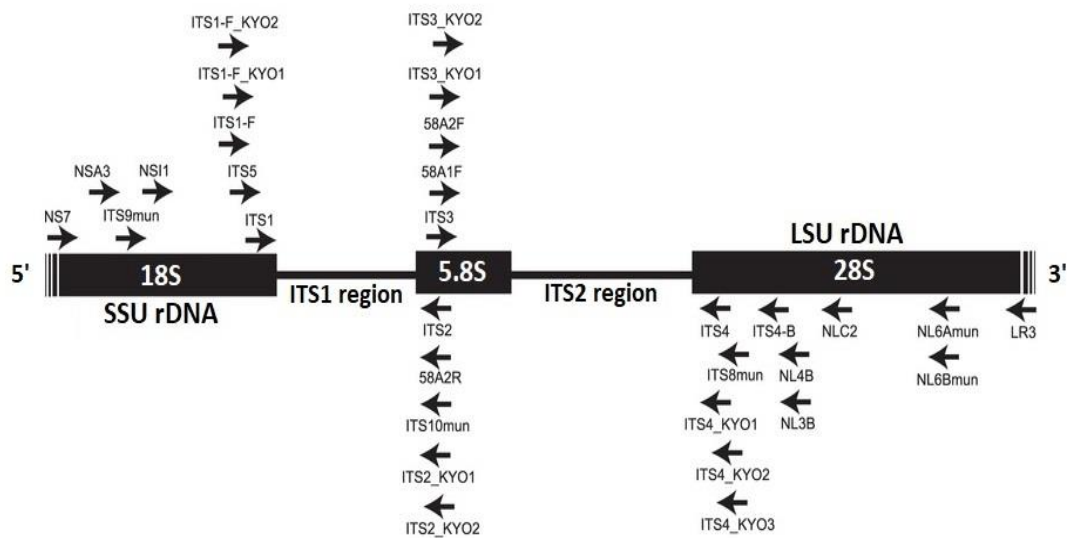


Figure 23 – rDNA region used in fungal identification. It is divided into SSU (18S and 5.8S) and LSU (28S). ITS regions are located between 18S subunit and 28S subunit and include 5.8S subunit. Primer for ITS region amplification are represented in black arrows

ITS regions contain several copies in the fungal genome (Nilsson *et al.*, 2009; Fajarningsih, 2016; Letchuman & Cosmecuticals, 2018; Ghosh *et al.*, 2019) and are easily amplified (Baldwin *et al.*, 1995; Letchuman & Cosmecuticals, 2018). This last aspect adds value to ITS regions used on metabarcoding approaches (Baldwin *et al.*, 1995; Letchuman & Cosmecuticals, 2018).

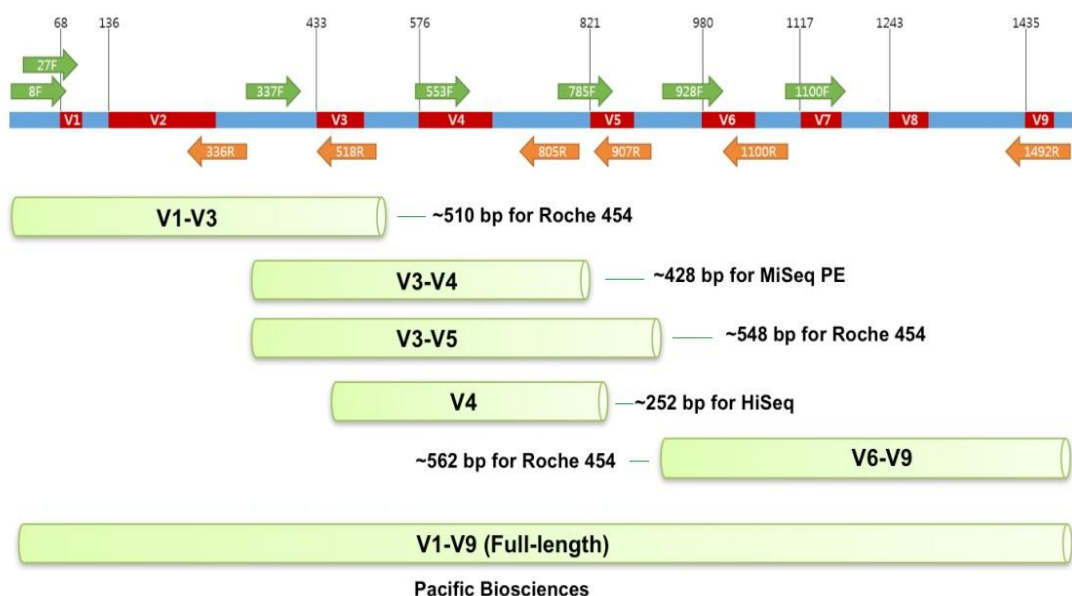


Figure 24 – 16S rDNA gene used on bacteria identification. It is divided into conserved regions (blue) and hypervariable regions (red). Primer for hypervariable region amplification is also presented (green arrow), as the sequence methodologies used on metagenomic approach

16S rDNA genes are DNA barcodes for bacterial identification (Woo *et al.*, 2008; Kim & Chun, 2014), due to their presence on almost all bacteria (Janda & Abbott, 2007). The 16S (SSU) rRNA gene codes for the 30S ribosomal RNA subunit and is composed by conserved regions interspaced by 9 hypervariable regions (V1-V9) (Figure 24) (Wang & Qian, 2009; Jo *et al.*, 2016). 16S rRNA is used on metagenomic approach (Janda & Abbott, 2007), but its hypervariable regions (V1-V9) only provide bacterial taxonomic identification, until genus level (Beckers *et al.*, 2016; Jo *et al.*, 2016).

Next Generation Sequencing (NGS) improved sequencing technologies, which led to a great advance on genomic analysis (De Sá *et al.*, 2018; Wilson *et al.*, 2019). In the past years several sequencing technologies have been used, such as 454 GS FLX, SOLiD (Sequencing by Oligonucleotide Ligation and Detection), Ion Torrent, PacBio, *Illumina HiSeq* and *Illumina MiSeq* (De Sá *et al.*, 2018).

These technologies differ on the biochemistry used for sequencing and on the amount of data produced (De Sá *et al.*, 2018). For example, *Illumina* platform uses sequencing by synthesis chemistry (SBS) (Mardis, 2008; Illumina, 2017; De Sá *et al.*, 2018). Due to the low costs per base and the high precision base to base, *Illumina* platform has been considered one of the most promising for the analysis of bacterial and fungal communities (Degnan & Ochman, 2012). *Illumina MiSeq* technology is the best for small genomes sequencing (throughput from 0.3 to 15 Gb) and *Illumina HiSeq* is required for studies that need high-throughput sequencing and can produce 1Tb of data (De Sá *et al.*, 2018).

After sequencing, data analysis is performed using bioinformatic tools (Prijbelski *et al.*, 2019)- In a metabarcoding approach the sequences are clustered into Operational Taxonomic Units (OTUs) (Matallana-Surget *et al.*, 2018). Through web services (*QUIME* – Quantitative insight into microbial ecology), each OTU is matched with a certain taxon (Caporaso *et al.*, 2010; Matallana-Surget *et al.*, 2018; Mataragas *et al.*, 2018). *SILVA* database is used for the identification of bacterial communities (Quast *et al.*, 2013; Yilmaz *et al.*, 2014; Glöckner *et al.*, 2017), and *UNITE alpha* database for fungal communities (Abarenkov *et al.*, 2010; Tedersoo *et al.*, 2018). Despite this, scientists have to be concerned about the human error on creating reference libraries for microorganism assemblage and with the decrease in the morphological description of new species (Kowalska *et al.*, 2019).

The aim of this work is the identification and composition analysis of soil microbial communities present in cork oak stands that were damaged by a wildfire. In particular, the soil microbial community recovering will be evaluated along time. To accomplish this, soil sampling

was performed 5-, 12- and 18-months post-fire on *Santa Marta das Cortiças* – Portugal. Microbial communities were evaluated by a metabarcoding approach, using 16S rDNA V23V4 for bacteria identification and ITS region for fungi identification, in *Illumina MiSeq* platform. Diversity analysis of obtained OTUs was then performed to compare soil microbial communities.

3.2. Material and Methods

3.2.1. *Quercus suber* L. study population

At 15th October of 2017, the cork oak stand from *Santa Maria das Cortiças* (Braga, Portugal) suffered a wildfire, initiated at Guimarães which went through 1200 ha. Soils were collected from different affected bark oak trees, after 5- (21st March 2018), 12- (1st October 2018) and 18- months (16th April of 2019) after wildfire occurrence (Table 12). Soils were taken from near nine existing cork oaks, which differ on fire damages (Table 13, Figure 25)



Figure 25 – Region map of the sampled cork oak forest (*S^a Marta das Cortiças*, Braga) used for the study of soil microbial communities by metabarcoding approach. Photo from 06-09-2017, Google earth Pro. Sampled trees are highlighted by a red sign.

The burnt condition was related with the appearance of damage caused by the wildfire across whole tree (almost 100%). Trees were externally carbonized, and soil displayed no plant cover (26A). Half-burnt trees were those which exhibit superficial fire damage (50%; 26B). These trees displayed a damage gradation, from severe damage in the base part of the tree to a healthier crown, suggesting that the wildfire did not reach the entire tree. In these cork oak trees, there was also no plant cover.

Table 12 – Sampled forest after 5-, 12- and 18-months after wildfire damage. Description of forest characteristics at the time of soil sampling.

Forest	Characteristics
	5 months post-fire (March 2018) • Stripped trees • No cover vegetation • Soil fulfilled with dead leaves (organic matter) and carbonized around trees
	12 months post-fire (October 2018) • Tree top with leaves • Soil covered with weeds and a dense shrubbery
	18 months post-fire (April 2019) • <i>Eucalyptus</i> plantlets growing near the affected wildfire trees • Soil showing signs of recovery (structure)

Table 13 - Fire damages and GPS coordinates of each sampled cork oak tree

N° of tree	State	GPS Coordinates
1	Burnt	N 41° 31' 1,34878'' W 8° 23' 40,77539''
2	Burnt	N 41° 31' 1,32707'' W 8° 23' 39,67187''
3	Burnt	N 41° 30' 59,81914'' W 8° 23' 39,79708''
4	Burnt	N 41° 30' 57,49129'' W 8° 23' 40,34968''
5	Non-Burnt	N 41° 30' 59,48872'' W 8° 23' 40,77044''
6	Non-Burnt	N 41° 30' 59,63946'' W 8° 23' 38,60779''
7	Non-Burnt	N 41° 30' 59,11177'' W 8° 23' 39,00666''
8	Half-Burnt	N 41° 31' 0,68'' W 8° 23' 38,41931''
9	Half-Burnt	N 41° 31' 0,83965'' W 8° 23' 37,66376''



Figure 26 – *Quercus suber* tree selection according to tree damage status. a) 100% damaged cork oak; b) 50% damaged cork oak; c) cork oak without fire damage

Although whole *Santa Marta das Cortiças* area was attacked by wildfire, some regions were just exposed to high temperatures, being possible to find non-burnt trees (Figure 26C).

From each sampled tree, three soil cores were collected with a core cutter (10 cm in depth and 5 cm in diameter). The cores were equally distributed around the tree and taken from under the middle of tree canopy. After removing the uppermost layer of soil that consisted of plant litter and other organic material, three independent soil cores (5 cm in diameter and 10 cm in depth) were collected from the cork oak soil and kept at 4°C until processing. In total, 81 soil cores (3 sampling times $\times$ 9 trees $\times$ 3 cores) were collected.

For chemical analysis, soils were grouped according to cork oak fire damages (burnt, half-burnt and not-burnt) and sampling time (5- and 18-months after fire), thus creating 6 soil samples. These samples were chemically analysed by *A2-Análises químicas*TM (Guimarães, Portugal). The chemical soil analysis included gravimetry, pH (H₂O), pH (CaCl₂), electrical conductivity, organic matter, organic carbon, total nitrogen; carbon: nitrogen ratio; phosphorus (P₂O₅), potassium (K₂O), calcium (CaO), magnesium (MgO), sodium; boron, sulphur, iron and manganese.

3.2.2. Experimental design

Soil cores from each tree were thoroughly mixed, sieved by a 45-mesh sieve and stored at -80°C until DNA extraction. For considering the same number of samples for each plant condition, soil cores were combined as depicted in Figure 27, creating 54 samples for DNA extraction (18 per sampling date).

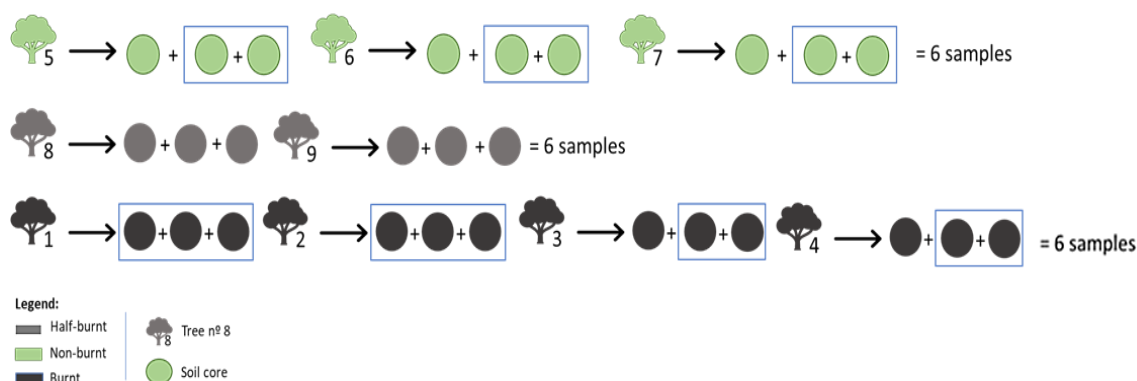


Figure 27 - Soil sampling method for metabarcoding approach on soil microbial communities.

3.2.3. Metabarcoding approach for soil microbial communities analysis

Soil DNA was extracted from 1g using the *DNeasy Power Soil Kit* (Qiagen, The Netherlands) with some changes, using the optimized protocol from chapter 2. The quantity and quality of obtained DNA were accessed using a *Nanodrop spectrometer ND-1000 3.8.1*, (Thermo Fisher Scientific) using $A_{260\text{ nm}}/A_{280\text{ nm}}$ and $A_{260\text{ nm}}/A_{230\text{ nm}}$ values. For accurately quantify the DNA, before sending to sequencing services, a fluorescent DNA quantification assay was performed with *Qubit dsDNA HS Assay Kit* (Thermo Fisher Scientific, Waltham, MA, USA), using *Qubit 4 fluorometer*.

For evaluating if DNA was amplifiable, a PCR amplification was performed using the pair of primers *16S V3V4 FW* and *16S V3V4 RV* for the 16S rRNA region and *ITS1F* and *ITS2* for ITS region in a PCR reaction of 25µL (Table 14). Amplification occurred on a *Bio-Rad T100 Thermal Cycles* using the following programme: 4 min at 94°C for initial denaturation, followed by 35 cycles of 30s at 94°C for denaturation, 30s at variable temperatures (53°C to 55°C) for annealing temperature and 30s at 72°C for the extension. PCR was ended with a final extension of 10 min, at 72°C. PCR products were evaluated by electrophoresis on an agarose gel (1%, w/w) prepared in 0.5x TAE buffer (0.01M Tris; pH 8.0; 47.5mM acetic acid; 25mM EDTA). For allowing the visualization of DNA, *green safe buffer* (nzytech) was added to the agarose gel (100 µL of *green safe buffer*/100mL gel). A mix of 8µL of DNA plus 2µL of green dye (nzytech) was loaded into the

agarose gel, as well as the molecular marker (*100 bp plus ready-to-use DNA Ladder*, bioron). Electrophoresis ran at 109V for 30min. The agarose gel was observed with an *UV transilluminator (VWR Genosmart)* and pictures were taken with an image acquisition system (*VWR Genosmart*).

Table 14 - PCR Components (25 µL) for 16S rRNA ITS region amplification, for bacteria and fungi respectively identification.

PCR components	Amount (µL)
ddH ₂ O	20.15
Complete NH ₄ reaction Buffer (10x): pH 8.8, 0.1% Tween 20, 25mM M _g Cl ₂ Bioron	2.5
dNTPs (10 mM)	0.25
Primer <i>16S V3V4 FW*</i> or <i>ITS1F**</i> (10 mM)	0.5
Primer <i>16S V3V4 RV*</i> or <i>ITS2**</i> (10 mM)	0.5
DSF- <i>Taq</i> DNA polymerase Bioron (5U/ µL)	0.1
DNA template	1
Total	25

* 16S V3V4 FW – TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCTA; 16S V3V4 RV – GTCTCGTGGGCTCGGAGATGTGTATAAGAGA CAGGAC; using these primers a 400 bp PCR product is expected.

** ITS1F – CTTGGTCATTAGAGGAAGTAA; ITS2 – GCTGCGTTCTTCATCGATGC; using these primers a 230 bp PCR product is expected

3.2.3.1. DNA sequence analysis and quality control

Due to budget limitations, only the bacterial community proceeded to sequencing by *Illumina*. From each of the total 54 soil DNA samples (3 sampling times x 3 burnt conditions x 6 soil samples), 10 µL were taken to perform DNA sequence and sent for sequencing to a service provider (Biocant; Cantanhede, Portugal).

Raw reads were extracted from *Illumina MiSeq@System* in *fastq* format and quality-filtered with *PRINSEQ version 0.20.4* (Schmieder & Edwards, 2011) to remove sequencing adapters, reads with less than 100 bases and trim bases with an average quality lower than Q25 in a window of 5 bases. The quality report of each library sequencing was viewed in *FastQC v0.11.8* (Andrews, 2010). The sequence trimming was performed in *Sickle* (Joshi & Fass, 2011). Additional quality filtering and overlapping paired-end reads merge was performed using *BayesHammer module of Spades 3.12.0 software* (Nikolenko *et al.*, 2013). Using *Usearch v11.0.667*, read pairs were merged (Edgar & Flyvbjerg, 2015). Detection and removal of sequencing adapters and primers, as well as the clipping of limited skewing and poor quality read ends, was performed by *Ea-utils (fastq-mcf) v 1.04.636* (Aronesty, 2013).

Sequence results organization into Operational Taxonomic Units (OTUs) at 97% of identity was performed using *micca 1.7.0 software* (Albanese *et al.*, 2015). At the same time, taxonomy

was assigned by using the SILVA database (Silva release 132) (Quast *et al.*, 2013; Yilmaz *et al.*, 2014; Glöckner *et al.*, 2017), in order to classify each bacterial OTU sequence and convert data into a *biom format*. This final analysis was achieved using *Qiime 2* (Caporaso *et al.*, 2010). Unknown classifications, OTUs identified as chloroplasts or mitochondria were removed from OTU table, as well as those low abundance OTUs (with less than 5 reads).

Analysis of α -diversity data was calculated using the *Past3 software v3.26* (Hammer, 2019). Rarefaction curves were constructed using *GraphPad Prism 7.04 software* and diversity indices determined. Venn diagram was obtained by *Excel software*.

3.3. Results and discussion

3.3.1. Chemical analysis of *Santa Marta das Cortiças* soils

For evaluating cork oak soil restauration after wildfire episode, chemical analysis on sampled soils collected 5- and 18-months after fire occurrence was performed (Table 15 and Table 16). Chemical analysis carried out on all soil samples revealed the presence of an acid soil on *Santa Marta das Cortiças* (Tables 15 and 16). As previously referred (chapter 2), acid soils are a characteristic of cork oak forests (Torres, 2008) and were also detected at Universidade do Minho sampled tree (Table 4, Chapter 2). Although fire intensity on the ground is reported to affect the soil pH values (Hamman *et al.*, 2007; Granged *et al.*, 2011; Mataix-Solera *et al.*, 2011), there was a significative differences on pH (H₂O) values ($P < 0.01$).

The higher values of organic matter found in half-burnt tree soils (25.54%), were due to low intensity fire, that promoted the falling of the remaining leaves and twigs (Mataix-Solera *et al.*, 2011). And comparing unburnt and burnt soils, 5 months post-fire, there was a slight decrease on organic matter on soils that suffered wildfire occurrence (from 15.89% to 8.40%), which could be due to the conversion of organic to inorganic matter through the carbonization process. *Santa Marta das Cortiças* forest presented a content of organic matter (OM) lower than half- and burnt tree soils [non-burnt soil ($8.4 \pm 0.01\%$)], which may be explained by the remains of cork oaks stripping. Burnt trees did not displayed any leaves and unburnt trees still preserved their leaves. Comparing *Santa Marta das Cortiças* soil to Universidade do Minho cork oak sampled soil the contente of OM from half- and burnt tree soils, at 5 months post-fire, is higher than cork oak sampled soil from Universidade do Minho. But OM content obtained for non-affected cork oak soil, from *Santa Marta das Cortiças* revealed to be lower. The effects of fire on organic matter are described to contribute to the variation of nutrients (Granged *et al.*, 2011).

Table 15 – Chemical analysis of soils collected on March 2018, 5-months post-fire occurrence, at *Santa Marta das Cortiças* (Braga).

Parametres	Burnt		Half-burnt		Non-burnt		Reference values
	Results	Interpretation	Results	Interpretation	Results	Interpretation	
Granulometry	Areno-Franca (75.7% Sand; 15.1% Clay; 9.2% Lime)		Areno-Franca (Sand 80.4%; 8.2% Clay; 11.4% Lime)		Areno-Franca (77.7% Sand; 11.8% Clay; 10.5% Lime)		
pH (HzO)	3.98 ± 0.01	Very acid	4.39 ± 0.01	Very acid	4.36 ± 0.01	Very acid	3.4 – 7.8
pH (CaCl ₂)	3.52 ± 0.01	Acid	3.44 ± 0.01	Acid	3.75 ± 0.01	Acid	-
Electrical conductivity	283 ± 2 µS/cm	Non saline	345 ± 2 µS/cm	Non saline	178 ± 2 µS/cm	Non saline	-
Organic matter	15.89 ± 0.01 %	Very high	25.54 ± 0.01 %	Very high	8.40 ± 0.01 %	Very high	-
Organic carbon	9.22 ± 0.04 %	-	14.81 ± 0.04 %	-	4.87 ± 0.04 %	-	-
Total nitrogen	0.67 ± 0.02 %	In excess	0.99 ± 0.02 %	In excess	0.32 ± 0.02 %	In excess	-
Carbon: nitrogen	13.7	Normal	15.0	High	15.1	High	-
Phosphorus (P ₂ O ₅)	60.1 ± 0.4 mg/kg	Low	31.5 ± 0.4 mg/kg	Very low	105.3 ± 0.4 mg/kg	High	98 – 162 mg/kg
Potassium (K ₂ O)	163.6 ± 1.3 mg/kg	In excess	216.7 ± 1.3 mg/kg	In excess	103.5 ± 1.3 mg/kg	High	74 – 140 mg/kg
Calcium (CaO)	127.6 ± 0.9 mg/kg	Very low	120.7 ± 0.9 mg/kg	Very low	312.4 ± 0.9 mg/kg	Very low	819 – 1047 mg/kg
Magnesium (MgO)	84.8 ± 0.4 mg/kg	Medium	206.7 ± 0.4 mg/kg	In excess	323.3 ± 0.4 mg/kg	In excess	100 – 205 mg/kg
Sulphur	35.8 ± 0.1 mg/kg	High	30.9 ± 0.1 mg/kg	High	15.4 ± 0.1 mg/kg	High	>10 mg/kg
Iron	358.2 ± 0.1 mg/kg	In excess	351.0 ± 0.1 mg/kg	In excess	177.0 ± 0.1 mg/kg	In excess	50 – 100 mg/kg
Manganese	425.1 ± 0.0 MnAl	In excess	355.4 ± 0.0 MnAl	In excess	379.1 ± 0.0 MnAl	In excess	25 – 100 MnAl*
Boron	0.77 ± 0.00 mg/kg	High	0.70 ± 0.00 mg/kg	High	0.63 ± 0.00 mg/kg	high	0.5 – 5 mg/kg
Sodium	35.0 ± 0.1 mg/kg	-	45.6 ± 0.1 mg/kg	-	22.6 ± 0.1 mg/kg	-	-

With the depletion of organic material on the soil surface, the concentration on nutrients, such as phosphorous, potassium, calcium, magnesium, among others, could be disturbed by a fire occurrence. This could occur due to subsequent rainfall, which move them to deeper soil after rainfall (Altun *et al.*, 2004), or through volatilization [312.4 mg/kg (non-burnt soil) to 127.6 mg/kg (burnt soil)]. In addition, the combustion of MgCO₃, forms MgO + CO₂. But the lower presence of Mg on burnt tree soils is explained by CO₂ reabsorption through MgO molecules, forming MgCO₃ at temperatures lower than 900°C (Parraa & Lopeza, 1996; Certini, 2005; Guerrero *et al.*, 2005).

After 18-months, the fire occurrence, some of these macronutrients increased their amounts on non-burnt tree soils (Calcium 487.5 mg/kg, Magnesium 337.2 mg/kg and sulphur 13.3 mg/kg) but decrease on burnt soils. This may be explained by lixiviation processes occurred throughout rainfalls and radiation through soils were subjected.

Table 16 – Chemical analysis of soils collected on April 2019, 18-months post-fire occurrence, at *Santa Marta das Cortiças* (Braga).

Parameters	Burnt		Hal-burnt		Non-burnt		Reference values
	Results	Interpretation	Results	Interpretation	Results	Interpretation	
Granulometry	Areno-Franca (Sand 80.0%; 9.6% Clay; 10.4% Lime)		Areno-Franca (Sand 79.4%; 8.2% Clay; 12.4% Lime)		Areno-Franca (Sand 79.3%; 11.1% Clay; 9.6% Lime)		
pH (H ₂ O)	4.22 ± 0.01	Very acid	4.49 ± 0.01	Very acid	4.35 ± 0.01	Very acid	3.4 – 7.8
pH (CaCl ₂)	3.68 ± 0.01	Acid	3.64 ± 0.01	Acid	3.41 ± 0.01	Acid	-
Electrical conductivity	143 ± 2 µS/cm	Non saline	109 ± 2 µS/cm	Non saline	97 ± 2 µS/cm	Non saline	-
Organic matter	14.20 ± 0.01 %	Very high	26.61 ± 0.01 %	Very high	16.46 ± 0.01 %	Very high	-
Organic carbon	8.24 ± 0.04 %	-	15.43 ± 0.04 %	-	9.55 ± 0.04 %	-	-
Total nitrogen	0.66 ± 0.02 %	In excess	1.12 ± 0.02 %	In excess	0.55 ± 0.02 %	In excess	-
Carbon: nitrogen	12.5	Normal	13.8	Normal	17.5	High	-
Phosphorus (P ₂ O ₅)	123.6 ± 0.4 mg/kg	High	177.5 ± 0.4 mg/kg	In excess	105.6 ± 0.4 mg/kg	High	98 – 162 mg/kg
Potassium (K ₂ O)	113.3 ± 1.3 mg/kg	High	251.3 ± 1.3 mg/kg	In excess	149.3 ± 1.3 mg/kg	In excess	74 – 140 mg/kg
Calcium (CaO)	174.8 ± 0.9 mg/kg	Very low	337.6 ± 0.9 mg/kg	Very low	487.5 ± 0.9 mg/kg	Low	819 – 1047 mg/kg
Magnesium (MgO)	59.4 ± 0.4 mg/kg	Medium	146.4 ± 0.4 mg/kg	High	337.2 ± 0.4 mg/kg	In excess	100 – 205 mg/kg
Sulphur	25.6 ± 0.1 mg/kg	High	21.8 ± 0.1 mg/kg	High	13.3 ± 0.1 mg/kg	High	>10 mg/kg
Iron	365.7 ± 0.1 mg/kg	In excess	481.2 ± 0.1 mg/kg	In excess	293.3 ± 0.1 mg/kg	In excess	50 – 100 mg/kg
Manganese	384.9 ± 0.0 MnAl	In excess	376.6 ± 0.0 MnAl	In excess	409.0 ± 0.0 MnAl	In excess	25 – 100 MnAl
Boron	0.49 ± 0.00 mg/kg	low	0.53 ± 0.00 mg/kg	High	0.69 ± 0.00 mg/kg	high	0.5 – 5 mg/kg
Sodium	29.6 ± 0.1 mg/kg	-	42.1 ± 0.1 mg/kg	-	41.3 ± 0.1 mg/kg	-	-

Statistical analysis (*One-Way ANOVA*), revealed significant differences between tree soil samples, $p < 0.01$ for soil sampling on March of 2018, and $p < 0.001$ for April 2019.

3.3.2. Amplification of soil DNA samples

As previously described, 54 soil samples were taken from *Santa Marta das Cortiças* in order to extract DNA (Annex 1) for evaluating soil microbial communities after a wildfire episode by molecular methods. A PCR optimization was performed to guarantee the amplification of 16S rDNA and ITS rRNA gene marker (Figure 28 e Figure 29). PCR optimization consisted on using a gradient of annealing temperatures, using the primer pairs *16S V3/V4 FW* and *16S V3/V4 RV* (for bacteria barcode); and *ITS1* and *ITSF2* (for fungi barcode). The electrophoresis revealed that 54°C and 53°C were the ideal annealing temperatures for amplifying rDNA 16S and ITS regions, respectively.

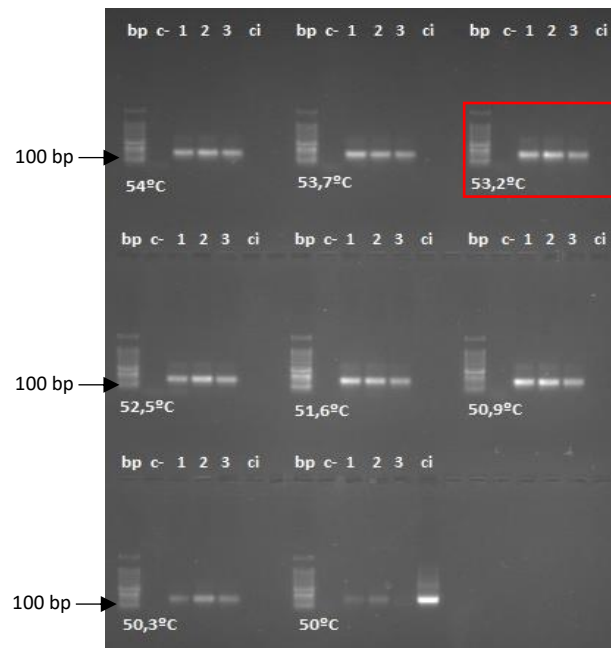


Figure 28 – Optimization of PCR for amplifying ITS region. An annealing temperature gradient (50°-53°) PCR was used to optimize PCR. DNA was extracted and used to amplify ITS region by using the ITSF1 and ITS2 primer pair Legend (bp) 100bp plus ready-to-use DNA Ladder Bioron; (c-) negative control; (1) [DNA] 3ng/ μ L; (2) [DNA] 4 ng/ μ L (3) [DNA] 6 ng/ μ L; (ci) [DNA] 53,6 ng/ μ L.. The most adequate temperature to perform PCR and amplify ITS region was 53°C (highlighted by a red rectangle).

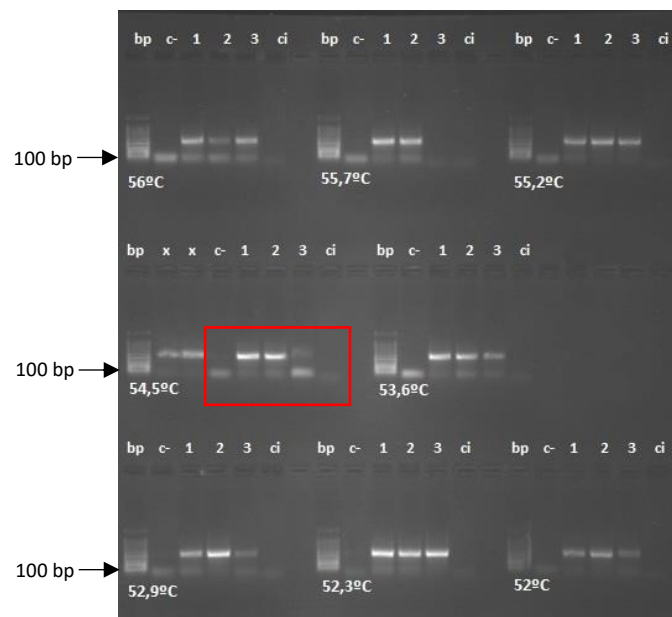


Figure 29 – Optimization of PCR for amplifying 16S region. An annealing temperature gradient (52°-56°) PCR was used to optimize PCR. DNA was extracted and used to amplify 16S V3V4 region by using the *16S V3V4FW* and *16S V3V4RV* primer pairs. Legend: (bp) 100bp plus ready-to-use DNA Ladder Bioron; (c-) negative control; (1) [DNA] 3ng/ μ L; (2) [DNA] 4 ng/ μ L (3) [DNA] 6 ng/ μ L; (ci) [DNA] 53,6 ng/ μ L. The most adequate temperature to perform PCR and amplify 16S V3V4 region was 54°C (highlighted by a red rectangle).

For ensuring the amplification of the rDNA genes marker for further sequence, 16S V3V4 and ITS regions were amplified in all DNA samples (Annex 2 and Annex 3).

DNA samples were sent to sequencing services to be sequenced by *Illumina MiSeq*. Sequence was only performed on bacterial communities due to budget limitations.

3.3.3. Data processing

Sequence data analysis from 16S region amplification was performed following several authors (Soh *et al.*, 2013; Pylro *et al.*, 2014; Mataragas *et al.*, 2018; Sadaippan *et al.*, 2020).

Table 17 – Data processing of reads obtained by *Illumina MiSeq* metabarcoding using 16S barcode in DNA samples obtained from soils of different damaged cork oak trees. Raw dataset was processed as described in Materials and Methods and clustered into OTUs (results without singletons and unclassified reads). Number of OTUs correspond to results after dataset subsampling and removing OTUs with less than 5 reads.

Sample		Reads processing					Taxonomic classification of OTUs						
Sampling date	Tree Damage	Name	Initial read pairs	After trimming	Merged reads	Unclassified reads	OTUs	Phylum	Class	Order	Family	Genus	
5 months post-fire (March 2018)	Non-burnt	A6S1F1	55624	55304	23445	13884	255	11	20	48	71	190	
		A6S23F1	57382	57214	24907	20262	507	12	23	52	81	231	
		A7S1F1	68942	68588	29567	20307	354	12	21	41	53	180	
		A7S23F1	77536	77036	32456	22125	504	14	29	52	71	219	
		A8S1F1	69334	69028	29725	20822	522	15	30	62	79	151	
		A8S23F1	60412	60194	26307	16396	349	8	12	36	51	166	
	Half-burnt	A9S1F1	-	-	-	-	-	-	-	-	-	-	-
		A9S2F1	70506	70182	30293	21272	519	14	29	53	71	222	
		A9S3F1	67380	67102	29614	22960	246	11	18	38	51	152	
		A10S1F1	92582	91954	39561	28123	414	3	4	18	33	72	
		A10S2F1	104178	103538	44056	31430	467	15	21	47	60	147	
		A10S3F1	89592	89004	38685	28135	358	16	21	46	55	182	
	Burnt	A1S123F1	60896	60500	25966	15024	309	6	16	38	52	139	
		A2S123F1	91738	91060	40107	32815	347	13	17	41	56	184	
		A4S1F1	83524	82938	35723	25782	515	16	31	64	80	196	
		A4S23F1	93386	92828	40083	28011	568	16	30	64	80	174	
		A5S1F1	68584	68120	29895	19186	344	10	16	41	60	184	
		A5S23F1	79836	79494	34709	18835	338	10	17	43	58	179	
	Total		1291432	1284084	555099	385369	3097	23	60	146	271	497	
12 months post-fire (October 2018)	Non-burnt	A6S1F3	61402	61142	26663	17477	441	12	21	49	71	191	
		A6S23F3	70230	69894	30415	17553	380	10	19	45	62	161	
		A7S1F3	32768	32524	13703	6191	176	5	11	23	33	112	
		A7S23F3	59478	59220	26010	13113	323	7	11	35	55	176	
		A8S1F3	102810	102426	44661	22532	452	9	19	42	68	187	
		A8S23F3	47924	47778	20638	11904	222	7	12	26	35	125	
	Half-burnt	A9S1F3	66126	65804	28584	19478	320	12	16	38	57	167	
		A9S2F3	80718	80266	34854	24394	316	12	17	34	50	180	
		A9S3F3	72682	72194	31372	23776	370	12	21	44	61	189	
		A10S1F3	40226	39990	17601	10108	173	7	11	32	47	124	
		A10S2F3	68838	68496	30396	19466	277	15	19	41	66	160	
		A10S3F3	65640	65290	28576	18199	352	13	18	46	67	191	
	Burnt	A1S123F3	45478	45364	20183	11135	271	8	15	41	65	166	
		A2S123F3	70840	70606	31375	20038	270	12	15	40	58	168	
		A4S1F3	52210	52030	23108	12104	290	8	12	35	57	156	
		A4S23F3	102420	102120	45094	19215	461	11	21	47	78	164	
		A5S1F3	92324	92044	41016	24236	370	10	17	41	66	200	
		A5S23F3	80956	80592	35227	21332	363	8	18	38	57	146	
	Total		1213070	1207780	529476	312251	2825	22	53	126	233	440	
18 months post-fire (April 2019)	Non-burnt	A6S1F5	66972	66732	28747	20106	483	11	19	53	83	233	
		A6S23F5	80588	80314	35692	16226	402	10	18	41	65	183	
		A7S1F5	100208	99482	43504	33882	622	14	23	63	85	237	
		A7S23F5	74594	74418	32843	18898	333	11	15	37	56	189	
		A8S1F5	75982	75712	32978	19434	439	13	24	51	64	177	
		A8S23F5	87840	87302	36240	20265	483	14	23	50	66	152	
	Half-burnt	A9S1F5	67372	67112	29066	21463	406	14	21	49	65	174	
		A9S2F5	61660	61394	26716	20146	363	14	21	50	68	175	
		A9S3F5	56952	56696	24189	15131	366	14	20	52	70	188	
		A10S1F5	76982	76670	33441	21583	417	15	19	51	76	211	
		A10S2F5	71010	70712	30777	21096	375	14	18	47	67	180	
		A10S3F5	63912	63704	27649	18822	376	17	22	50	78	179	
	Burnt	A1S123F5	93730	93314	40730	25754	493	15	23	51	74	214	
		A2S123F5	132390	131874	57887	38258	501	15	23	52	77	220	
		A4S1F5	115442	115086	50357	28354	476	15	21	53	67	204	
		A4S23F5	84296	83938	36471	21165	497	15	26	54	79	174	
		A5S1F5	107600	107014	46202	30186	370	13	20	45	55	185	
		A5S23F5	106056	105620	46366	30574	590	16	24	57	80	266	
	Total		1523586	1517094	659855	421343	3205	21	58	148	268	509	
TOTAL		4028088	4008958	1744430	1118963	3354	29	83	207	382	717		

A total of 4,028,088 raw reads were obtained from cork oak soils of *Santa Marta das Cortiças* (Table 17). After sequence analysis, 92 OTUs were allocated as unclassified, 3 classified as chloroplasts, 3 as mitochondria and 1.144 sequences were removed due to their abundance (≤ 5). At the end a total of 3354 identified OTUs were classified.

3.3.4. Bacterial taxonomic composition

The taxonomic assignment of 16S (bacteria) sequences with *SILVA* database was performed with the pooled samples from soils displaying different damaged trees (Burnt, Half-burnt and Non-burnt) and from different time periods after wildfire occurrence (5-, 12- and 18-months). Results reveal that since forest fire in *Santa Marta das Cortiças*, at 12th October 2017, microbial communities present in the soil have suffered variations in their composition and structure (Figure 30) and (Figure 31), (Annex 7 to Annex 15).

At March 2018 (5 months after fire), the cork oak soils of *Santa Marta das Cortiças* were mainly composed by *Proteobacteria* (34.88%), followed by *Acidobacteria* (29.21%), and *Actinobacteria* (25.41%) (Figure 30A, Annex 7). In addition to these phyla, *Chloroflexi* (4.56%), *Planctomycetes* (1.84%) and *Verrucomicrobia* (1.53%) were found at lower percentages. *Bacterioidetes*, *Firmicutes* and *Gemmatimonadetes* were found in a low abundance ($<0.5\%$). Over time, the native communities of cork oak soil have undergone slight changes in their abundance (Figure 30C, Annex 10) and (Figure 30E, Annex 13). One year after the wildfire in *Santa Marta das Cortiças*, some of the aforementioned phyla presented variations in abundance when compared to the first harvesting. *Proteobacteria* (from 34.88% to 31.98%) and *Acidobacteria* (from 29.21% to 22.85%) showed the most evident decreases, while *Actinobacteria* (25.41% to 39.29%) revealed a considerable increase. But in April 2019 (18 months after the forest fire) (Figure 30E, Annex 13), the phyla that had decreased in abundance in October 2018 (12 months after the forest fire), increased their abundance (*Proteobacteria* from 31.98% to 36.75%; and *Acidobacteria* from 22.85% to 27.01%). *Actinobacteria* also recovered to values more similar to the first sampling date (28.00%). The observed changes should have resulted from the season effect on microbial communities, as the most dissimilar community was found in October (12 months after wildfire occurrence), while the most similar were taken both during spring (March-April).

Forest fires do not burn to the same intensity / severity within forests (Bento-Gonçalves *et al.*, 2012). Evidence of this is the presence of half- and burnt trees near to non-burnt trees in the forest of *Santa Marta das Cortiças*. This differentiation is due to the type of fuel found at the site

and the edaphoclimatic conditions during the forest fire (Allison & Martiny, 2009). This variation in the burning of trees resulted in changes on the soil bacterial communities from differently affected trees. Thus, 5 months after fire occurrence (March, 2018), the soil of half-burnt trees exhibited as the most evident differences a greater abundance of *Acidobacteria* (from 29.21% to 30.41%), *Verrucomicrobia* (2.78%), and *Firmicutes* (1.07%) and a decrease on *Proteobacteria* (from 34.88% to 31.54%) and *Actinobacteria* (from 28.21% to 24.12%) (Figure 30A, Annex 8).. The remaining phyla remained did not change more that 1%. After 12 months from the occurrence of wildfire, *Proteobacteria* was the most abundant phylum (39.80%), followed by *Actinobacteria* (37.98%), *Acidobacteria* (13.08%), *Chloroflexi* (4.51%) and *Firmicutes* (1.13%). The remaining phyla found showed abundances <1%. But 18 months after wildfire (Figure 30E, Annex 14), all these phyla decreased their abundance, except for *Proteobacteria* (48.67%) which reach the highest abundance value. *Actinobacteria* (29.04%), *Chloroflexi* (2.31%) and *Planctomycetes* (1.17%) also decreased their abundances.

As for the soil communities of the burnt trees, 5 months post-fire the most abundant phylum was *Proteobacteria* (37.29%), followed by *Actinobacteria* and *Acidobacteria* (23.86% and 22.61%, respectively) (Figure 30A, Annex 9). In fact, the abundance of *Chloroflexi* was also higher (7.12%) than *Chloroflexi* in native cork oak soil communities, as well as *Firmicutes* (3.13%). Twelve months after wildfire in *Santa Marta das Cortiças*, microbial communities continue to be abundant in the soils of burnt trees, with *Actinobacteria* being superior to *Proteobacteria* (44.96% and 32.79% respectively), as well as *Chloroflexi* and *Firmicutes* (6.53% and 1.56%) (Figure 30C, Annex 12). *Acidobacteria* showed lower values than those of non-burnt tree soils (12.51%). Finally, except for *Chloroflexi*, (Figure 30E, Annex 15, in which the abundance values obtained, 18 months post-fire, are higher than those from non-burnt tree soils (7.48%), all other phyla give slight decreases when compared to those ones to.

Finally, the time factor (March 2018, October 2018 and April 2019), the environmental conditions that the soil was subjected to after the forest fire and the edaphoclimatic conditions when collecting the samples (Winter, Autumn and Spring) influence the type of bacterial community found in the cork oak soil in *Santa Marta das Cortiças* (Figure 30B, D and E). *Proteobacteria* and *Acidobacteria* being more sensitive to edaphoclimatic variations, over time. And if we look at what happens to the communities of burnt soils, these phyla are also the ones that suffer the most variation (Figure 30B, D and E). Nevertheless, this variation among all phyla, is smaller through time and tree damage.

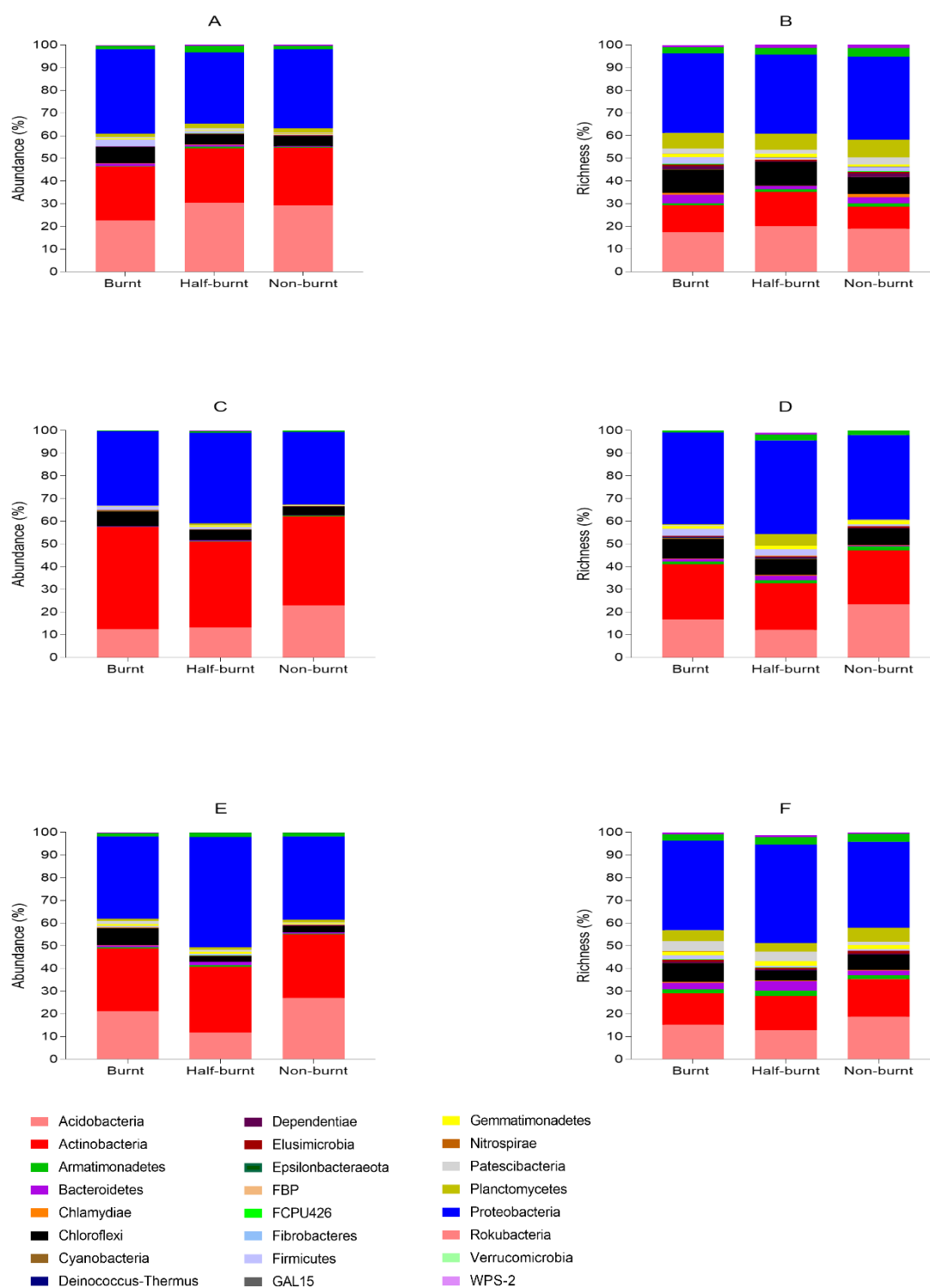


Figure 30 – Abundance and richness of bacterial phyla detected on St^a Marta das Cortiças soil as revealed by *Illumina MiSeq 16S* amplicon sequencing. Phylum abundance: A – 5 months post-fire (March 2018); C – 12 months post-fire (October 2018) and E – 18 months post-fire (April 2019) identified at 97%; Phylum richness: B – 5 months post-fire (March 2018); D – 12 months post-fire (October 2018) and F - 18 months post-fire (April 2019), identified at 97%.

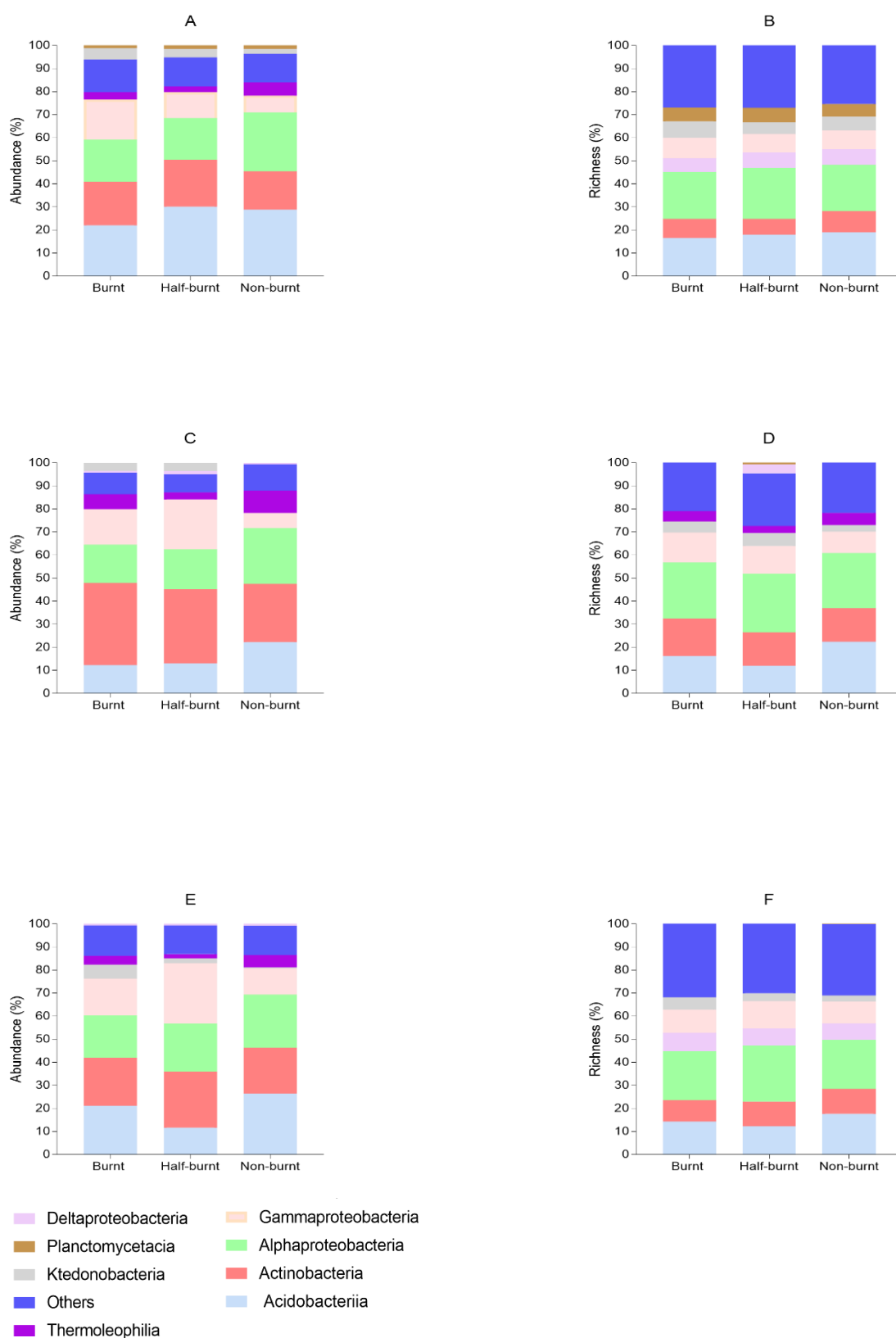


Figure 31 – Abundance and richness of bacterial class detected on St^a Marta das Cortiças soil as revealed by Illumina MiSeq 16S amplicon sequencing. Class abundance: A – 5 months post-fire (March 2018); C – 12 months post-fire (October 2018) and E – 18 months post-fire (April 2019) identified at 97%; Class richness: B – 5 months post-fire (March 2018); D – 12 months post-fire (October 2018) and F – 18 months post-fire (April 2019), identified at 97%.

The same conclusions are taken for bacterial classes changes, found on *Santa Marta das Cortiças* soils, either affected or not affected by fire. The most abundant classes in the cork oak soil not affected by fire (5 months after fire) were *Alphaproteobacteria* (25.59%), *Gammaproteobacteria* (7.24%) and *Deltaproteobacteria* (2.07%), belonging to the phylum *Proteobacteria* (Figure 31A, Annex 7). From *Actinobacteria*, the most abundant classes were *Actinobacteria* (16.63%) and *Thermoleophila* (5.79%); while from *Acidobacteria*, the *Acidobacteria* class was the prevalent (28.76%). After 12 months of fire occurrence, (Figure 31C, Annex 10), the abundances of these classes changed, with a decrease on *Alphaproteobacteria* and *Acidobacteria*, (24.16% and 22.28% respectively), and an increase in *Actinobacteria*, *Gammaproteobacteria*, *Thermoleophila* and *Deltaproteobacteria* (25.21%, 22.28%, 9.62% and 1.27%, respectively). However, 18 months post-fire, (Figure 31E, Annex 13), communities again suffer variations in their abundance. In this case, *Acidobacteria* and *Deltaproteobacteria*, the classes that increase their abundance in cork oak soil were not affected by fire (26.24% and 2.45%).

Fifty percent of damage to cork oak trees created disturbances in the microbial phyla present in soils, but also in the classes, through March 2018 (Figure 31A, Annex 8), October 2018 (Figure 31C, Annex 11) and April 2019 (Figure 31E, Annex 14). Some bacterial classes abundances increased as *Actinobacteria* [20.20% (March 2018); 32.31% (October 2018) and 24.46% (April 2019)], *Gammaproteobacteria* [11.22% (March 2018); 21.59% (October 2018) and 26.31% (April 2019)], and *Ktedonobacteria* [3.65% (March 2018); 4.19% (October 2018) and 2.07% (April 2019)]. Others classes decreased their abundance when compared to non-affected cork oak soils, such as *Alphaproteobacteria* [18.14% (March 2018); 17.31% (October 2018) and 20.78% (April 2019)] and *Thermoleophila* [2.41% (March 2018); 3.01% (October 2018) and 1.94% (April 2019)]. Small variations on microbial classes throughout time on half-burnt tree soils were detected along time. Also, *Bacilli* class (*Firmicutes* phylum) was identified in small amounts (<2%), higher than non-affected cork oak soils, at half-burnt tree soils collected on March and October (5- and 12 months post-fire in *Santa Marta das Cortiças*). But in April 2019, 18 months post-fire, *Bacilli*'s abundance was lower when compared with non-affected cork oak soils (<1%).

Regarding to burnt cork oak tree soils, the highest abundant classes of bacteria in March 2018 (Figure 31A, Annex 9) when compared to non-burnt cork oak soils, were *Acidobacteria* (22.07%), *Actinobacteria* (18.67%), *Alphaproteobacteria* (18.44%), *Gammaproteobacteria* (17.27%), *Ktedonobacteria* (4.82%) and *Bacilli* (3.12%). But *Thermoleophila* (3.23%) and *Acidimicrobiia* (1.81%) were present in lower abundances when compared to non-burnt cork oak

soils. After 12 months from fire occurrence, the abundances of these classes changed, displaying a higher abundance of *Actinobacteria*, *Bacilli*, *Gammaproteobacteria* and *Ktedonobacteria* (35.58%; 1.56%; 15.39% and 4.23% respectively; Figure 31C, Annex 12). Other classes presented decreased values of abundance when compared to non-burnt cork oak soils. However, 18 months after fire, communities suffer small variations in their abundance (Figure 31E, Annex 15). In this case, *Acidimicrobiia* (2.68%), *Actinobacteria* (21%), *Gammaproteobacteria* (16.14%) and *Ktedonobacteria* (5.97%), were the classes that had their abundance higher than in cork oak soils not affected by fire.

In ecological successions, the abundance of *Proteobacteria* and *Acidobacteria* are greater than other phyla (Zhang *et al.*, 2016). From *Proteobacteria*, forest fire increases *Betaproteobacteria* and decreases delta- and *Alphaproteobacteria* (Xiang *et al.*, 2014). But phyla abundance (e.g. *Actinobacteria* and *Proteobacteria*) is influenced by abiotic factors such as precipitation, soil texture and pH, which occurred post-fire (Zeng *et al.*, 2016). Nevertheless, bacterial sensitiveness to those factors, plus fire severity and organic matter content post-fire, determinates microbial community recovery speed in ecosystem (Bach *et al.*, 2010; Banning *et al.*, 2011; Zeng *et al.*, 2016).

Bacterial abundance can also be influenced by the appearance of invasive or exogenous vegetation (*Eucalyptus spp* - Table 12). These habitats contribute for microbial communities variations throughout ecological successions (Bach *et al.*, 2010; Zeng *et al.*, 2016), explaining the variations detected on *Santa Marta das Cortiças* soils either affected or not affected by fire. Plant cover after wildfire can promote the growth of some bacteria and inhibit the growth / appearance of others, through soil chemical modifications (Zhang *et al.*, 2018). Indeed, pH is reported to influence *Proteobacteria*, *Actinobacteria* and *Chloroflexi* phyla, where a high pH values is know to be a limiting factor (Xiang *et al.*, 2014; Zeng *et al.*, 2016). Nevertheless, pH do not have a direct influence on *Acidobacteria* growth (Xiang *et al.*, 2014; Zeng *et al.*, 2016). *Proteobacteria* prefer soils rich in nutrients, while *Acidobacteria* phyla thrive on poorer soils (Zhang *et al.*, 2016). Soils with high concentrations of clay, can better protect microbial communities from heat and pH fluctuations (Bach *et al.*, 2010). Soil chemical composition also influences the microbial communities at the restoration of the ecosystem after a wildfire (Bach *et al.*, 2010; Xiang *et al.*, 2014).

Bacterial responses when subjected to abiotic stress factors (wildfires) can be different among phyla and class (Xiang *et al.*, 2014). Fire severity controls the responses (resilience) of bacterial communities in the face of these disorders (Allison & Martiny, 2009; Baho *et al.*, 2012; Bento-Gonçalves *et al.*, 2012; Holden *et al.*, 2016). This may explain the higher abundance, of soil bacterial communities, of half-burnt tree soils when compared with burnt tree soils. The dynamics of bacterial communities follow a pattern in the development of ecosystems. This pattern can be predicted and contextualized if, the various edaphoclimatic factors were considered (Banning *et al.*, 2011). These changes on relative abundance phyla are better described on bar graphs displaying the relative abundance of phyla (Figure 30A, C and E) or classes (Figure 31A, C and E).

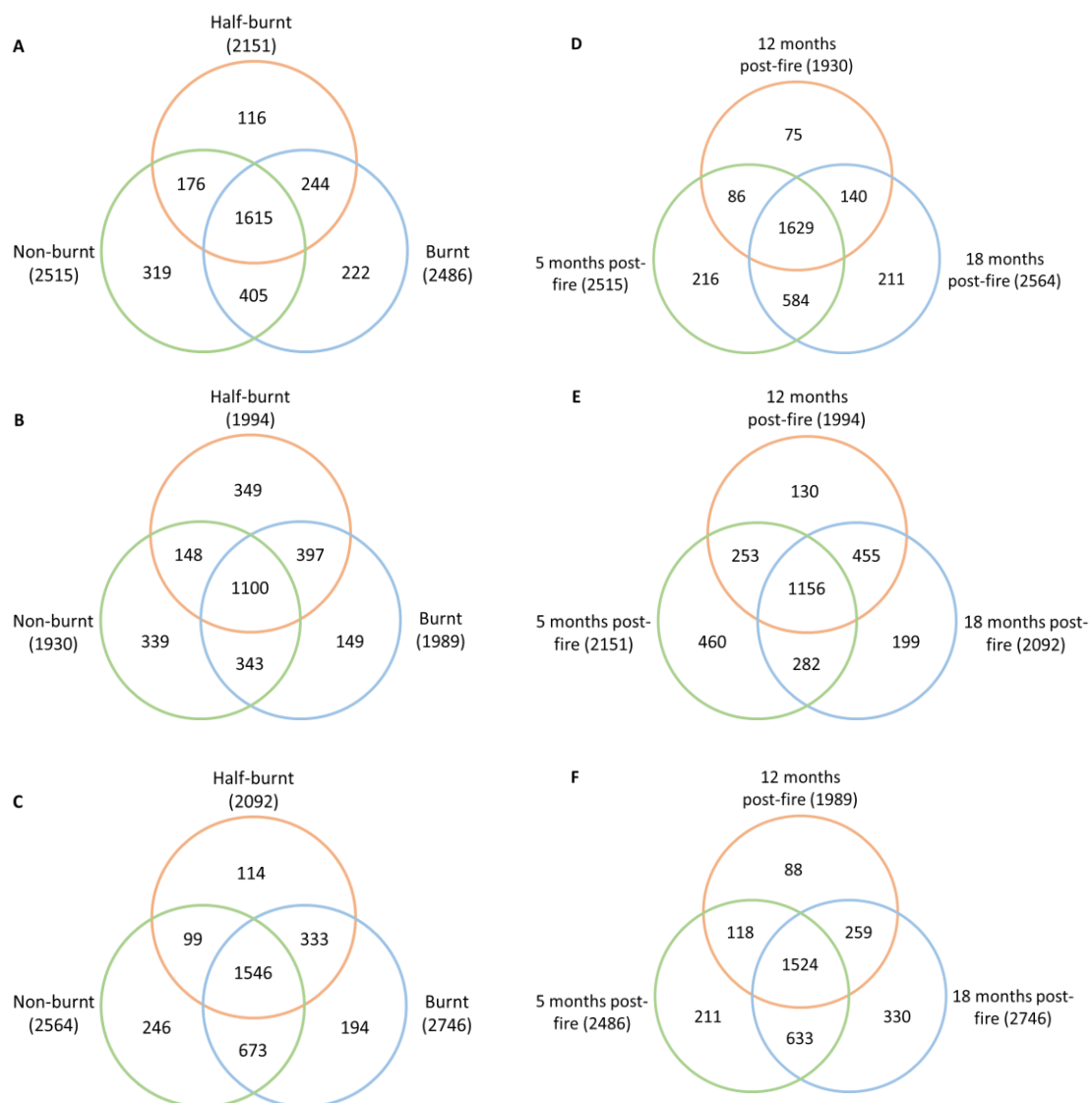


Figure 32 – Venn diagram of shared bacterial OTUs 5 months postfire (A); 12 months post-fire (B) and 18 months post-fire (C). And bacterial OTUs shared between non-burnt cork oak soil (D); half-burnt cork oak soil (E) and between burnt cork oak soils (F) is also provided. The OTUs were classified up to genus level (97 % identity) and represent total of 3354 genus. OTUs number identified in each sample are in parentheses.

The number of OTUs shared between the different types of trees depending on time period is variable (Annex 17). At 5 months post-fire from the 3.354 OTUs identified, 319 belonged only to non-burnt tree soils, 222 belonged to burnt tree soils and 116 to half-burnt tree soils (Figure 32A). Seven months later (12 months after fire), the number of OTUs exclusive to each type of soil, increases to 339, 149 and 349 respectively (Figure 32B). Throughout recovery time, the structure of the bacterial communities becomes similar (Banning *et al.*, 2011; Xiang *et al.*, 2014). However, 18 months after fire occurrence, the number of shared OTUs increases, promoting a decrease on exclusive OTUs to 246, 194 and 114 respectively (Figure 32C). However, these values are higher than those found for cork oak soils 5 months after the forest fire. Therefore, it was possible to evaluate the number of OTUs unique to each type of tree (Figure 32D, E and F).

3.3.4.1. Bacterial diversity

Bacterial diversity was assessed by plotting rarefaction curves (Figure 33) and also by determining different diversity parameters. Rarefaction curves revealed greater microbial diversity after 18 months and lowest 12 months after fire occurrence. Cork oak soils provided from non-burnt trees are the ones with higher diversity, followed by burnt trees soils and half-burnt soils. As a plateau was reached in all curves, we can infer that the analysed bacterial communities are well represented. *Richness* (S) was estimated by the number of different OTUs observed in the sample. However, this parameter may underestimate the real richness of a certain environment as few species may not be detected (Gotelli & Coldwell, 2011; Calle, 2019). Therefore, different diversity indices were used for depicting diversity of microbial communities, such as *Simpson* ($1-D$), *Shannon* (H'), or *Fisher_alpha* (Table 18). Both the rarefaction curves and diversity parameters indicated that diversity on cork oak (non-burnt tree soils) studied forest is higher 18 months post-fire, followed by 5- and then 12-months post-fire. Due to an increase of environmental temperatures on April 2019 (Spring). Also, a decrease in microbial diversity is observed for 50% damaged cork oak soils. Although it increases with fire intensity (burnt cork oak soils). Furthermore, the homogeneity of communities, as evaluated by *Equitability index* (J), decreases during the first 12 months post-fire, indicating a high dominance of few species within the community in relation to others, but increases after 18 months.

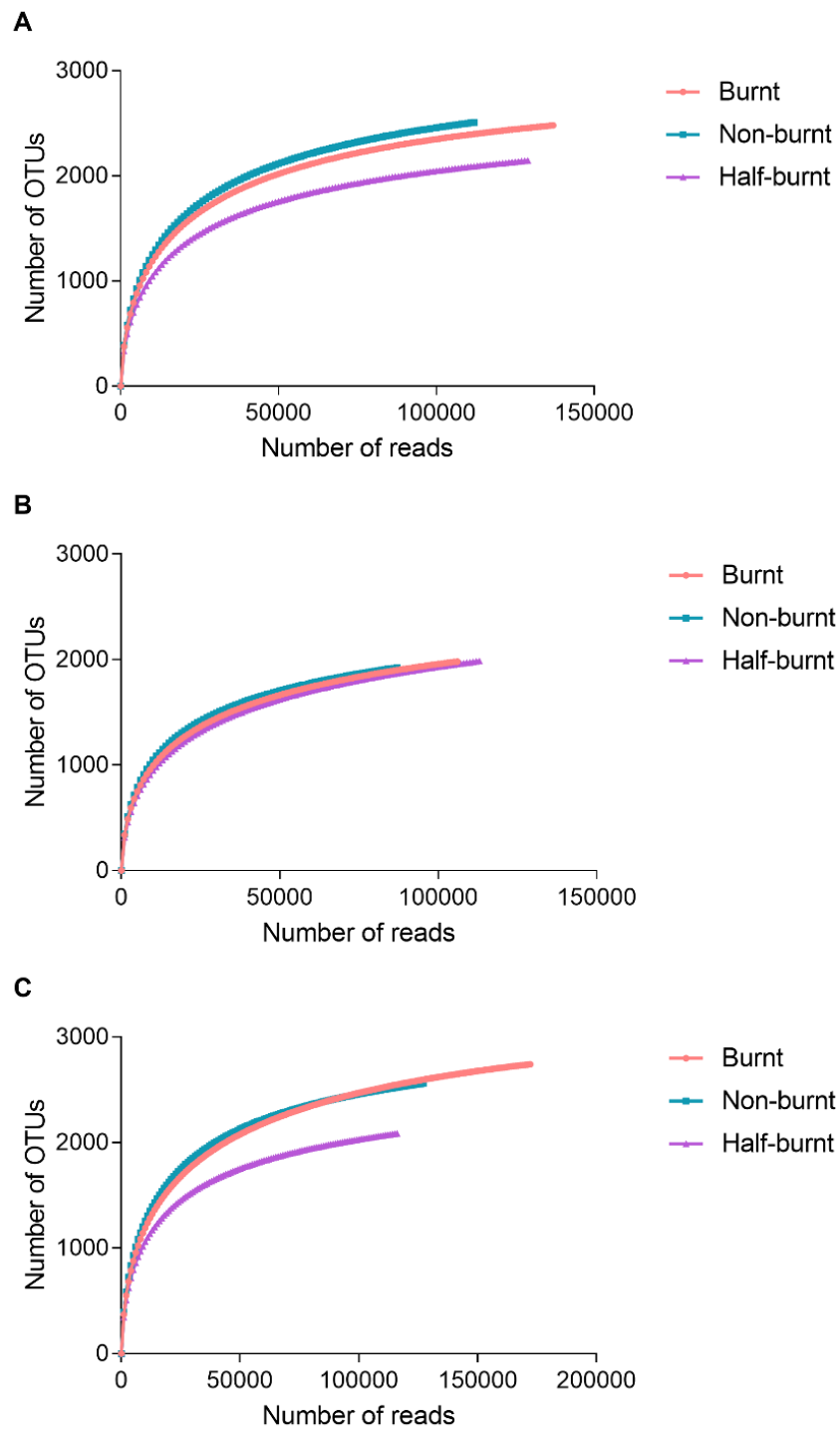


Figure 33 – Rarefaction curves for bacterial community (number of OTUs) at 97 % identity. Samples came from A – 5 months post-fire; B – 12 months post-fire and 18 months post-fire (C). Rarefaction curves were obtained at *Past5 software v3.26* (Hammer, 2019) and plotted in *GraphPad Prism 7.04*

Table 18 - Diversity parameters for cork oak soil samples harvested 5-, 12- and 18-months post-fire at *Santa Marta das Cortiças*. S – OTUs number.

Time post-fire	Tree damage	S	Simpson (1-D)	Shannon (H')	Equitability index (J)	Fisher_alpha
5 months (March 2018)	Non-burnt	2514	0.9907	5.882	0.7512	455.5
	Half-burnt	2151	0.9863	5.513	0.7184	365.7
	Burnt	2486	0.9922	5.886	0.7528	430.1
12 months (October 2018)	Non-burnt	1930	0.9863	5.567	0.7359	348.2
	Half-burnt	1994	0.9904	5.548	0.7302	342.7
	Burnt	1989	0.9899	5.639	0.7424	346.3
18 months (April 2019)	Non-burnt	2564	0.9905	5.895	0.751	454.1
	Half-burnt	2092	0.9909	5.683	0.7433	361.4
	Burnt	2746	0.9921	5.862	0.7404	463.3

3.4. Conclusions

The results revealed that during the experiment there were not great changes on the bacterial communities present on cork oak soils that were not affected by the fire. In addition, slight variations for half- and burnt tree soils were found. These variations are due to the ecological succession occurring on the soil of *Santa Marta das Cortiças*. This succession is characterized, in this case, by the restoration of soil microbial communities.

However, among the most abundant phyla in the soils of unburned trees were *Proteobacteria*, *Acidobacteria* and *Actinobacteria*. Over time, these phyla revealed seasonal changes. For example, lower environmental temperatures (during the winter up to March) increased *Actinobacteria* abundance on soil samples not affected by wildfire. But higher environmental temperatures increased the abundance of *Acidobacteria* (Spring). These results indicate that bacterial communities are influenced by edaphoclimatic factors.

Half-burnt cork oak soils had a greater OTU abundance than burnt oak soils throughout recovery time. This variation may also be explained by soil chemical composition, present on burnt cork oak soils. Such soils displayed a high content of phosphorus, which is a limiting factor for bacterial (*Proteobacteria* and *Actinobacteria*) expansion (Zeng *et al.*, 2016). Soil acidity also influences the presence of some bacterial communities on soils (*Acidobacteria*). Also, some bacteria prefer poor soils than nutrient rich soils.

3.5. Bibliography

- Abarenkov K, Nilsson RH, Larsson K, Alexander IJ, Eberhardt U, Erland S, Høiland K, Kjølter R, Larsson E, Pennanen T, *et al.* 2010. The UNITE database for molecular identification of fungi – recent updates and future perspectives. *New Phytologist* 35.
- Albanese D, Fontana P, De Filippo C, Cavalieri D, Donati C. 2015. MICCA: A complete and accurate software for taxonomic profiling of metagenomic data. *Scientific Reports* 5: 1–7.
- Allison SD, Martiny JBH. 2009. Resistance, resilience, and redundancy in microbial communities. *In the Light of Evolution* 2: 149–166.
- Altun L, Bilgili E, Sağlam B, Küçük Ö, Yılmaz M, Tüfekçioğlu A. 2004. Soil organic matter , soil pH and soil nutrient dynamics in forest stands after fire. In: Natural Resource Management for Sustainable Development. International Soil Conference, 10.
- Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. *Babraham Institute*.
- Aronesty E. 2013. Comparison of Sequencing Utility Programs. *The Open Bioinformatics Journal* 7: 1–8.
- Bach EM, Baer SG, Meyer CK, Six J. 2010. Soil texture affects soil microbial and structural recovery during grassland restoration. *Soil Biology and Biochemistry* 42: 2182–2191.
- Baho DL, Peter H, Tranvik LJ. 2012. Resistance and resilience of microbial communities - Temporal and spatial insurance against perturbations. *Environmental Microbiology* 14: 2283–2292.
- Baldwin BG, Sanderson MJ, Porter JM, Wojciechowski MF, Campbell CS, Donoghue MJ. 1995. The its Region of Nuclear Ribosomal DNA: A Valuable Source of Evidence on Angiosperm Phylogeny. *Annals of the Missouri Botanical Garden* 82: 247.
- Banning NC, Gleeson DB, Grigg AH, Grant CD, Andersen GL, Brodie EL, Murphy D V. 2011. Soil microbial community successional patterns during forest ecosystem restoration. *Applied and Environmental Microbiology* 77: 6158–6164.
- Beckers B, Beeck M Op De, Thijs S, Truyens S, Weyens N. 2016. Performance of 16s rDNA Primer Pairs in the Study of Rhizosphere and Endosphere Bacterial Microbiomes in Metabarcoding Studies Study Site Description and Sampling. 7.
- Bento-Gonçalves A, Vieira A, Úbeda X, Martin D. 2012. Fire and soils: Key concepts and recent advances. *Geoderma* 191: 3–13.
- Calle ML. 2019. Statistical Analysis of Metagenomics Data. *Genomics & Informatics* 17: e6.
- Caporaso JG, Kuczynski J, Stombaugh J, Bittinger K, Bushman FD, Costello EK, Fierer N, Peña AG, Goodrich JK, Gordon JI, *et al.* 2010. QIIME allows analysis of high-throughput community sequencing data. *Nature methods* 7: 335–6.
- Certini G. 2005. Effects of fire on properties of forest soils: A review. *Oecologia* 143: 1–10.
- Das S, Dash HR, Mangwani N, Chakraborty J, Kumari S. 2014. Understanding molecular identification and polyphasic taxonomic approaches for genetic relatedness and phylogenetic relationships of microorganisms. *Journal of Microbiological Methods* 103: 80–100.
- Degnan PH, Ochman H. 2012. Illumina-based analysis of microbial community diversity. *ISME Journal* 6: 183–194.
- Edgar RC. 2013. UPARSE: Highly accurate OTU sequences from microbial amplicon reads. *Nature Methods* 10: 996–998.
- Edgar RC, Flyvbjerg H. 2015. Error filtering, pair assembly and error correction for next-generation sequencing reads. *Bioinformatics* 31: 3476–3482.
- Fajarningsih ND. 2016. Internal Transcribed Spacer (ITS) as Dna Barcoding to Identify Fungal Species: a Review. *Squalen Bulletin of Marine and Fisheries Postharvest and Biotechnology* 11: 37.
- Ghosh A, Mehta A, Khan AM. 2019. Metagenomic Analysis and its Applications. In: Encyclopedia of Bioinformatics and Computational Biology. Elsevier, 184–193.
- Ginzburg O, Steinberger Y. 2012. Effects of forest wildfire on soil microbial-community activity and chemical components on a temporal-seasonal scale. *Plant and Soil* 360: 243–257.
- Glöckner FO, Yılmaz P, Quast C, Gerken J, Beccati A, Ciuprina A, Bruns G, Yarza P, Peplies J, Westram R, *et al.* 2017. 25 years of serving the community with ribosomal RNA gene reference databases and tools. *Journal of Biotechnology* 261: 169–176.
- Gotelli NJ, Coldwell RK. 2011. Estimating species richness. In: Biological diversity: frontiers in measurement

and assessment. 39–54.

Granged AJ, Zavala LM, Jordán A, Bárcenas-Moreno G. 2011. Post-fire evolution of soil properties and vegetation cover in a Mediterranean heathland after experimental burning: A 3-year study. *Geoderma* **164**: 85–94.

Guerrero C, Mataix-Solera J, Gómez I, García-Orenes F, Jordán MM. 2005. Microbial recolonization and chemical changes in a soil heated at different temperatures. *International Journal of Wildland Fire* **14**: 385–400.

Hamman ST, Burke IC, Stromberger ME. 2007. Relationships between microbial community structure and soil environmental conditions in a recently burned system. *Soil Biology and Biochemistry* **39**: 1703–1711.

Hammer Ø. 2019. Manual Past 3.25.

Hernández M, Calabi Ma, Conrad R, Dumont MG. 2020. Analysis of the microbial communities in soils of different ages following volcanic eruptions. *Pedosphere* **30**: 126–134.

Holden SR, Rogers BM, Treseder KK, Randerson JT. 2016. Fire severity influences the response of soil microbes to a boreal forest fire. *Environmental Research Letters* **11**.

Illumina I. 2017. An introduction to Next-Generation Sequencing Technology. : 1–16.

Janda JM, Abbott SL. 2007. 16S rRNA gene sequencing for bacterial identification in the diagnostic laboratory: Pluses, perils, and pitfalls. *Journal of Clinical Microbiology* **45**: 2761–2764.

Jo JH, Kennedy EA, Kong HH. 2016. Research Techniques Made Simple: Bacterial 16S Ribosomal RNA Gene Sequencing in Cutaneous Research. *Journal of Investigative Dermatology* **136**: e23–e27.

Joshi NA, Fass JN. 2011. Sickel: A sliding-window, adaptive, quality-based trimming tool for FastQ files. (Version 1.33) [Software]. Available at <https://github.com/najoshi/sickle>.

Kim M, Chun J. 2014. 16S rRNA gene-based identification of bacteria and archaea using the EzTaxon server. In: *Methods in Microbiology*. Elsevier Ltd., 61–74.

King GM, Weber CF. 2007. Distribution, diversity and ecology of aerobic CO-oxidizing bacteria. *Nature Reviews Microbiology* **5**: 107–118.

Kirk JL, Beaudette L a, Hart M, Moutoglou P, Klironomos JN, Lee H, Trevors JT. 2004. Methods of studying soil microbial diversity. *Journal of Microbiological Methods* **58**: 169–188.

Kowalska Z, Pniewski F, Latała A. 2019. DNA barcoding – A new device in phycologist's toolbox. *Ecology and Hydrobiology*. 1–11.

Letchuman S, Cosmecuticals O. 2018. Short Introduction of DNA Barcoding. *International Journal of Research* **05**: 673–686.

Mardis ER. 2008. The impact of next-generation sequencing technology on genetics. *Trends in Genetics* **24**: 133–141.

Mataix-Solera J, Cerdà A, Arcenegui V, Jordán A, Zavala LM. 2011. Fire effects on soil aggregation: A review. *Earth-Science Reviews* **109**: 44–60.

Matallana-Surget S, Jagtap PD, Griffin TJ, Beraud M, Wattiez R. 2018. *Comparative Metaproteomics to Study Environmental Changes*. Elsevier Inc.

Mataragas M, Alessandria V, Ferrocino I, Rantsiou K, Coccolin L. 2018. A bioinformatics pipeline integrating predictive metagenomics profiling for the analysis of 16S rDNA/rRNA sequencing data originated from foods. *Food Microbiology* **76**: 279–286.

Naidoo K, Steenkamp ET, Coetzee MPA, Wingfield MJ, Wingfield BD. 2013. Concerted Evolution in the Ribosomal RNA Cistron. *PLOS ONE* **8**.

Nikolenko SI, Korobeynikov AI, Alekseyev MA. 2013. BayesHammer: Bayesian clustering for error correction in single-cell sequencing. *BMC Genomics* **14**.

Nilsson RH, Ryberg M, Abarenkov K, Sjökvist E, Kristiansson E. 2009. The ITS region as a target for characterization of fungal communities using emerging sequencing technologies. *FEMS Microbiology Letters* **296**: 97–101.

Parraa JG, Lopeza TI. 1996. in *Soils Affected By a Forest Fire*. *Environment* **181**: 231–236.

Prijbelski AD, Korobeynikov AI, Lapidus AL. 2019. Sequence Analysis. In: *Encyclopedia of Bioinformatics and Computational Biology*. Elsevier, 292–322.

Pyro VS, Roesch LFW, Morais DK, Clark IM, Hirsch PR, Tótola MR. 2014. Data analysis for 16S microbial profiling from different benchtop sequencing platforms. *Journal of Microbiological Methods* **107**: 30–37.

Quast C, Pruesse E, Yilmaz P, Gerken J, Schweer T, Yarza P, Peplies J, Glöckner FO. 2013. The SILVA

ribosomal RNA gene database project: Improved data processing and web-based tools. *Nucleic Acids Research* **41**: 590–596.

Rocha R, Almeida C, Azevedo F. 2015. Metodologias para a identificação de microrganismos patogênicos em amostras alimentares : a técnica de PNA-FISH. *Universidade do Minho, Campus de Gualtar*. 38–40.

De Sá PHCG, Guimarães LC, das Graças DA, de Oliveira Veras AA, Barh D, Azevedo V, da Costa da Silva AL, Ramos RTJ. 2018. Next-generation sequencing and data analysis: Strategies, tools, pipelines and protocols. *Omics Technologies and Bio-engineering: Towards Improving Quality of Life* **1**: 191–207.

Sadaipappan B, Kannan S, Palaniappan S, Manikkam R, Ramasamy B, Anilkumar N, Subramanian M. 2020. Metagenomic 16S rDNA amplicon data of microbial diversity and its predicted metabolic functions in the Southern Ocean (Antarctic). *Data in Brief* **28**: 104876.

Schmieder R, Edwards R. 2011. Quality control and preprocessing of metagenomic datasets. *Bioinformatics* **27**: 863–864.

Schoch CL, Seifert KA, Huhndorf S, Robert V, Spouge JL, Levesque CA, Chen W, Bolchacova E, Voigt K, Crous PW, *et al.* 2012. Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. *Proceedings of the National Academy of Sciences* **109**: 6241–6246.

Soh J, Dong X, Caffrey SM, Voordouw G, Sensen CW. 2013. Phoenix 2: A locally installable large-scale 16S rRNA gene sequence analysis pipeline with Web interface. *Journal of Biotechnology* **167**: 393–403.

Strickland MS, Rousk J. 2010. Considering fungal: Bacterial dominance in soils - Methods, controls, and ecosystem implications. *Soil Biology and Biochemistry* **42**: 1385–1395.

Tedersoo L, Sánchez-Ramírez S, Kõljalg U, Bahram M, Döring M, Schigel D, May T, Ryberg M, Abarenkov K. 2018. High-level classification of the Fungi and a tool for evolutionary ecological analyses. *Fungal Diversity* **90**: 135–159.

Torres E. 2008. Cork Oak Woodlands on the Edge: Ecology, Adaptive Management, and Restoration. *Restoration Ecology* **18**: 615–617.

Tresbach RH, Cerqueira NM, Medeiros SR, Gutierrez HJP, Hernández NO, Rodrigues MDN. 2015. DNA Barcoding: Uma Ferramenta de Apoio Molecular para Identificação de Espécies de Peixes. *Scientia Agraria Paranaensis* **14**: 77–81.

Wang Y, Qian PY. 2009. Conservative fragments in bacterial 16S rRNA genes and primer design for 16S ribosomal DNA amplicons in metagenomic studies. *PLoS ONE* **4**.

Weber CF, King GM. 2010. Quantification of Burkholderia coxL Genes in Hawaiian Volcanic Deposits. *Applied and Environmental Microbiology* **76**: 2212–2217.

Wilson J-J, Sing K-W, Jaturas N. 2019. DNA Barcoding: Bioinformatics Workflows for Beginners. *Encyclopedia of Bioinformatics and Computational Biology*: 985–995.

Woo PCY, Lau SKP, Teng JLL, Tse H, Yuen K-Y. 2008. Then and now: use of 16S rDNA gene sequencing for bacterial identification and discovery of novel bacteria in clinical microbiology laboratories. *Clinical Microbiology and Infection* **14**: 908–934.

Xiang X, Shi Y, Yang J, Kong J, Lin X, Zhang H, Zeng J, Chu H. 2014. Rapid recovery of soil bacterial communities after wildfire in a Chinese boreal forest. *Scientific Reports* **4**: 1–8.

Yilmaz P, Parfrey LW, Yarza P, Gerken J, Priesse E, Quast C, Schweer T, Peplies J, Ludwig W, Glöckner FO. 2014. The SILVA and ‘all-species Living Tree Project (LTP)’ taxonomic frameworks. *Nucleic Acids Research* **42**: 643–648.

Zeng Q, Dong Y, An S. 2016. Bacterial community responses to soils along a latitudinal and vegetation gradient on the Loess Plateau, China. *PLoS ONE* **11**: 1–17.

Zhang C, Liu G, Xue S, Wang G. 2016. Soil bacterial community dynamics reflect changes in plant community and soil properties during the secondary succession of abandoned farmland in the Loess Plateau. *Soil Biology and Biochemistry* **97**: 40–49.

Zhang W, Qiao W, Gao D, Dai Y, Deng J, Yang G, Han X, Ren G. 2018. Relationship between soil nutrient properties and biological activities along a restoration chronosequence of Pinus tabulaeformis plantation forests in the Ziwuling Mountains, China. *Catena* **161**: 85–95.

Chapter 4: Final conclusions and Future perspectives

The analysis of the soil microbiome of *Santa Marta das Cortiças* performed in this work reveals that edaphoclimatic factors present when collecting the samples and to which the bacteria were subjected after the forest fire (rains, winds, solar radiation, etc.) should be considered. Since the development of *Bacillus spp* is enhanced by increased heat (results from chapter 2), a greater abundance of *Firmicutes* in soil samples affected by the forest fire of *Santa Marta das Cortiças* (half- and burnt tree soils) would be expected. However, what was found, was the highest incidence of gram-negative bacteria (*Proteobacteria*), followed by others, such as *Acidobacteria*, *Actinobacteria* and *Chloroflexi*. *Firmicutes* phyla was present in abundance values <3% in all soil samples except for non-burnt tree soils. This is could be to the possibility of some *Proteobacteria* (as *Burkholderia*) and *Actinobacteria*, be able to oxidize carbon monoxide (CO), to carbon dioxide (CO₂), under conditions of CO <1000ppm (King & Weber, 2007; Hernández *et al.*, 2020). This mechanism is used due the presence of CO, provided from organic matter combustion at the wildfire (Zhang *et al.*, 2018). Because Oak forests fires can reach 300°C to 700°C (Ginzburg & Steinberger, 2012). In addition, studies revealed that a high number of *coxL* genes copies (encodes CO dehydrogenase) contributes to the expansion of CO oxidizing microbial communities during biological succession (Weber & King, 2010). Nevertheless, a deeper study, on bacterial genes (metaproteomic approach) should be performed to realize which genes were most (in)active on bacterial soil communities from *Santa Marta das Cortiças*.

There were no higher variations on soil bacterial communities through time (richness), but in order to see those differences, soil sampling should be carried out sooner, perhaps 1 week or month post-fire. This soil harvest, closer to the event of forest disturbance (fire), would bring higher variations in the composition of the soil bacterial communities analyzed, as well as in the abundance between them. Also, differentiating sharply according to the damage that fire caused to cork oaks of *Santa Marta das Cortiças*, and along forest recovery time.

For future perspectives, the establishment of a direct relationship between the physical conditions of the trees and soil microbiome could be also performed, for understanding the influence of microbial communities on plant status post-fire. Thus, a metabarcoding analysis on fungal communities, present on *Santa Marta das Cortiças* forest, could also be carried out. In addition, a metaproteomic approach, possibly, would provide knowledge about interactions that exist between fungal and bacterial communities. Plus, this approach could also lead to a undersanding of soil microbial communities' relationship between cork oak trees.

Annex

Annex 1 – Quantification of soil DNA, extracted from the selected 14 bacterial morphotypes at 125°C. Ratios $A_{260\text{ nm}}/A_{280\text{ nm}}$ and $A_{260\text{ nm}}/A_{230\text{ nm}}$ are also provided.

Bacteria	ng/ μL	$A_{260\text{ nm}}/A_{280\text{ nm}}$	$A_{260\text{ nm}}/A_{230\text{ nm}}$
B1	19.5	2.54	1.14
B2	32.9	2.26	1.15
B3	46.6	2.09	0.83
B4	25.8	2.00	1.90
B5	31.4	1.83	0.77
B6	13.9	1.95	0.96
B7	20.7	1.81	0.73
B8	40.3	1.71	1.41
B9	16.0	1.82	1.63
B10	11.5	1.59	1.40
B11	41.4	1.69	1.37
B12	20.3	1.82	1.86
B13	34.5	1.76	0.85
B14	39.2	1.64	0.72

Annex 2 – Obtained sequences of the selected 14 bacterial morphotypes at 125°C. Bacterial identification was performed through 16S amplicom.

>B1

NNNNN

>B2

CCCCATTATGACCTGGGCTACACACGTGCTACAATGGACGGTACAAAGAGCTGCAAGACCGCGAGGTGGAGCTAA
TCTCATAAAACCGTTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGCTGGAATCGTAGTAATCGCG
GATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAAACAC
CCGAAGTCGGTGGGTAACCTTTATGGAGCCAGCCGCCTAAGGTGGGACAGATGATTGGGGTGAAGTCGTAACAA
GGTAACCGTAAAGG

>B3

AGTCGGGTCAATCATCATCGCCCCTTATGCCCTGCGCTCTCACGTGCTACAATGTCCCGTACTATGAGCTGCGGG
CGCGAGGTGGAGCTAATCTCATACACCGTTCTCGTTTCGGCTTGTAGGCTGCGACTCGCCTTCTTGGTGCTGGA
ATCGTAGTTATCGCGGATCCGCATGCCGCGGTGATTACGTTCCCGGGCCTTGTACCCCCGCCCCGTCTCTCCT
CGCAGCGTTTGTACCACCGAGTCGGTGGGGTATCCTTTGTGGGGCCCGCCGCTTGGTGGGGCAGTTCGATTG
GGGTGAACGTCGTTAACGGGTATCCGTAAAC

>B4

ATCATCATGCCCTTATGACCTGGGCTACACACGTGCTACAATGGATGGTACAAAGGGCTGCAAGACCGCGAGGT
CAAGCCAATCCCATAAAACCATTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGCTGGAATCGCTAG
TAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTT

TGTAACACCCGAAGTCGGTGGAGTAACCGTAAGGAGCTAGCCGCCTAAGGTGGGACAGATGATTGGGGTGTAGA
GTCCTAACAAAGGTGATACCGTAAATT

>B5

TCATCATGCCCCCTTATGACCTGGGCTACACACGTGCTACAATGGACGGTACAAAGAGCTGCAAGACCGCGAGGTG
GAGCTAATCTCATAAAACCGTTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGCTGGAATCGCTAGTA
ATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTG
TAACACCCGAAGTCGGTGGGGTAACCTTTATGGAGCCAGCCGCCTAAGGTGGGACAGATGATTGGGGTGAAGTC
GTAACAAGTGAATCCGTATATT

>B6

AATCTCTGCCCCCTTATGACCTGGGCTACACACGTGCTACAATGGACGGTACAAAGAGCTGCAAGACCGCGAGGTG
GAGCTAATCTCATAAAACCGTTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGCTGGAATCGCTAGTA
ATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTG
TAACACCCGAAGTCGGTGGGGTAACCTTTATGGAGCCAGCCGCCTAAGGTGGGACAGATGATTGGGGTGAAGTC
GTAACAAGTGAATCCGTATAACC

>B7

TCATCATGCCCCCTTATGACCTGGGCTACACACGTGCTACAATGGACGGTACAAAGAGCTGCAAGACCGCGAGGTG
GAGCTAATCTCATAAAACCGTTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGCTGGAATCGCTAGTA
ATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTG
TAACACCCGAAGTCGGTGGGGTAACCTTTATGGAGCCAGCCGCCTAAGGTGGGACAGATGATTGGGGTGAAGTC
GTAACAAGTGAACCGTAAAC

>B8

ATGCCCCCTTATGACCTGGGCTAAACGTGCTACAATGGATGGTGTGAGAGCTGCAAGTGTGTGAGGTGGAGCTAA
TCTCTTCACCCGTTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTCCTTGGGCTGGAATCGCTAGTTTCGCGGAT
CAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAAACCCCG
AAGTCGGTGGGGTAACCTTTATGGAGCCAGCCGCCTAAGGTGGGACAGATGATTGGGGTGAAGTCGTAACAAGGT
AATCCGTAAAAA

>B9

GTCAATCATCATGCCCCCTTATGACCTGGGCTACACACGTGCTACAATGGACGGTACAAAGAGCTGCAAAACCGCG
AGGTGGAGCTAATCTCATAAAACCGTTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGCTGGAATCG
CTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAG
AGTTTGTAAACCCGAAGTCGGTGAAGTAACCTTTATGGAGCCAGCCGCCTAAGGTGGGACAGATGATTGGGGTGA
AAGTCGTAACAAGGTAACCGTAAAG

>B10

AAGTCATCGTGCATGCTTATGACCTGAGCCTGCTCACGTTGCTACGATGGCACC GCACACAGGAGATGCGTTAC
CGCCTAGGAGGAGCTCATCACGCAAAACGAATGAGGTGTAGAAGTGCATTCTCATACTCCGCCTACATGAAGCTC
CGAATCTGTAAATACATCGACAAATCAGCTCTAGCGAAATTCGAATACTTATCGCGGGACCTGTACACTGCCGCG
CCTGTGCAACAACCAGCGACAGTTTAGTAACGGACGCTGTCACGTGGGGTAACATGTGATGCTTCCAGCATAACT
AAGGGTGTGCACTTATGAATGATGCGAATTTGTAACGTCGTGTTTCAATACTCTGTAGGCTTTGACAGCCCTTGCA
TTCGACAGCAGGGTATGGAAGCCGGCCCGCACCGCTTCTTGAATAACGTAACGATTGGGGTAGTCGAAAGTCGTA
ACAAGGTAACCGTAAT

>B11

TCATCATGCCCCCTTATGACCTGGGCTACACACGTGCTACAATGGACAGAACAAAGGGCAGCGAAACCGCGAGGT
AAGCCAATCCACAAATCTGTTCTCAGTTCGGATCGAGTCTGCAACTCGACTGCGTGAAGCTGGAATCGCTAGT
AATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTT

GTAACACCCGAAGTCGGTGAGGTAACCTTTTAGGAGCCAGCCGCCGAAGGTGGGACAGATGATTGGGGTGAAGT
CGTAACAAGGTAACCGTAAAAG

>B12

CCGTGCTACAATGGACGGTACAATAGCTGCAAGACCGCGAGGGGGGAGCTAATCTCATAAAACCGTTCTCAGTTCTG
GATTGTAGGCTGCAACTCCCCTACATGAATCTGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACG
TTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAAACACCCGAAGTCGGTGGGGTAACCTTTAT
GGAGCCAGCCNCCTAAGGTGGGACAGATGATTGGGGTGAAGTCGTAACAAGGNAACCGTAANC

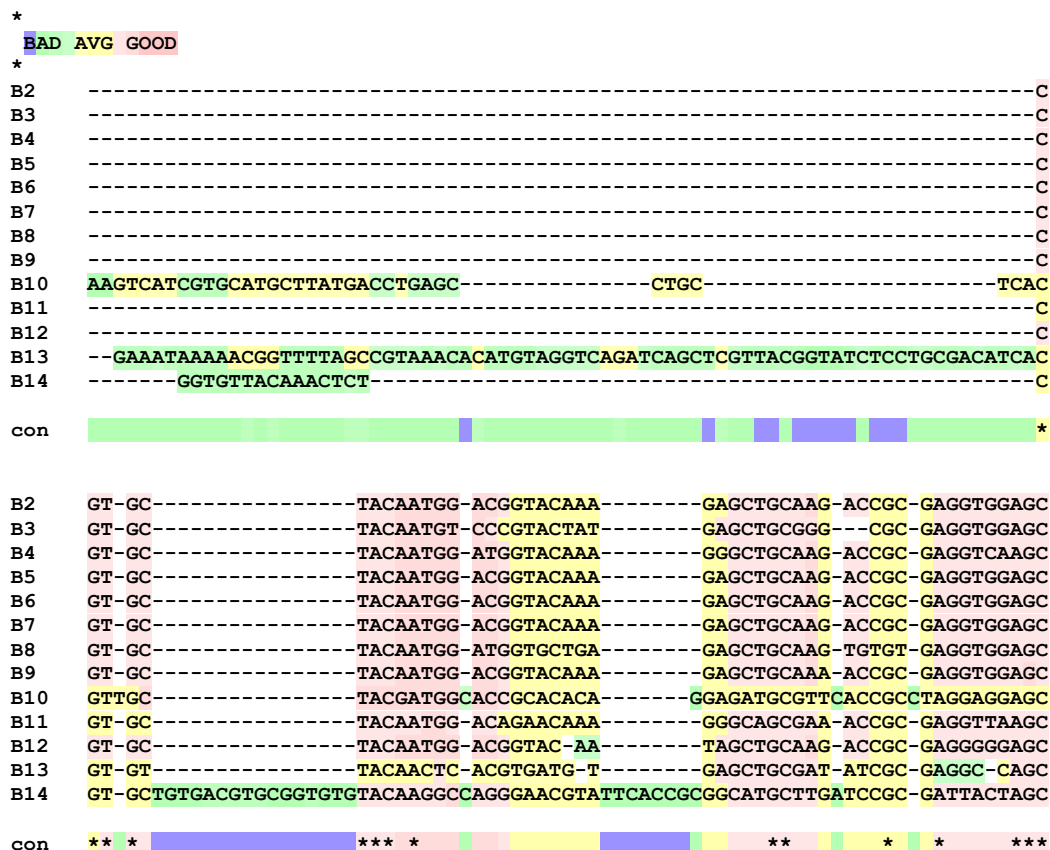
>B13

GAAATAAAACGGTTTTAGCCGTAAACACATGTAGGTCAGATCAGCTCGTTACGGTATCTCCTGCGACATCACGTG
TTACAACTCACGTGATGTGAGCTGCGATATCGCGAGGCCAGCCAATCTCTTCACAGCGTTCTGAGGTCGCACTGT
AACCAGCAATTCGAGCACCTTATACTCGAATCGCTACCAATCGTGCATCCTCATGATGCGTTGAATACATTGGCTT
GACTTGTAGATCTTGCAGGTCTTTGCACCATAGATTGTAACACGCGAAGTCGGTGGAGTATCCGTAGCGTGCTAA
CTTCCACGACGTGGCCACAGCATGATTCGCGGGTGTAGAGCTCCTAACAAGGTATACCGTAAAAC

>B14

GTAGGGAGAGACCCATTAGGCGGCTGGCTCCGAAAAGGTATAGCACCCAGCCGACATTGGGGTGTACAACT
CTCGTGCTGTGACGTGCGGTGTGTACAAGGCCAGGGAACGTATTCACCGCGGCATGCTTGATCCGCGATTACTAG
CGATTCCAGCTTCATGTAGGCGAGTTGCAGCCTACAATCCGAAGTGAAGACGGTTTTATGAGATTAGCTCCACCT
CGCGGTCTTGAGCTCTTTGTACCGTCCATTGTAGCACGTGTGTAGCCAGGTGATAAGGGGCATGATGATTGA
CGTCATCCCACCTTCTCTCGGTGTTGATCGACCGGACCGGATGGTATCTAAAAC

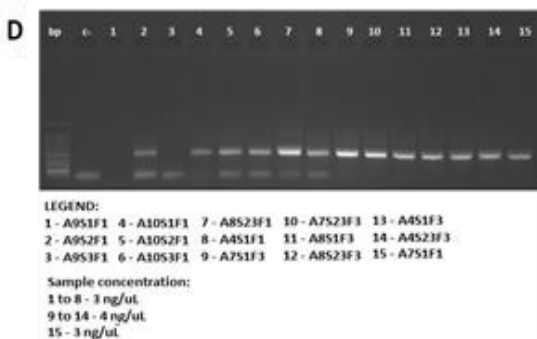
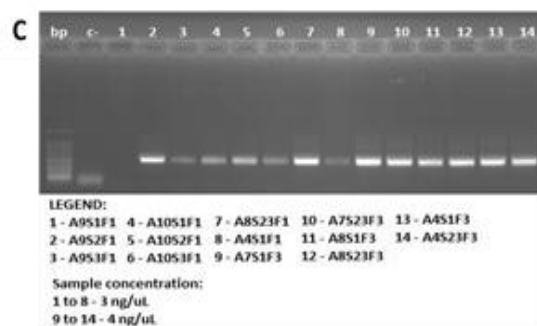
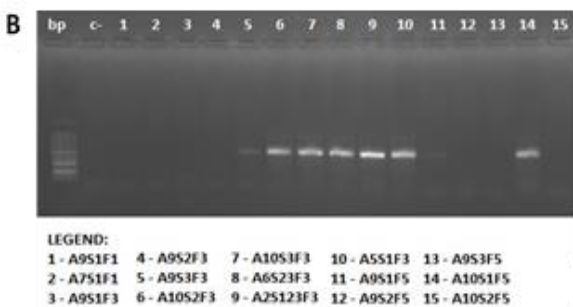
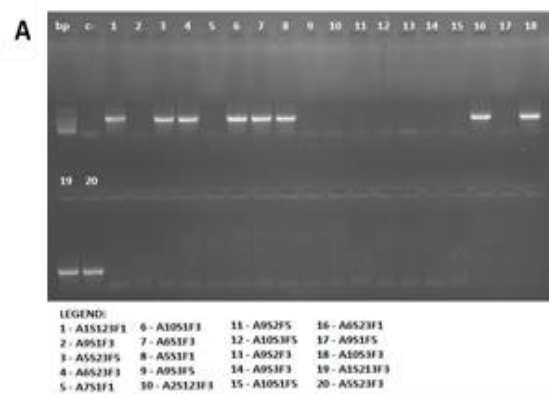
Annex 3 – *T-COFFEE*, Version_11.00.d625267 multiple sequence alignment of the most heat resistant bacteria.



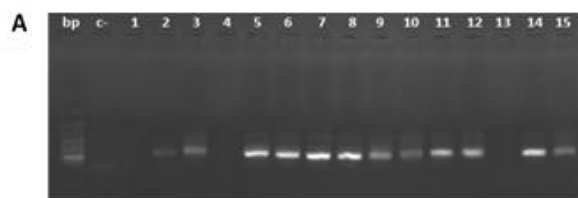
Annex 4 – Quantification of soil DNA extracted from soil samples from St^a Marta das Cortiças by nanodrop and Qubit method, for microbial communities' analysis by metabarcoding approach

Tree damage	5 months					12 months					18 months				
	Sample	nanodrop	Qubit	$A_{260\text{ nm}}/A_{280\text{ nm}}$	$A_{260\text{ nm}}/A_{230\text{ nm}}$	Sample	nanodrop	Qubit	$A_{260\text{ nm}}/A_{280\text{ nm}}$	$A_{260\text{ nm}}/A_{230\text{ nm}}$	Sample	nanodrop	Qubit	$A_{260\text{ nm}}/A_{280\text{ nm}}$	$A_{260\text{ nm}}/A_{230\text{ nm}}$
		ng / μL						ng / μL					ng / μL		
Non-burnt	A6S1F1	58.20	31.20	1.67	1.37	A6S1F3	13.60	8.60	1.54	1.04	A6S1F5	5.40	2.26	1.38	0.68
	A6S23F1	4.80	1.37	1.45	0.62	A6S23F3	23.80	17.60	1.59	1.12	A6S23F5	49.80	41.60	1.86	1.89
	A7S1F1	98.40	39.60	1.51	1.16	A7S1F3	62.40	54.40	1.80	1.65	A7S1F5	94.90	90.20	1.85	1.96
	A7S23F1	53.60	34.20	1.75	1.59	A7S23F3	56.90	42.00	1.72	1.46	A7S23F5	76.90	61.20	1.82	1.96
	A8S1F1	49.50	36.80	1.67	1.65	A8S1F3	52.60	37.00	1.64	1.55	A8S1F5	67.90	56.20	1.83	1.86
	A8S23F1	46.30	36.00	1.76	1.76	A8S23F3	54.60	60.80	1.82	1.84	A8S23F5	60.50	52.40	1.82	1.75
Half-burnt	A9S1F1	127.40	4.80	1.33	0.90	A9S1F3	24.30	12.90	1.58	1.00	A9S1F5	99.90	27.20	1.47	1.06
	A9S2F1	49.50	18.10	1.60	1.26	A9S2F3	19.40	10.00	1.59	0.97	A9S2F5	113.20	18.70	1.45	0.96
	A9S3F1	67.60	4.32	1.36	0.86	A9S3F3	38.40	24.40	1.71	1.25	A9S3F5	51.50	18.50	1.56	1.12
	A10S1F1	153.20	43.20	1.43	0.99	A10S1F3	14.40	10.10	1.60	1.07	A10S1F5	28.80	18.20	1.66	1.38
	A10S2F1	107.70	61.20	1.63	1.29	A10S2F3	11.20	6.88	1.67	0.95	A10S2F5	14.20	7.46	1.79	1.14
	A10S3F1	117.10	27.00	1.45	1.01	A10S3F3	28.10	18.60	1.56	1.21	A10S3F5	24.90	12.70	1.82	1.14
Burnt	A1S123F1	46.60	33.80	1.79	1.80	A1S123F3	22.60	18.30	1.61	1.13	A1S123F5	25.60	6.40	1.74	1.33
	A2S123F1	45.50	16.00	1.37	0.83	A2S123F3	21.50	2.94	1.41	0.94	A2S123F5	48.20	11.30	1.46	0.89
	A4S1F1	176.70	93.80	1.54	1.29	A4S1F3	53.70	49.60	1.84	2.21	A4S1F5	94.20	78.80	1.86	1.89
	A4S23F1	107.50	69.40	1.70	1.64	A4S23F3	68.70	69.40	1.83	1.97	A4S23F5	55.80	480.00	1.83	2.01
	A5S1F1	15.30	8.30	1.55	0.93	A5S1F3	14.50	10.70	1.80	1.04	A5S1F5	21.40	13.20	1.09	1.75
	A5S23F1	45.50	32.80	1.71	1.56	A5S23F3	25.70	18.80	1.70	1.35	A5S23F5	26.90	18.60	1.75	1.62

Annex 5 - Electrophoresis of 16S V3V4 region from soil samples of St^a Marta das Cortiças. DNA was extracted and used to amplify 16S V3V4 region by using the 16S V3V4FW and 16S V3V4 RV primer pair. (A, B) PCR performed on non-diluted DNA samples; (C, D, E) PCR performed on 24x DNA diluted samples; bp – 100bp plus ready-to-use DNA Ladder Bioron.

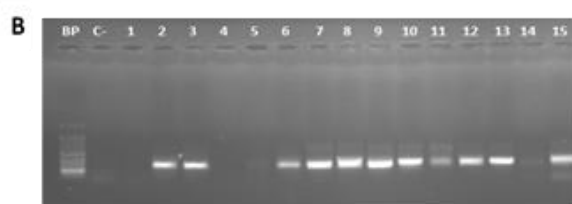


Annex 6 - Electrophoresis of ITS region from soil samples of St^a Marta das Cortiças. DNA was extracted and used to amplify ITS region by using the ITSF1 and ITS2 primer pair. (A, B, C) PCR performed on non-diluted DNA samples; (D, F, E) PCR performed on 24x DNA diluted samples; bp – 100bp plus ready-to-use DNA Ladder Bioron



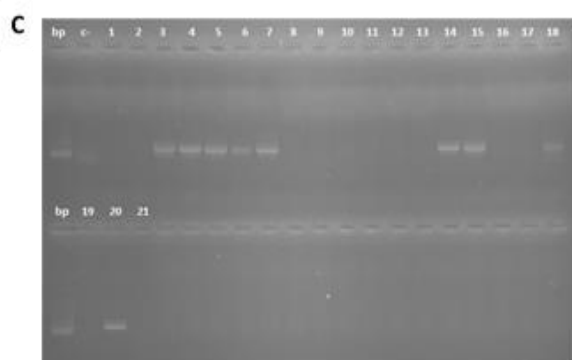
LEGEND:

1 - A9S1F1 4 - A9S1F3 7 - A10S1F3 10 - A6S1F3 13 - A2S123F3
2 - A5S1F1 5 - A9S2F3 8 - A10S2F3 11 - A6S23F3 14 - A5S1F3
3 - A6S23F1 6 - A9S3F3 9 - A10S3F3 12 - A1S123F3 15 - A5S23F3



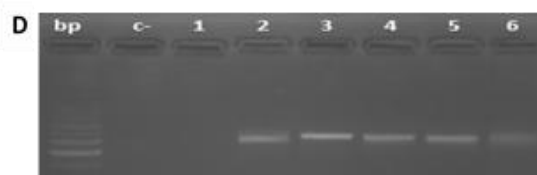
LEGEND:

1 - A10S3F1 4 - A9S1F5 7 - A10S1F5 10 - A7S23F5 13 - A4S1F5
2 - A9S1F3 5 - A9S2F5 8 - A10S2F3 11 - A8S1F5 14 - A9S1F1
3 - A2S123F3 6 - A9S3F5 9 - A10S3F5 12 - A2S123F5 15 - A9S1F1_A



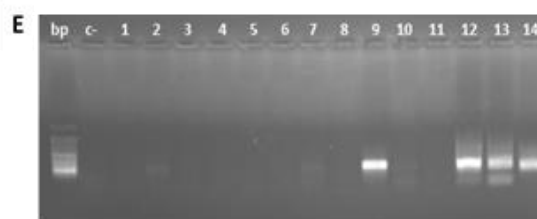
LEGEND:

1 - A9S2F5 5 - A5S23F5 9 - A4S1F5 13 - A7S23F5 17 - A10S2F5 21 - A9S1F1
2 - A9S1F5 6 - A8S23F5 10 - A8S1F5 14 - A1S123F1 18 - A4S23F5
3 - A1S123F5 7 - A6S1F5 11 - A5S3F5 15 - A6S23F5 19 - A10S3F1
4 - A5S1F5 8 - A2S123F5 12 - A10S1F5 16 - A10S3F5 20 - A7S1F5



Legend:

1- A9S1F1 4- A10S2F1
2- A9S3F1 5- A4S1F1
3- A10S1F1 6- A8S1F3

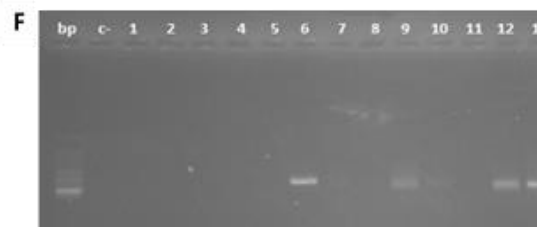


LEGEND:

1 - A9S1F1 4 - A10S1F1 7 - A8S23F1 10 - A7S23F3 13 - A4S1F3
2 - A9S2F1 5 - A10S2F1 8 - A4S1F1 11 - A8S1F3 14 - A4S23F3
3 - A9S3F1 6 - A10S3F1 9 - A7 F3 12 - A8S23F3

Sample concentration:

1 to 8 - 3 ng/ul
9 to 14 - 4 ng/ul

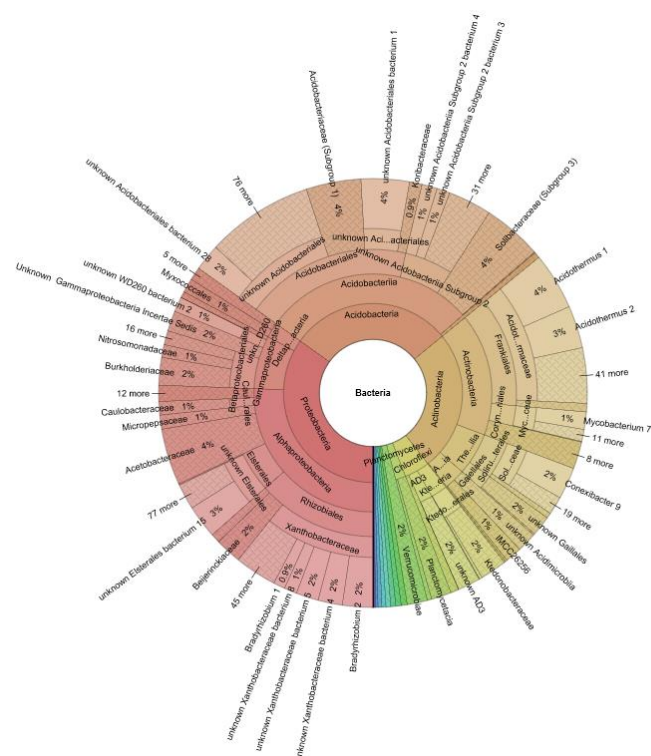


LEGEND:

1- A9S1F1 4- A10S1F1 7- A7S1F1 10- A2S1S2S3F1 13- A5S2S3F1
2- A9S2F1 5- A10S3F1 8- A7S1S2F1 11- A4S1F1
3- A9S3F1 6- A6S1F1 9- A8S1F1 12- A4S2S3F1

Sample concentration: 4 ng/ul

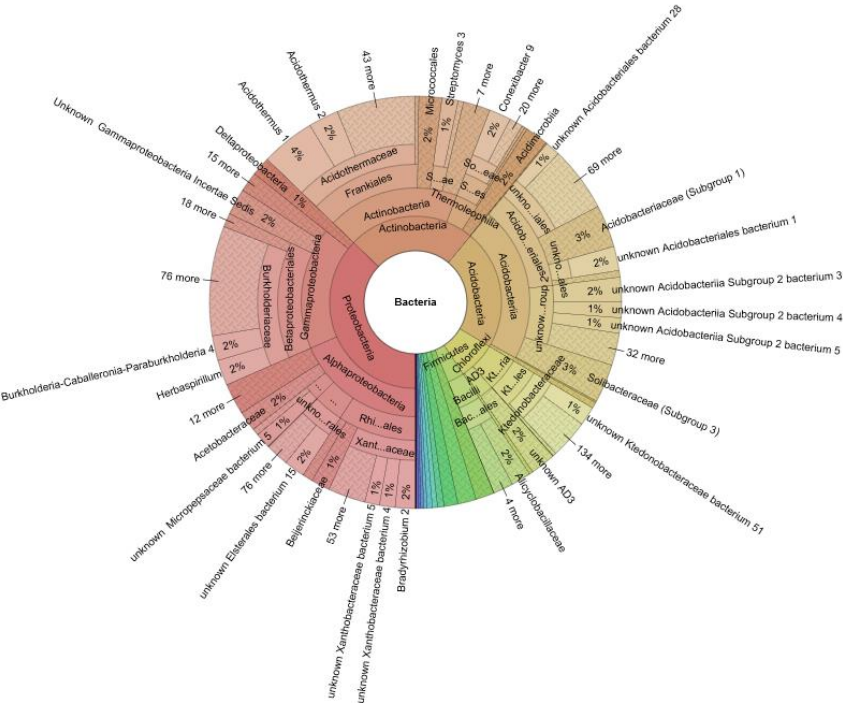
Annex 7 - Representation of bacterial taxonomic abundance, 5 months post-fire (March 2018) occurrence on *Santa Marta das Cortiças* of a non-burnt cork oaks soil. OTUs are identified until genus level (97 % identity).



Annex 8 - Representation of bacterial taxonomic abundance, 5 months post-fire (March 2018) occurrence on *Santa Marta das Cortiças* of a half-burnt cork oaks soil. OTUs are identified until genus level (97 % identity).



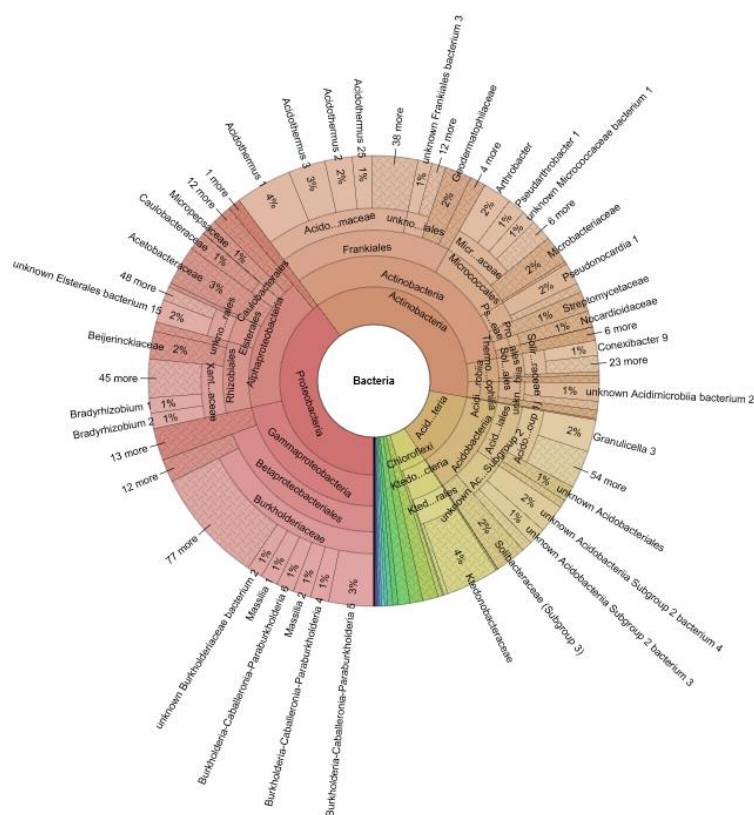
Annex 9 - Representation of bacterial taxonomic abundance, 5 months post-fire (March 2018) occurrence on *Santa Marta das Cortiças* of burnt cork oaks soil. OTUs are identified until genus level (97 % identity).



Annex 10 - Representation of bacterial taxonomic abundance, 12 months post-fire (October 2018) occurrence on *Santa Marta das Cortiças* of non-burnt cork oaks soil. OTUs are identified until genus level (97 % identity).



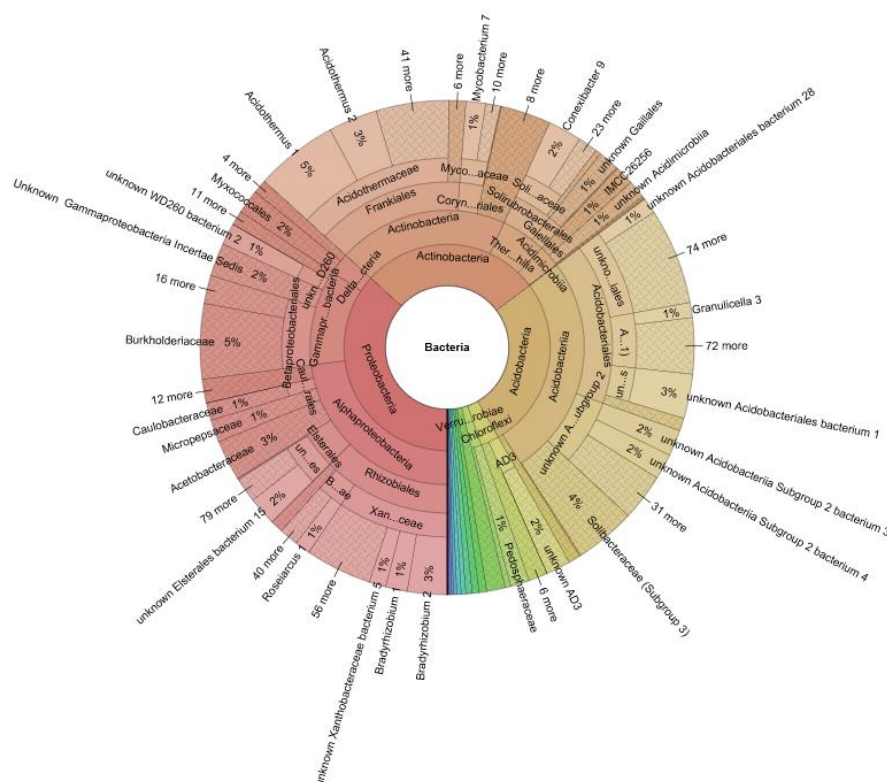
Annex 11 - Representation of bacterial taxonomic abundance, 12 months post-fire (October 2018) occurrence on *Santa Marta das Cortiças* of a half-burnt cork oaks soil. OTUs are identified until genus level (97 % identity).



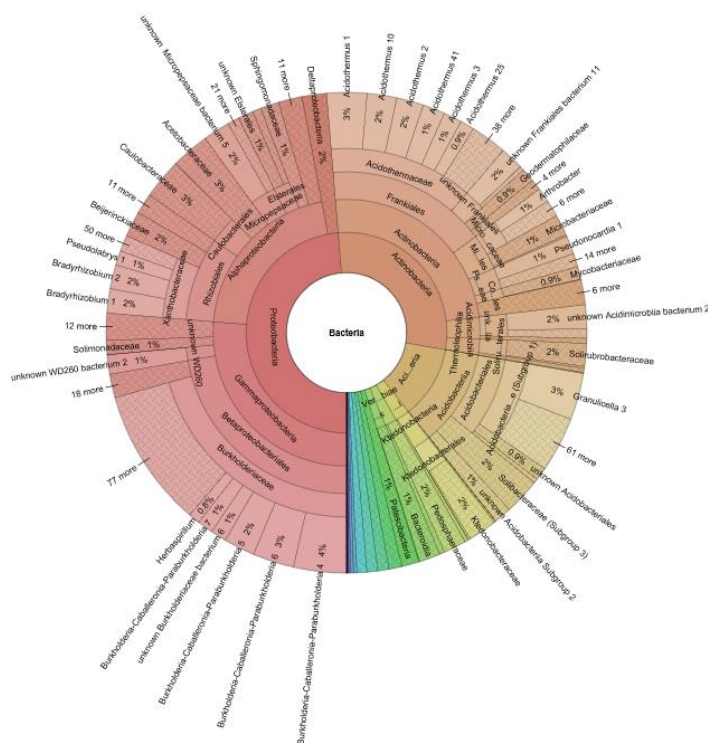
Annex 12 - Representation of bacterial taxonomic abundance, 12 months post-fire (October 2018) occurrence on *Santa Marta das Cortiças* of burnt cork oaks soil. OTUs are identified until genus level (97 % identity).



Annex 13 - Representation of bacterial taxonomic abundance, 18 months post-fire (April 2019) occurrence on *Santa Marta das Cortiças* of non-burnt cork oaks soil. OTUs are identified until genus level (97 % identity).



Annex 14 - Representation of bacterial taxonomic abundance, 18 months post-fire (April 2019) occurrence on *Santa Marta das Cortiças* of hal-burnt cork oaks soil. OTUs are identified until genus level (97 % identity).



Annex 15 - Representation of bacterial taxonomic abundance, 18 months post-fire (April 2019) occurrence on *Santa Marta das Cortiças* of burnt cork oaks soil. OTUs are identified until genus level (97 % identity).



Annex 16 – Bacterial OTUs identified by *Illumina MiSeq* sequencing of 16S amplicon. Bacterial sequences were classified till genus level with an identity of 97%; 0, 15 and 30 min of temperature (100°C) application.

Phylum	Class	Genus	0 min	15 min	30 min
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Acidipila 2</i>	13	1	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 13</i>	10	4	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 7</i>	6	0	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Koribacter 1</i>	9	3	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 10</i>	8	1	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 12</i>	6	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 2</i>	17	5	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 4</i>	7	1	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 48</i>	7	0	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 51</i>	17	7	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 53</i>	6	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 7</i>	84	37	8
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 8</i>	17	17	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Granulicella 1</i>	20	14	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	uncultured <i>Acidobacteriaceae</i> (Subgroup 1) 1	9	1	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	uncultured <i>Acidobacteriaceae</i> (Subgroup 1) 12	9	5	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	uncultured <i>Acidobacteriaceae</i> (Subgroup 1) 2	5	0	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	uncultured <i>Acidobacteriaceae</i> (Subgroup 1) 3	7	2	1

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	uncultured <i>Acidobacteriaceae</i> bacterium 28	11	2	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	uncultured <i>Acidobacteriaceae</i> bacterium 31	32	9	6
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	uncultured <i>Acidobacteriaceae</i> bacterium 35	18	2	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	uncultured <i>Acidobacteriaceae</i> bacterium 36	8	10	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	uncultured <i>Acidobacteriaceae</i> bacterium 37	3	2	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	uncultured <i>Acidobacteriaceae</i> bacterium 54	8	1	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	uncultured <i>Acidobacteriaceae</i> bacterium 80	33	3	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	uncultured <i>Acidobacteriaceae</i> bacterium 81	7	1	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	uncultured <i>Acidobacteriaceae</i> bacterium 88	1	4	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	unknown <i>Acidobacteriales</i> bacterium 1	53	12	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	unknown <i>Acidobacteriales</i> bacterium 13	17	17	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	unknown <i>Acidobacteriales</i> bacterium 18	21	2	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	unknown Subgroup 2 bacterium 12	4	1	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	unknown Subgroup 2 bacterium 20	2	5	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	unknown Subgroup 2 bacterium 3	20	14	13
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	unknown Subgroup 2 bacterium 8	87	63	20
<i>Acidobacteria</i>	<i>Blastocatellia</i> (Subgroup 4)	RB41 1	19	3	3
<i>Acidobacteria</i>	<i>Blastocatellia</i> (Subgroup 4)	RB41 2	9	0	2
<i>Acidobacteria</i>	<i>Blastocatellia</i> (Subgroup 4)	RB41 4	6	0	0
<i>Acidobacteria</i>	<i>Holophagae</i>	unknown Subgroup 7 bacterium 5	5	3	1
<i>Acidobacteria</i>	Subgroup 11	unknown Subgroup 11 bacterium 1	6	0	0
<i>Acidobacteria</i>	Subgroup 11	unknown Subgroup 11 bacterium 2	7	0	1
<i>Acidobacteria</i>	Subgroup 22	unknown Subgroup 22 bacterium 1	10	10	8
<i>Acidobacteria</i>	Subgroup 22	unknown Subgroup 22 bacterium 2	9	4	8
<i>Acidobacteria</i>	Subgroup 5	unknown Subgroup 5 bacterium 1	5	5	2

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Acidobacteria</i>	<i>Subgroup 5</i>	<i>unknown Subgroup 5 bacterium 3</i>	36	37	22
<i>Acidobacteria</i>	<i>Subgroup 5</i>	<i>unknown Subgroup 5 bacterium 4</i>	13	6	6
<i>Acidobacteria</i>	<i>Subgroup 5</i>	<i>unknown Subgroup 5 bacterium 7</i>	7	2	2
<i>Acidobacteria</i>	<i>Subgroup 5</i>	<i>unknown Subgroup 5 bacterium 8</i>	25	15	6
<i>Acidobacteria</i>	<i>Subgroup 6</i>	<i>unknown Subgroup 6 bacterium 1</i>	3	4	0
<i>Acidobacteria</i>	<i>Subgroup 6</i>	<i>unknown Subgroup 6 bacterium 10</i>	7	6	2
<i>Acidobacteria</i>	<i>Subgroup 6</i>	<i>unknown Subgroup 6 bacterium 11</i>	5	7	3
<i>Acidobacteria</i>	<i>Subgroup 6</i>	<i>unknown Subgroup 6 bacterium 12</i>	7	9	3
<i>Acidobacteria</i>	<i>Subgroup 6</i>	<i>unknown Subgroup 6 bacterium 3</i>	1	6	2
<i>Acidobacteria</i>	<i>Subgroup 6</i>	<i>unknown Subgroup 6 bacterium 4</i>	4	4	2
<i>Acidobacteria</i>	<i>Subgroup 6</i>	<i>unknown Subgroup 6 bacterium 5</i>	4	13	7
<i>Acidobacteria</i>	<i>Subgroup 6</i>	<i>unknown Subgroup 6 bacterium 6</i>	7	4	1
<i>Acidobacteria</i>	<i>Subgroup 6</i>	<i>unknown Subgroup 6 bacterium 9</i>	15	7	5
<i>Acidobacteria</i>	<i>Thermoanaerobaculia</i>	<i>Subgroup 10 4</i>	6	4	2
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>CL500-29 marine group 1</i>	19	33	23
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>CL500-29 marine group 2</i>	3	7	7
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>CL500-29 marine group 3</i>	4	10	7
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>CL500-29 marine group 4</i>	8	1	3
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>CL500-29 marine group 5</i>	1	4	4
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>Iamia 1</i>	8	18	10
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>Iamia 2</i>	16	17	9
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>Iamia 3</i>	8	3	6
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>Iamia 4</i>	8	5	2
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>Illumatobacter 1</i>	3	11	9
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>Illumatobacter 2</i>	7	8	6
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>IMCC26207</i>	7	4	6
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiaceae bacterium</i>	3	5	7
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Illumatobacteraceae bacterium 2</i>	19	4	8
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Illumatobacteraceae bacterium 3</i>	17	12	15
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Illumatobacteraceae bacterium 4</i>	15	12	6
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 12</i>	14	20	4
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 16</i>	19	15	10
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 2</i>	11	14	4
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 4</i>	46	35	25

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichaceae bacterium 1</i>	6	2	3
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichaceae bacterium 11</i>	5	3	1
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichaceae bacterium 16</i>	5	3	1
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichaceae bacterium 18</i>	2	6	2
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichaceae bacterium 27</i>	4	2	0
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichaceae bacterium 3</i>	1	6	4
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichaceae bacterium 5</i>	30	13	11
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichaceae bacterium 6</i>	2	18	6
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichaceae bacterium 7</i>	8	7	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidothermus 1</i>	107	44	28
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidothermus 15</i>	7	5	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidothermus 2</i>	13	5	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidothermus 3</i>	11	3	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidothermus 4</i>	8	0	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinoallomurus 1</i>	14	42	68
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomadura 2</i>	2	4	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomadura 4</i>	1	4	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetospora</i>	3	7	14
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinophytocola 2</i>	14	14	7
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinophytocola 3</i>	12	13	7
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinophytocola 4</i>	13	0	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinoplanes 1</i>	21	36	31
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinoplanes 2</i>	11	18	15
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinoplanes 3</i>	4	2	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 8</i>	16	0	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Amycolatopsis 1</i>	11	30	9
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Blastococcus 1</i>	1	6	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Blastococcus 2</i>	4	3	5
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Catenulispota 1</i>	11	5	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Cellulomonas 1</i>	35	88	81
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Crossiella 1</i>	9	4	14
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Dactylosporangium</i>	17	16	10
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Demequina</i>	18	49	47
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Herbihabitans</i>	4	2	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitans 11</i>	6	1	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitans 2</i>	5	3	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitans 5</i>	12	15	8
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitans 9</i>	17	5	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Kibdelosporangium</i>	9	12	9
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Kribbella 1</i>	5	12	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Kribbella 2</i>	24	28	8
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Lapillicoccus</i>	43	36	20
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Leifsonia 1</i>	9	14	16
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Leifsonia 2</i>	11	20	18
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Leifsonia 3</i>	9	17	8
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Luedemannella</i>	56	99	73
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Lysinimonas</i>	6	24	31
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Marmoricola 1</i>	14	15	16

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Marmoricola 3</i>	10	12	10
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Microbacterium 1</i>	10	29	38
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Microbacterium 2</i>	29	25	15
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Microbacterium 3</i>	5	16	15
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Microbispora 1</i>	0	6	7
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Microlunatus</i>	15	15	11
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Micromonospora 1</i>	21	48	94
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Micromonospora 2</i>	2	4	13
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Modestobacter 2</i>	16	2	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 1</i>	29	34	35
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 10</i>	15	18	10
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 11</i>	10	7	13
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 2</i>	93	123	95
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 3</i>	28	36	42
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 5</i>	35	65	66
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 6</i>	3	11	15
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 7</i>	3	5	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 8</i>	2	8	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 9</i>	12	22	17
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nakamurella 1</i>	41	40	28
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nakamurella 2</i>	1	5	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nakamurella 3</i>	19	21	7
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 10</i>	3	12	24
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 11</i>	3	4	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 12</i>	11	18	5
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 13</i>	4	11	14
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 15</i>	5	5	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 16</i>	2	9	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 17</i>	19	34	38
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 19</i>	7	8	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 2</i>	44	31	15
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 20</i>	1	7	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 21</i>	0	4	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 22</i>	5	10	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 23</i>	8	2	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 3</i>	63	52	37
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 4</i>	11	46	46
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 5</i>	10	12	33
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 7</i>	17	21	17
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioides 9</i>	6	4	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Parafrioglobacterium 1</i>	26	2	12
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardia 1</i>	13	15	18
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardia 3</i>	34	33	33
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardia 4</i>	31	31	35
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardia 5</i>	25	15	16
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Rhodococcus 1</i>	2	6	5
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Rhodococcus 2</i>	5	1	15
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Skermania</i>	2	3	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces 1</i>	2	3	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces 11</i>	3	9	12
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces 12</i>	1	17	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces 13</i>	3	15	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces 18</i>	6	2	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces 20</i>	0	4	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces 3</i>	58	37	29
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces 4</i>	26	18	15
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces 6</i>	5	11	6

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces 7</i>	9	19	10
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces 8</i>	7	10	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptosporangium 1</i>	0	10	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptosporangium 2</i>	3	10	10
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Tetrasphaera</i>	6	6	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 13</i>	6	3	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 15</i>	3	5	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Actinobacteria bacterium 1</i>	1	8	17
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Geodermatophilaceae bacterium</i>	2	2	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Kineosporiaceae bacterium 1</i>	15	11	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Kineosporiaceae bacterium 2</i>	17	42	48
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Kineosporiaceae bacterium 3</i>	5	7	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Microbacteriaceae bacterium 1</i>	19	47	93
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Microbacteriaceae bacterium 6</i>	0	3	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Micrococcaceae bacterium 1</i>	9	11	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Micrococcales bacterium 1</i>	5	2	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Micromonosporaceae bacterium 2</i>	5	1	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Micromonosporaceae bacterium 3</i>	16	66	119
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Micromonosporaceae bacterium 4</i>	24	41	96
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Micromonosporaceae bacterium 5</i>	5	0	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Micromonosporaceae bacterium 7</i>	1	3	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown PeM15 bacterium 1</i>	0	3	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown PeM15 bacterium 2</i>	13	26	14
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Propionibacteriaceae bacterium</i>	6	4	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Pseudonocardiaceae bacterium 1</i>	2	1	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Pseudonocardiaceae bacterium 2</i>	1	5	2

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Pseudonocardiaceae bacterium 3</i>	1	4	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Sporichthyaceae bacterium 2</i>	3	1	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Sporichthyaceae bacterium 5</i>	17	31	13
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Thermomonosporaceae bacterium</i>	0	3	3
<i>Actinobacteria</i>	<i>MB-A2-108</i>	<i>unknown MB-A2-108 bacterium 1</i>	72	77	34
<i>Actinobacteria</i>	<i>MB-A2-108</i>	<i>unknown MB-A2-108 bacterium 11</i>	20	18	9
<i>Actinobacteria</i>	<i>MB-A2-108</i>	<i>unknown MB-A2-108 bacterium 12</i>	7	13	2
<i>Actinobacteria</i>	<i>MB-A2-108</i>	<i>unknown MB-A2-108 bacterium 2</i>	46	49	19
<i>Actinobacteria</i>	<i>MB-A2-108</i>	<i>unknown MB-A2-108 bacterium 3</i>	50	46	18
<i>Actinobacteria</i>	<i>MB-A2-108</i>	<i>unknown MB-A2-108 bacterium 4</i>	30	27	6
<i>Actinobacteria</i>	<i>MB-A2-108</i>	<i>unknown MB-A2-108 bacterium 5</i>	6	22	5
<i>Actinobacteria</i>	<i>MB-A2-108</i>	<i>unknown MB-A2-108 bacterium 6</i>	5	15	9
<i>Actinobacteria</i>	<i>MB-A2-108</i>	<i>unknown MB-A2-108 bacterium 7</i>	10	8	6
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 1</i>	83	31	15
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 2</i>	169	83	59
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 4</i>	12	8	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Gaiella 1</i>	12	8	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Gaiella 10</i>	4	2	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Gaiella 2</i>	58	66	33
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Gaiella 3</i>	68	40	35
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Gaiella 4</i>	21	30	21
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Gaiella 5</i>	11	7	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Gaiella 6</i>	20	21	14
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Gaiella 7</i>	21	14	8
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Gaiella 8</i>	5	1	0
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 1</i>	7	10	9
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 2</i>	7	1	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 3</i>	61	30	20
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 6</i>	69	24	17
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 7</i>	14	1	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 8</i>	3	4	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 1</i>	159	102	83
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 10</i>	7	5	6
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 11</i>	10	8	9
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 14</i>	8	15	4
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 15</i>	6	3	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 17</i>	4	3	0

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 2</i>	42	33	33
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 4</i>	59	62	33
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 6</i>	33	36	13
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 7</i>	3	5	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 8</i>	8	3	0
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 9</i>	8	1	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 1</i>	102	107	40
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 10</i>	21	25	8
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 11</i>	58	29	19
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 12</i>	6	4	5
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 13</i>	35	32	15
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 14</i>	18	53	10
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 15</i>	33	29	16
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 16</i>	10	22	4
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 17</i>	40	30	4
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 19</i>	15	15	9
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 2</i>	14	13	4
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 20</i>	2	2	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 24</i>	12	9	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 26</i>	12	2	5
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 27</i>	15	18	4
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 30</i>	5	6	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 31</i>	9	4	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 33</i>	3	8	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 34</i>	6	6	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 35</i>	3	5	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 36</i>	21	25	16
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 37</i>	15	3	0
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 38</i>	10	1	1

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 4</i>	79	153	47
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 40</i>	3	5	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 41</i>	5	9	4
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 42</i>	5	4	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 43</i>	23	22	7
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 44</i>	5	3	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 45</i>	5	0	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 46</i>	1	8	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 55</i>	2	3	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 57</i>	38	25	13
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 59</i>	6	7	0
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 6</i>	27	9	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 63</i>	12	14	6
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 8</i>	23	8	10
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaiellales bacterium 9</i>	21	9	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Solirubrobacteraceae bacterium 6</i>	4	0	4
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Thermoleophilia bacterium 1</i>	18	69	45
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Thermoleophilia bacterium 2</i>	2	6	7
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Adhaeribacter</i>	10	10	4
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Chryseobacterium 1</i>	22	4	4
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Flavisolibacter 1</i>	4	5	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Flavobacterium 1</i>	245	155	111
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Flavobacterium 2</i>	31	42	50
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Flavobacterium 3</i>	7	3	3
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Flavobacterium 4</i>	15	10	3
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Ohtaekwangia 1</i>	7	16	22
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Ohtaekwangia 2</i>	3	12	9
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Ohtaekwangia 3</i>	1	2	8
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Ohtaekwangia 4</i>	1	7	8
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>OLB12</i>	2	2	7
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Sporocytophaga 4</i>	3	1	2
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown 37-13 bacterium 2</i>	4	4	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Bacteroidetes VC2.1 Bac22 bacterium 1</i>	2	5	8
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Bacteroidetes VC2.1 Bac22 bacterium 2</i>	3	4	6

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 19</i>	6	7	6
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 1</i>	34	52	42
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 11</i>	1	5	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 12</i>	9	8	18
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 14</i>	2	5	2
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 17</i>	7	1	2
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 2</i>	40	36	23
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 3</i>	19	17	21
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 4</i>	9	18	22
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 5</i>	3	16	11
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 6</i>	10	10	11
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 7</i>	9	11	6
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 8</i>	1	7	4
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 9</i>	8	6	4
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Saprospiraceae bacterium</i>	12	8	9
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown AKYH767 bacterium 1</i>	2	3	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown AKYH767 bacterium 2</i>	11	4	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown AKYH767 bacterium 5</i>	10	3	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown env.OPS 17 bacterium 12</i>	6	0	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown env.OPS 17 bacterium 14</i>	6	1	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown env.OPS 17 bacterium 16</i>	2	4	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown env.OPS 17 bacterium 17</i>	3	4	5
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown env.OPS 17 bacterium 25</i>	1	4	5
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown env.OPS 17 bacterium 9</i>	18	13	11
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown KD3-93 bacterium 2</i>	2	2	2
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown NS11-12 marine group bacterium 3</i>	15	10	6
<i>Bacteroidetes</i>	<i>Ignavibacteria</i>	<i>unknown BSV26 bacterium</i>	18	8	2
<i>Bacteroidetes</i>	<i>Ignavibacteria</i>	<i>unknown OPB56 bacterium 2</i>	2	3	3

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Protochlamydia 1</i>	0	5	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Rhabdochlamydia 10</i>	2	5	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Neochlamydia 2</i>	3	2	2
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Parachlamydiaceae bacterium 1</i>	1	4	3
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Parachlamydiaceae bacterium 7</i>	2	6	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Simkaniaceae bacterium 4</i>	0	4	10
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown cvE6 bacterium 4</i>	0	7	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown cvE6 bacterium 9</i>	1	7	2
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 2</i>	13	13	10
<i>Chloroflexi</i>	<i>Chloroflexia</i>	<i>unknown JG30-KF-CM45 bacterium 1</i>	1	8	6
<i>Chloroflexi</i>	<i>Chloroflexia</i>	<i>unknown Roseiflexaceae bacterium 1</i>	17	53	24
<i>Chloroflexi</i>	<i>Chloroflexia</i>	<i>unknown Roseiflexaceae bacterium 3</i>	10	60	17
<i>Chloroflexi</i>	<i>Chloroflexia</i>	<i>unknown Roseiflexaceae bacterium 4</i>	7	9	4
<i>Chloroflexi</i>	<i>Chloroflexia</i>	<i>unknown Roseiflexaceae bacterium 5</i>	2	3	2
<i>Chloroflexi</i>	<i>Chloroflexia</i>	<i>unknown Roseiflexaceae bacterium 6</i>	2	5	0
<i>Chloroflexi</i>	<i>Chloroflexia</i>	<i>unknown Roseiflexaceae bacterium 7</i>	2	5	1
<i>Chloroflexi</i>	<i>Chloroflexia</i>	<i>unknown Roseiflexaceae bacterium 9</i>	0	6	1
<i>Chloroflexi</i>	<i>Dehalococcoidia</i>	<i>unknown S085 bacterium 4</i>	8	1	0
<i>Chloroflexi</i>	<i>KD4-96</i>	<i>unknown KD4-96 bacterium 1</i>	26	61	29
<i>Chloroflexi</i>	<i>KD4-96</i>	<i>unknown KD4-96 bacterium 2</i>	3	4	3
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 13</i>	4	17	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 3</i>	5	31	15
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 4</i>	12	32	7
<i>Chloroflexi</i>	<i>TK10</i>	<i>unknown TK10 bacterium 11</i>	14	2	1
<i>Chloroflexi</i>	<i>TK10</i>	<i>unknown TK10 bacterium 15</i>	3	3	5
<i>Chloroflexi</i>	<i>TK10</i>	<i>unknown TK10 bacterium 27</i>	26	13	5
<i>Chloroflexi</i>	<i>TK10</i>	<i>unknown TK10 bacterium 28</i>	12	5	5
<i>Chloroflexi</i>	<i>TK10</i>	<i>unknown TK10 bacterium 30</i>	4	4	5
<i>Chloroflexi</i>	<i>TK10</i>	<i>unknown TK10 bacterium 5</i>	9	3	2

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Chloroflexi</i>	<i>TK10</i>	<i>unknown TK10 bacterium 8</i>	12	4	1
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 3</i>	5	4	0
<i>Elusimicrobia</i>	<i>Elusimicrobia</i>	<i>unknown Lineage IV bacterium 2</i>	1	5	1
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unknown Lineage IIa bacterium 1</i>	8	3	3
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unknown Lineage IIa bacterium 2</i>	1	2	3
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unknown Lineage IIa bacterium 4</i>	5	3	0
<i>Entothaeonellaeota</i>	<i>Entothaeonellia</i>	<i>unknown Entothaeonellaceae bacterium</i>	18	6	5
<i>FCPU426</i>	<i>unknown FCPU426</i>	<i>unknown FCPU426 bacterium 1</i>	1	2	3
<i>Fibrobacteres</i>	<i>Fibrobacteria</i>	<i>unknown Fibrobacteraceae bacterium 1</i>	5	7	2
<i>Fibrobacteres</i>	<i>Fibrobacteria</i>	<i>unknown Fibrobacteraceae bacterium 2</i>	3	8	8
<i>Fibrobacteres</i>	<i>Fibrobacteria</i>	<i>unknown Fibrobacteraceae bacterium 4</i>	3	3	5
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Ammoniphilus</i>	3	19	151
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Aneurinibacillus 1</i>	0	3	11
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 1</i>	7	4834	13085
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 10</i>	0	27	75
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 11</i>	0	10	9
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 12</i>	4	4	19
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 13</i>	0	2	17
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 15</i>	0	5	9
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 17</i>	0	8	3
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 2</i>	9	2243	1590
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 3</i>	5	50	192
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 4</i>	1	329	190
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 5</i>	3	427	1088
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 6</i>	6	12	91
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 7</i>	3	149	607
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 8</i>	1	10	93
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 9</i>	1	9	58
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Brevibacillus</i>	0	0	10
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Cohnella 1</i>	1	3	30
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Cohnella 2</i>	0	2	8
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Cohnella 4</i>	0	3	8
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Cohnella 6</i>	0	4	11
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Domibacillus</i>	2	1	23
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Lysinibacillus</i>	5	61	110
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 1</i>	0	287	451
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 10</i>	2	59	32
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 11</i>	0	47	67
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 12</i>	0	32	33
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 14</i>	2	71	118
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 17</i>	0	14	13
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 18</i>	3	17	56
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 20</i>	0	18	5

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 22</i>	0	3	21
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 23</i>	0	15	16
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 25</i>	0	0	11
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 26</i>	0	2	14
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 27</i>	1	2	6
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 28</i>	1	1	16
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 29</i>	0	22	28
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 30</i>	0	5	21
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 31</i>	0	1	10
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 34</i>	0	1	6
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 35</i>	0	5	4
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 36</i>	0	0	11
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 4</i>	1	106	197
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 43</i>	1	4	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 45</i>	0	2	8
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 48</i>	1	0	5
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 49</i>	0	3	8
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 5</i>	0	0	11
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 50</i>	0	1	6
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 54</i>	1	0	7
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 56</i>	0	2	8
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 58</i>	0	5	12
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 59</i>	0	2	9
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 6</i>	1	41	104
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 7</i>	2	38	89
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 9</i>	1	30	50
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Rummeliibacillus</i>	0	33	131
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Shimazuella 1</i>	0	24	42
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Shimazuella 2</i>	0	4	50
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Solibacillus</i>	2	1	6
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Sporosarcina 1</i>	40	207	1303
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Sporosarcina 2</i>	2	6	71
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Sporosarcina 3</i>	0	3	6
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Sporosarcina 4</i>	2	4	18
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Thermoactinomyces</i>	1	2	11
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Tumebacillus 1</i>	3	590	2675
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Tumebacillus 2</i>	0	234	113
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Tumebacillus 5</i>	0	79	41
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Tumebacillus 6</i>	0	1	12
<i>Firmicutes</i>	<i>Bacilli</i>	<i>unknown Bacillaceae bacterium 1</i>	0	61	164
<i>Firmicutes</i>	<i>Bacilli</i>	<i>unknown Bacillaceae bacterium 2</i>	0	2	12
<i>Firmicutes</i>	<i>Bacilli</i>	<i>unknown Paenibacillaceae bacterium 1</i>	0	0	11
<i>Firmicutes</i>	<i>Bacilli</i>	<i>unknown Sporolactobacillaceae bacterium</i>	0	2	7
<i>Firmicutes</i>	<i>Clostridia</i>	<i>Clostridium sensu stricto 1 1</i>	1	0	20
<i>Firmicutes</i>	<i>Clostridia</i>	<i>Clostridium sensu stricto 1 2</i>	1	6	14
<i>Firmicutes</i>	<i>Clostridia</i>	<i>Clostridium sensu stricto 1 3</i>	0	1	6
<i>Firmicutes</i>	<i>Clostridia</i>	<i>Clostridium sensu stricto 12</i>	0	0	6

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Firmicutes</i>	<i>Clostridia</i>	<i>Clostridium sensu stricto</i> 2	0	0	6
<i>Firmicutes</i>	<i>Clostridia</i>	<i>Paeniclostridium</i>	2	24	86
<i>Firmicutes</i>	<i>Clostridia</i>	<i>Terrisporobacter</i>	0	1	5
<i>Firmicutes</i>	<i>Clostridia</i>	unknown <i>Clostridiaceae</i> 1 bacterium	0	0	17
<i>Firmicutes</i>	<i>Clostridia</i>	unknown <i>Peptostreptococcaceae</i> bacterium	0	1	23
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 10	6	7	2
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 12	21	18	6
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 14	2	3	1
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 16	13	15	8
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 17	10	7	3
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 2	5	7	5
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 21	7	4	6
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 25	6	4	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 26	12	3	5
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 33	4	2	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 34	1	5	1
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 41	1	3	2
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 42	7	0	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 7	4	1	3
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 10	9	4	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 16	2	7	1
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 18	7	1	1
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 19	5	1	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 4	38	40	15
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 5	6	8	2
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 6	10	35	30
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 7	44	21	13
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 9	13	21	7
<i>Latescibacteria</i>	<i>Latescibacteria</i>	unknown <i>Latescibacteraceae</i> bacterium	6	3	4
<i>Nitrospirae</i>	<i>Nitrospira</i>	<i>Nitrospira</i> 1	23	10	12
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>Candidatus</i> <i>Yanofskybacteria</i> bacterium 2	3	6	1

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown Candidatus Adlerbacteria bacterium 13</i>	0	2	4
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown Parcubacteria bacterium 13</i>	0	6	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknownunknown Candidatus Kaiserbacteria bacterium 18</i>	0	13	1
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknownunknown Candidatus Kaiserbacteria bacterium 27</i>	5	8	7
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknownunknown Candidatus Kaiserbacteria bacterium 29</i>	0	6	3
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>nknown Saccharimonadales bacterium 4</i>	3	8	4
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>nknown Saccharimonadales bacterium 6</i>	7	4	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>nknown Saccharimonadales bacterium 7</i>	3	6	2
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>nknown Saccharimonadales bacterium 89</i>	3	5	2
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>nknown Saccharimonadales bacterium 96</i>	3	13	3
<i>Planctomycetes</i>	<i>BD7-11</i>	<i>unknown BD7-11 bacterium</i>	1	4	2
<i>Planctomycetes</i>	<i>OM190</i>	<i>unknown OM190 bacterium 1</i>	18	12	10
<i>Planctomycetes</i>	<i>OM190</i>	<i>unknown OM190 bacterium 2</i>	5	5	2
<i>Planctomycetes</i>	<i>OM190</i>	<i>unknown OM190 bacterium 3</i>	16	3	3
<i>Planctomycetes</i>	<i>OM190</i>	<i>unknown OM190 bacterium 4</i>	7	4	0
<i>Planctomycetes</i>	<i>OM190</i>	<i>unknown OM190 bacterium 5</i>	3	4	0
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>SM1A02 1</i>	11	29	3
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>SM1A02 2</i>	20	9	4
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>SM1A02 3</i>	7	16	6
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>SM1A02 4</i>	3	2	3
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>SM1A02 5</i>	6	0	2
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>SM1A02 6</i>	1	3	4
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>SM1A02 7</i>	6	2	2
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>SM1A02 8</i>	2	5	2
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>SM1A02 9</i>	3	3	0
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown WD2101 soil group bacterium 25</i>	5	2	1
<i>Planctomycetes</i>	<i>Pla4 lineage</i>	<i>unknown Pla4 lineage bacterium 3</i>	40	29	12
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Pir4 lineage 1</i>	19	33	46
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Pir4 lineage 2</i>	2	4	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Pirellula 1</i>	6	2	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Pirellula 2</i>	14	2	3

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Schlesneria 1</i>	10	1	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 101</i>	3	3	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 1</i>	9	5	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 18</i>	4	2	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 21</i>	2	4	4
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 8</i>	9	6	2
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 16</i>	4	4	2
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 17</i>	3	3	0
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 19</i>	2	2	3
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 4</i>	7	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Afipia 1</i>	5	0	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium 2</i>	12	9	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Amaricoccus 1</i>	5	2	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Amaricoccus 2</i>	3	4	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bauldia 1</i>	18	3	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bradyrhizobium 1</i>	333	168	180
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bradyrhizobium 2</i>	82	34	42
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Candidatus Alysiosphaera 1</i>	4	3	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Candidatus Alysiosphaera 2</i>	3	2	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Candidatus Alysiosphaera 3</i>	2	1	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Caulobacter 1</i>	8	5	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Caulobacter 2</i>	5	2	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Devosia 1</i>	16	14	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Devosia 2</i>	2	6	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Devosia 3</i>	2	5	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Dongia 1</i>	54	17	34
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Ellin6055 1</i>	19	12	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Hirschia 1</i>	3	9	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Hyphomicrobium 1</i>	12	8	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Mesorhizobium 1</i>	4	2	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Mesorhizobium 2</i>	29	12	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Mesorhizobium 3</i>	7	3	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Microvirga 3</i>	7	7	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Microvirga 6</i>	3	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Nordella 1</i>	4	2	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Novosphingobium 3</i>	4	4	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pedomicrobium 1</i>	51	26	16
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pedomicrobium 3</i>	17	4	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Phenyllobacterium 1</i>	34	18	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pseudolabrys 3</i>	32	24	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pseudolabrys 4</i>	9	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Reyranella 1</i>	28	11	11
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Reyranella 2</i>	6	1	0

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Reyranella 3</i>	38	8	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodomicrobium</i>	7	14	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Roseiarcus 1</i>	8	1	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Skermanella 2</i>	1	3	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 1</i>	50	11	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 10</i>	4	3	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 11</i>	1	1	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 13</i>	7	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 2</i>	12	2	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 3</i>	19	7	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 4</i>	6	3	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>SWB02 1</i>	3	3	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown A0839 bacterium 2</i>	8	8	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 2</i>	7	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 3</i>	6	1	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 4</i>	5	1	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Alphaproteobacteria bacterium 10</i>	5	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Alphaproteobacteria bacterium 18</i>	3	3	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Alphaproteobacteria bacterium 4</i>	16	10	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Alphaproteobacteria bacterium 8</i>	44	5	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 1</i>	8	7	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 17</i>	2	3	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 3</i>	4	3	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 5</i>	4	4	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 6</i>	7	5	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 7</i>	7	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 9</i>	11	6	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteriales bacterium 15</i>	3	3	3

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 29</i>	4	6	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 42</i>	3	1	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 60</i>	9	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 87</i>	8	4	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 95</i>	13	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Geminicoccaceae bacterium</i>	6	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown KF-JG30-B3 bacterium 1</i>	2	1	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown KF-JG30-B3 bacterium 3</i>	6	4	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Methyloligellaceae bacterium 1</i>	68	58	55
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Methyloligellaceae bacterium 2</i>	12	14	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 1</i>	52	51	34
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 10</i>	4	5	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 12</i>	4	2	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 24</i>	2	4	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 3</i>	31	20	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 4</i>	7	7	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhizobiales bacterium 1</i>	9	7	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhizobiales bacterium 2</i>	8	2	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillaceae bacterium 1</i>	6	1	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 21</i>	2	4	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Sphingomonadaceae bacterium</i>	18	12	13
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacteraceae bacterium 1</i>	5	3	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacteraceae bacterium 10</i>	3	19	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacteraceae bacterium 12</i>	4	1	1

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Xanthobacteraceae</i> <i>bacterium 15</i>	11	31	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Xanthobacteraceae</i> <i>bacterium 16</i>	4	4	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Xanthobacteraceae</i> <i>bacterium 18</i>	4	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Xanthobacteraceae</i> <i>bacterium 2</i>	43	22	12
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Xanthobacteraceae</i> <i>bacterium 27</i>	8	6	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Xanthobacteraceae</i> <i>bacterium 28</i>	52	40	32
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Xanthobacteraceae</i> <i>bacterium 29</i>	2	3	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Xanthobacteraceae</i> <i>bacterium 38</i>	19	7	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Xanthobacteraceae</i> <i>bacterium 4</i>	98	120	98
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Xanthobacteraceae</i> <i>bacterium 5</i>	49	28	14
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Xanthobacteraceae</i> <i>bacterium 6</i>	17	19	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Xanthobacteraceae</i> <i>bacterium 8</i>	4	1	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Xanthobacteraceae</i> <i>bacterium 9</i>	24	12	20
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 20</i>	3	2	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 4</i>	26	13	9
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 5</i>	9	3	12
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 9</i>	2	6	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio 28</i>	2	6	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio 8</i>	3	3	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 1</i>	119	81	54
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 12</i>	5	3	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 16</i>	2	3	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 2</i>	14	8	7
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 3</i>	13	1	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 4</i>	8	3	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 42</i>	6	8	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 5</i>	14	10	15
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 6</i>	6	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 7</i>	3	2	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 9</i>	9	8	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Minicystis</i>	2	5	9

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Oligoflexus 1</i>	10	15	15
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>OM27 clade 1</i>	1	3	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>OM27 clade 2</i>	1	2	8
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 2</i>	5	8	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 9</i>	9	6	10
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Peredibacter 1</i>	2	2	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Phaselicystis 1</i>	18	22	10
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Vulgatibacter 1</i>	0	3	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 108</i>	5	7	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 110</i>	0	4	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 111</i>	0	5	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 112</i>	1	8	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 17</i>	0	4	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 62</i>	2	5	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 7</i>	11	6	9
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 8</i>	2	4	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 98</i>	1	6	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Archangiaceae bacterium</i>	9	3	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown bacteriap25 bacterium 1</i>	8	5	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown bacteriap25 bacterium 2</i>	6	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Blrii41 bacterium 1</i>	40	20	27
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Blrii41 bacterium 2</i>	11	8	7
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Blrii41 bacterium 3</i>	40	80	65
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Blrii41 bacterium 4</i>	23	9	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Blrii41 bacterium 5</i>	1	1	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Blrii41 bacterium 6</i>	3	2	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Blrii41 bacterium 7</i>	28	23	13
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown KD3-10 bacterium 1</i>	7	9	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Myxococcales bacterium 4</i>	7	8	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P30B-42 bacterium 1</i>	11	4	8
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P30B-42 bacterium 16</i>	2	5	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P30B-42 bacterium 6</i>	2	2	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Polyangiaceae bacterium 1</i>	7	8	10

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Polyangiaceae bacterium 3</i>	3	9	14
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Polyangiaceae bacterium 4</i>	3	4	8
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Sandaracinaceae bacterium 1</i>	3	47	25
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Sandaracinaceae bacterium 2</i>	6	18	8
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Sandaracinaceae bacterium 3</i>	5	8	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Sandaracinaceae bacterium 5</i>	2	6	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown SAR324 clade(Marine group B) bacterium 2</i>	0	5	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>[Polyangium] brachysporum group</i>	5	2	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>AAP99</i>	9	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 11</i>	6	3	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 12</i>	26	9	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 14</i>	5	1	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 16</i>	12	3	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 3</i>	4	1	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 5</i>	136	180	86
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 8</i>	5	1	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 9</i>	9	4	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Aquabacterium 1</i>	59	23	12
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Arenimonas</i>	12	15	14
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia-Caballeronia-Paraburkholderia 2</i>	5	5	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia-Caballeronia-Paraburkholderia 3</i>	4	2	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia-Caballeronia-Paraburkholderia 5</i>	33	34	30
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia-Caballeronia-Paraburkholderia 6</i>	2	6	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia-Caballeronia-Paraburkholderia 8</i>	5	5	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Caenimonas 1</i>	26	45	34
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Caenimonas 2</i>	23	16	27
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Dokdonella</i>	9	6	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ellin6067 1</i>	44	19	6
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ellin6067 2</i>	27	11	6
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ellin6067 3</i>	78	69	38
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ellin6067 4</i>	29	47	28
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ellin6067 8</i>	12	6	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>GOUTA6</i>	41	17	13
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Herbaspirillum</i>	15	11	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>IS-44 1</i>	101	73	52
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>IS-44 2</i>	22	7	7
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>IS-44 3</i>	24	16	11
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>JTB255 marine benthic group</i>	7	4	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Lysobacter</i>	6	2	1

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Massilia 1</i>	10	8	10
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Massilia 4</i>	5	2	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Massilia 7</i>	5	7	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Methylophilus</i>	3	2	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>mle1-7</i>	25	5	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 1</i>	296	129	99
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 10</i>	8	5	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 3</i>	51	27	15
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 4</i>	2	4	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 5</i>	22	14	9
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 7</i>	7	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Nitrosospira</i>	7	0	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Noviherbaspirillum 1</i>	6	4	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Noviherbaspirillum 2</i>	8	9	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>OM60(NOR5) clade</i>	6	4	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Porticoccus</i>	2	2	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pseudomonas 1</i>	8	0	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pseudomonas 3</i>	1	4	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ramlibacter 1</i>	6	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Rhizobacter</i>	41	43	38
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Rhodanobacter 1</i>	6	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Rhodanobacter 2</i>	7	4	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Rhodoferax 2</i>	5	2	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Stenotrophomonas 1</i>	6	6	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Steroidobacter 1</i>	21	13	8
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Variovorax</i>	4	1	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown K189A clade bacterium</i>	3	4	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 11</i>	89	19	14
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 12</i>	7	1	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 3</i>	1	2	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 4</i>	4	2	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Betaproteobacteriales bacterium 8</i>	42	4	7
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 16</i>	64	12	9
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 17</i>	3	4	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 2</i>	3	1	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 21</i>	14	18	10
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 6</i>	75	42	39
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 7</i>	61	57	38

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown JG36-TzT-191 bacterium 3</i>	31	4	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown KF-JG30-C25 bacterium 1</i>	24	19	15
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Moraxellaceae bacterium 1</i>	1	7	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Neisseriaceae bacterium 8</i>	4	4	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown PLTA13 bacterium 1</i>	19	7	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown R7C24 bacterium 1</i>	17	43	30
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown R7C24 bacterium 2</i>	0	7	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Rhodanobacteraceae bacterium 2</i>	2	4	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Rhodanobacteraceae bacterium 3</i>	147	43	25
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Rhodocyclaceae bacterium 1</i>	2	14	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I-84 bacterium 1</i>	18	14	11
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I-84 bacterium 10</i>	3	2	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I-84 bacterium 2</i>	24	18	19
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I-84 bacterium 3</i>	64	17	7
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I-84 bacterium 4</i>	43	27	27
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I-84 bacterium 6</i>	29	16	11
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I-84 bacterium 7</i>	6	5	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I-84 bacterium 8</i>	2	1	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Steroidobacteraceae bacterium 2</i>	23	28	29
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Steroidobacteraceae bacterium 4</i>	2	6	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown TRA3-20 bacterium 2</i>	5	12	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown TRA3-20 bacterium 3</i>	8	6	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown TRA3-20 bacterium 4</i>	9	6	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown TRA3-20 bacterium 5</i>	18	7	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown TRA3-20 bacterium 8</i>	2	3	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown WD260 bacterium 2</i>	7	0	1

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown</i> <i>Xanthomonadaceae</i> <i>bacterium 6</i>	6	2	1
<i>Rokubacteria</i>	<i>NC10</i>	<i>unknown Rokubacteriales</i> <i>bacterium 2</i>	5	1	2
<i>Spirochaetes</i>	<i>Leptospirae</i>	<i>Turneriella</i>	1	5	4
<i>Spirochaetes</i>	<i>Spirochaetia</i>	<i>Spirochaeta 2 1</i>	6	6	8
<i>Spirochaetes</i>	<i>Spirochaetia</i>	<i>Spirochaeta 2 2</i>	4	10	4
<i>Spirochaetes</i>	<i>Spirochaetia</i>	<i>Spirochaeta 2 3</i>	5	3	1
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 1</i>	14	5	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 2</i>	16	4	6
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 3</i>	3	1	2
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 4</i>	33	10	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 7</i>	6	2	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Candidatus Udaeobacter 1</i>	23	11	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Candidatus Udaeobacter 2</i>	6	4	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Candidatus Udaeobacter 4</i>	8	5	6
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Lacunisphaera 3</i>	4	6	17
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Opitutus 2</i>	4	3	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Pedosphaera 1</i>	18	7	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Pedosphaera 2</i>	2	11	8
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedosphaeraceae</i> <i>bacterium 1</i>	2	0	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedosphaeraceae</i> <i>bacterium 1</i>	7	7	2
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedosphaeraceae</i> <i>bacterium 12</i>	22	9	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedosphaeraceae</i> <i>bacterium 13</i>	4	1	2
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedosphaeraceae</i> <i>bacterium 14</i>	11	1	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedosphaeraceae</i> <i>bacterium 15</i>	3	2	1
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedosphaeraceae</i> <i>bacterium 16</i>	15	3	2
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedosphaeraceae</i> <i>bacterium 17</i>	16	4	6
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedosphaeraceae</i> <i>bacterium 19</i>	17	7	7
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedosphaeraceae</i> <i>bacterium 2</i>	37	8	2
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedosphaeraceae</i> <i>bacterium 20</i>	5	8	2
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedosphaeraceae</i> <i>bacterium 21</i>	16	3	1

Annex 16 (Continuation)

Phylum	Class	Genus	0 min	15 min	30 min
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 24</i>	8	10	5
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 25</i>	14	2	2
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 26</i>	9	7	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 28</i>	16	4	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 31</i>	6	2	2
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 32</i>	7	3	5
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 34</i>	7	1	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 37</i>	4	3	1
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 38</i>	1	5	1
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 4</i>	4	0	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 48</i>	4	1	2
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 5</i>	15	7	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 56</i>	19	11	6
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 57</i>	6	3	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 60</i>	2	5	1
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 62</i>	2	3	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown</i> <i>Pedospaeraceae</i> <i>bacterium 7</i>	35	13	5

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriaceae bacterium 30</i>	23	13	0	2	5	0	1	13	5
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriaceae bacterium 31</i>	6	1	14	1	0	2	4	1	17
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriaceae bacterium 32</i>	1	9	5	1	8	4	2	48	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriaceae bacterium 33</i>	10	8	2	0	0	1	0	4	7
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriaceae bacterium 34</i>	9	37	22	1	1	21	1	1	18
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriaceae bacterium 35</i>	6	21	6	9	35	9	16	18	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriaceae bacterium 4</i>	7	16	6	0	0	2	1	0	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriaceae bacterium 7</i>	289	410	847	77	36	373	303	102	486
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriaceae bacterium 8</i>	444	415	346	101	34	214	181	3	178
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriaceae bacterium 9</i>	67	96	152	39	27	38	24	122	118
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Koribacter 1</i>	356	550	417	238	159	330	241	73	379
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Koribacter 10</i>	12	11	4	1	3	2	6	1	7
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Koribacter 11</i>	0	0	23	0	0	10	4	13	26
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Koribacter 2</i>	165	501	213	61	150	120	211	71	227
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Koribacter 3</i>	13	21	223	6	10	125	54	84	319
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Koribacter 4</i>	0	0	65	0	0	9	0	3	34
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Koribacter 5</i>	12	23	2	7	37	1	11	6	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Koribacter 6</i>	6	4	0	3	1	1	4	0	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Koribacter 7</i>	146	169	99	53	55	44	70	7	70
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Koribacter 8</i>	16	20	19	5	1	11	13	3	10
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Koribacter 9</i>	1	0	3	2	0	5	2	0	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 10</i>	1	0	18	0	0	9	0	0	47
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 11</i>	4	0	29	1	0	9	0	0	17
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 12</i>	0	46	0	0	0	0	0	8	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 14</i>	7	11	8	6	5	1	13	0	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 15</i>	28	7	17	18	6	7	34	5	19

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 16</i>	143	84	69	44	18	25	205	0	19
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 17</i>	9	9	21	5	2	13	12	0	24
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 18</i>	5	7	39	3	1	34	11	0	27
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 19</i>	0	0	3	0	0	1	0	0	7
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 2</i>	115	369	162	120	34	63	398	5	79
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 20</i>	2	2	2	1	0	1	1	0	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 22</i>	0	0	1	0	1	0	1	0	5
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 24</i>	9	4	11	4	1	9	10	1	10
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 26</i>	1	0	0	0	0	4	0	0	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 27</i>	0	0	4	0	0	0	0	0	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 28</i>	1634	2367	2273	383	201	634	1087	122	1311
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 29</i>	684	36	189	236	74	25	3263	286	57
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 3</i>	301	253	340	59	11	139	190	7	478
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 30</i>	830	992	587	338	65	413	787	79	795
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 31</i>	452	840	796	184	438	561	206	90	585
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 32</i>	561	428	639	167	20	332	393	20	500
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 33</i>	265	86	335	208	4	94	648	7	161
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 34</i>	217	201	542	65	13	423	207	17	905
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 35</i>	63	0	954	27	1	314	24	3	574
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 36</i>	19	8	410	16	18	74	165	57	370
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 37</i>	191	6	58	171	3	24	175	13	40
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 38</i>	294	298	146	54	0	55	328	5	128
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 39</i>	34	24	94	5	1	92	28	5	135
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 4</i>	258	237	165	151	40	84	129	24	113

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 40</i>	140	148	121	16	6	62	90	7	87
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 41</i>	28	24	55	10	1	18	23	2	74
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 42</i>	26	40	70	11	0	17	21	2	24
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 43</i>	73	41	109	18	2	59	22	2	51
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 44</i>	22	5	179	4	1	143	36	4	328
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 45</i>	27	0	18	0	0	31	4	0	15
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 46</i>	15	13	43	7	0	15	20	0	47
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 47</i>	1	1	15	3	1	6	2	3	45
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 48</i>	4	0	2	0	0	39	6	0	28
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 49</i>	25	0	2	1	0	12	1	0	7
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 5</i>	82	189	56	11	0	8	103	2	23
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 50</i>	9	10	9	2	0	9	2	1	29
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 51</i>	12	0	2	19	0	0	4	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 52</i>	6	2	10	5	0	17	9	4	54
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 53</i>	2	0	21	0	0	3	0	0	9
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 54</i>	3	2	25	2	1	16	6	1	20
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 55</i>	9	5	7	0	0	2	33	0	5
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 56</i>	6	6	13	2	1	6	1	0	12
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 57</i>	2	0	13	4	0	2	4	0	5
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 58</i>	1	0	26	1	0	9	1	2	28
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 59</i>	42	3	47	81	0	14	127	0	8
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 6</i>	437	422	573	300	128	168	943	91	368
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 60</i>	44	26	77	10	4	36	36	0	33
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 61</i>	0	0	10	0	0	2	4	5	4

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half-burnt	Non-burnt	Burnt	Half-burnt	Non-burnt	Burnt	Half-burnt	Non-burnt
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 62</i>	2	0	5	2	0	1	0	0	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 63</i>	1	3	14	0	0	8	3	1	11
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 64</i>	3	9	7	0	0	12	1	0	5
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 65</i>	0	0	2	0	0	8	0	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 66</i>	6	1	6	1	0	0	5	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 67</i>	2	4	2	0	0	1	1	0	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 68</i>	0	0	4	0	0	4	1	0	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 69</i>	4	0	2	2	0	0	12	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 7</i>	32	1	39	10	0	21	24	0	68
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 70</i>	0	0	1	0	0	9	0	0	7
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 71</i>	0	0	0	0	0	4	0	0	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 74</i>	1	1	2	1	0	3	0	0	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 76</i>	557	464	572	142	86	310	135	36	259
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 77</i>	123	191	129	3	1	103	23	13	403
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 78</i>	549	362	832	271	41	296	460	32	532
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 79</i>	88	0	11	14	0	62	16	0	12
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 8</i>	4	11	56	0	0	24	6	1	173
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 80</i>	0	0	21	0	0	6	0	0	16
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 81</i>	1	0	53	0	0	5	0	1	7
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 82</i>	10	3	7	3	0	4	1	0	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 83</i>	3	1	12	0	0	2	1	0	8
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 84</i>	111	56	104	33	24	79	14	6	95
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 85</i>	4	0	0	0	0	0	8	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 86</i>	60	8	35	13	0	21	46	3	24

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 87</i>	17	4	24	4	1	1	7	0	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 88</i>	17	31	33	6	1	13	14	0	19
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 89</i>	0	1	11	0	0	5	4	0	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 9</i>	1	24	19	1	0	2	4	48	16
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriales bacterium 1</i>	2627	1673	4115	996	241	2685	1940	83	3711
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 12 bacterium</i>	14	6	8	1	0	11	11	0	20
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 13 bacterium 1</i>	73	64	18	19	10	15	52	0	25
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 13 bacterium 10</i>	8	2	4	0	0	3	0	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 13 bacterium 2</i>	28	55	22	4	1	4	18	6	43
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 13 bacterium 3</i>	23	22	14	3	2	14	15	1	26
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 13 bacterium 4</i>	10	15	1	2	1	2	7	3	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 13 bacterium 5</i>	4	21	5	0	0	3	9	0	5
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 13 bacterium 6</i>	1	0	4	0	0	0	0	0	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 13 bacterium 7</i>	2	0	1	2	0	0	1	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 13 bacterium 8</i>	1	0	3	1	0	2	0	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 1</i>	29	37	90	2	7	41	31	9	236
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 10</i>	197	258	263	17	20	201	204	168	427
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 11</i>	211	34	91	85	2	24	1109	1	11
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 12</i>	39	82	31	13	1	20	36	8	83
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 13</i>	57	51	14	6	0	16	27	0	24

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 14</i>	34	56	35	10	1	24	30	6	66
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 15</i>	41	23	26	7	2	17	51	1	32
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 16</i>	5	30	19	6	6	20	14	1	21
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 17</i>	15	0	8	3	0	16	11	0	10
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 18</i>	205	156	308	48	2	96	281	3	125
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 19</i>	34	2	1	3	0	0	8	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 2</i>	8	0	0	2	0	7	0	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 20</i>	10	49	20	0	0	19	9	0	46
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 21</i>	2	17	2	4	0	2	3	2	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 22</i>	17	35	41	4	0	27	19	0	35
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 23</i>	1	12	4	0	0	0	1	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 24</i>	12	0	0	7	0	2	0	0	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 25</i>	99	179	108	10	7	93	90	3	101
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 26</i>	12	19	5	5	0	7	11	2	9
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 27</i>	13	14	95	8	1	19	36	1	73
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 28</i>	10	9	17	4	1	14	18	2	18
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 29</i>	2	0	1	0	1	1	0	0	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown Acidobacteriia Subgroup 2 bacterium 3</i>	2631	4177	1119	847	1426	918	4844	480	2183

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 30</i>	5	14	4	3	2	14	3	2	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 31</i>	0	14	0	2	1	0	0	0	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 32</i>	3	0	0	0	0	0	26	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 33</i>	0	2	0	3	0	1	1	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 35</i>	3	3	1	1	0	1	4	0	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 37</i>	0	1	1	3	0	0	2	0	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 38</i>	0	0	3	0	0	1	0	0	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 39</i>	54	200	64	5	2	31	31	0	82
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 4</i>	1757	7063	1315	754	2333	730	2225	450	2151
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 40</i>	45	21	5	12	2	9	26	0	11
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 41</i>	8	1	0	0	0	0	2	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 5</i>	1675	1322	689	116	197	312	1206	61	813
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 6</i>	1159	951	704	221	12	714	810	22	720
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 7</i>	778	372	506	224	149	276	966	119	360
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 8</i>	234	825	431	73	451	181	160	42	377
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>unknown</i> <i>Acidobacteriia</i> <i>Subgroup 2</i> <i>bacterium 9</i>	160	276	125	33	13	111	173	8	222
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 1</i>	4	0	8	17	1	3	4	2	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 10</i>	11	10	6	21	1	5	10	0	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 11</i>	0	0	0	0	0	4	0	7	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 12</i>	4	0	2	0	0	0	1	0	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 13</i>	0	0	0	3	0	4	4	1	8
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 15</i>	3	2	0	1	0	1	0	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 16</i>	1	0	4	0	0	0	1	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 17</i>	21	8	15	2	0	23	12	0	18
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 19</i>	385	524	425	303	179	386	372	35	437
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 2</i>	0	0	6	2	2	3	1	0	5

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 20</i>	64	77	142	74	132	89	104	93	58
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 21</i>	31	165	22	73	145	4	30	122	6
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 22</i>	55	69	149	28	6	55	40	24	108
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 23</i>	46	12	170	8	0	75	28	3	117
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 24</i>	39	1	0	106	71	1	177	75	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 25</i>	9	53	98	16	9	48	35	25	78
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 26</i>	14	26	40	28	29	39	32	49	38
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 27</i>	43	25	56	8	0	53	20	1	42
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 28</i>	34	8	41	31	2	50	34	7	29
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 29</i>	20	21	45	15	3	27	23	17	55
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 3</i>	124	194	325	43	5	188	93	9	255
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 30</i>	2	0	23	50	45	8	30	68	16
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 31</i>	3	4	13	13	1	10	6	5	29
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 32</i>	7	46	17	3	0	15	8	1	20
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 33</i>	23	5	9	11	2	14	11	0	9
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 34</i>	13	32	25	2	2	16	4	11	16
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 35</i>	8	5	19	4	2	19	6	2	22
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 36</i>	1	0	15	0	0	19	0	0	19
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 37</i>	3	0	14	0	2	11	8	6	31
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 38</i>	0	4	3	0	2	10	7	9	27
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 39</i>	0	0	12	15	5	3	11	7	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 4</i>	98	185	118	54	116	88	143	81	127
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 40</i>	5	11	27	0	1	14	2	4	26
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 41</i>	7	8	8	1	0	14	1	0	6
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 42</i>	1	0	0	11	29	0	6	10	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 43</i>	20	10	10	18	0	11	2	0	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 44</i>	2	1	8	6	12	4	2	13	6
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 45</i>	1	1	0	8	10	1	7	13	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 46</i>	12	3	6	1	0	8	4	0	7
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 47</i>	0	0	3	3	4	19	2	1	12
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 48</i>	0	15	19	0	4	4	1	3	5
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 49</i>	0	12	7	0	1	5	4	9	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 5</i>	98	111	80	53	38	56	68	12	73
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 50</i>	7	3	5	2	2	3	1	3	5
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 51</i>	0	0	2	6	8	5	3	5	7
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 52</i>	1	0	7	0	7	3	8	39	17
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 53</i>	6	8	5	0	0	4	3	0	8
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 54</i>	3	0	10	4	0	7	4	0	7
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 55</i>	0	0	1	2	5	5	1	4	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 56</i>	1	0	18	1	0	2	0	0	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 57</i>	0	4	10	0	2	4	1	6	16
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 58</i>	4	7	29	6	5	19	8	8	16
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 59</i>	14	0	0	0	0	0	0	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 6</i>	73	32	131	57	19	54	88	11	50
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 60</i>	9	1	5	1	0	1	2	0	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 61</i>	5	5	14	4	1	2	4	4	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 62</i>	1	0	0	12	6	0	0	1	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 63</i>	0	0	0	6	5	0	1	6	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 64</i>	2	0	5	1	0	3	1	0	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 65</i>	0	0	4	2	0	2	2	0	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 66</i>	9	9	4	5	0	4	5	1	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 67</i>	10	8	8	6	1	2	13	0	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 68</i>	30	40	37	6	4	31	22	0	67
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 69</i>	12	8	20	5	1	21	10	20	40
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 7</i>	12	22	33	6	4	8	24	0	21
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 70</i>	0	0	1	0	0	1	0	0	6
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 73</i>	0	0	2	0	1	11	2	1	6
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 74</i>	0	0	1	0	0	4	0	0	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 75</i>	0	0	0	1	0	0	1	5	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 76</i>	0	0	0	2	2	0	1	4	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 78</i>	6	0	4	2	0	11	6	3	8
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 8</i>	39	28	21	13	0	10	16	0	17
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 80</i>	0	1	1	1	1	5	3	1	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 81</i>	0	1	3	0	0	4	0	0	4
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 84</i>	20	44	69	5	56	14	6	13	7
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 85</i>	9	25	67	5	24	58	20	14	87
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 86</i>	6	0	0	44	24	0	2	2	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 87</i>	10	7	8	3	1	6	3	0	7
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 88</i>	9	0	3	4	0	7	3	0	6
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 89</i>	0	0	11	1	0	12	3	1	5
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 9</i>	4	1	23	2	2	7	4	16	21

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 90</i>	0	0	2	0	7	3	0	1	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 91</i>	4	0	3	1	1	8	3	11	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 92</i>	12	6	18	2	0	4	8	0	8
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 93</i>	2	0	0	0	4	1	1	1	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 94</i>	2	0	3	0	0	0	1	0	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Bryobacter 96</i>	3	1	1	0	0	1	0	0	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 1</i>	19	48	66	5	1	56	20	0	46
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 10</i>	213	33	15	78	100	3	116	167	15
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 11</i>	0	1	1	2	6	5	15	58	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 12</i>	11	19	28	2	0	13	1	5	14
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 13</i>	4	24	3	3	0	12	6	1	9
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 14</i>	2	2	14	0	1	10	4	0	17
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 15</i>	6	1	2	0	0	3	5	0	5
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 16</i>	1	10	6	1	6	16	10	61	14
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 18</i>	436	92	72	507	599	99	588	607	130
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 19</i>	90	188	158	55	77	81	195	272	154
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 2</i>	2	5	12	1	0	7	12	1	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 20</i>	109	62	118	55	22	121	59	11	119
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 21</i>	51	50	68	20	5	73	56	34	140
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 22</i>	34	2	22	10	7	60	12	92	54
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 23</i>	95	29	51	39	9	88	40	2	65
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 24</i>	12	4	30	29	0	38	58	0	38
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 25</i>	38	20	15	15	2	16	28	1	15
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 26</i>	33	61	60	10	2	39	33	7	63
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 27</i>	8	23	24	12	1	11	13	0	6
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 28</i>	6	35	29	3	1	7	11	4	12
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 29</i>	1	0	3	1	20	5	6	16	6
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 3</i>	2	2	2	1	0	5	2	0	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 30</i>	8	12	13	2	0	10	8	1	18
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 31</i>	0	7	6	0	2	3	0	2	15
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 32</i>	7	12	3	8	6	2	0	1	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 33</i>	0	18	13	1	1	2	2	1	1
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 34</i>	59	39	44	18	2	50	37	0	42
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 35</i>	44	17	39	33	2	41	57	0	30
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 36</i>	0	0	0	0	1	0	0	9	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 37</i>	0	1	11	3	0	5	1	0	10
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 38</i>	0	0	8	0	0	3	0	0	3
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 39</i>	0	3	0	1	1	0	0	0	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 4</i>	432	176	183	398	14	191	373	9	203
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 40</i>	0	0	7	0	0	2	0	0	1

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 41</i>	10	9	4	3	2	12	3	1	16
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 42</i>	0	1	5	0	0	1	0	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 43</i>	139	305	191	63	56	217	134	15	257
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 44</i>	90	151	109	59	49	123	138	67	187
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 45</i>	51	32	41	83	59	27	102	69	29
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 46</i>	69	24	40	11	1	33	49	0	26
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 47</i>	50	63	84	13	11	87	48	6	113
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 48</i>	30	31	21	17	1	38	29	1	37
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 49</i>	13	4	27	11	1	18	27	0	44
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 5</i>	159	378	358	78	119	258	257	177	406
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 50</i>	13	29	23	4	0	44	14	0	57
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 51</i>	8	20	33	12	0	40	9	0	57
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 52</i>	4	4	34	11	1	15	25	18	47
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 53</i>	22	14	21	11	0	10	23	0	26
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 54</i>	2	5	4	1	1	4	0	7	10
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 55</i>	23	14	14	14	5	28	25	3	28
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 56</i>	17	34	63	20	18	42	42	36	58
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 57</i>	1	9	10	0	2	7	2	6	12
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 58</i>	2	2	8	4	0	18	2	1	13
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 59</i>	87	110	98	83	14	104	61	19	58
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 6</i>	91	90	117	77	109	131	52	59	126
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 60</i>	3	1	9	3	0	8	3	0	10
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 62</i>	7	2	0	1	2	0	0	0	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 63</i>	0	0	0	0	3	12	0	1	6
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 65</i>	0	4	0	0	2	0	0	2	0
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 66</i>	0	0	1	0	1	2	1	0	2
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 7</i>	5	2	6	37	72	17	76	54	8
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 8</i>	23	1	13	72	42	5	21	26	8
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Candidatus Solibacter 9</i>	10	5	18	7	19	25	15	27	16
<i>Acidobacteria</i>	<i>Acidobacteriia</i>	<i>Paludibaculum</i>	7	0	0	14	21	0	0	3	0
<i>Acidobacteria</i>	<i>Blastocatellia</i> (Subgroup 4)	unknown 11-24 bacterium 1	0	0	0	1	0	4	0	0	1
<i>Acidobacteria</i>	<i>Blastocatellia</i> (Subgroup 4)	unknown 11-24 bacterium 2	0	0	0	1	3	2	0	2	0
<i>Acidobacteria</i>	<i>Blastocatellia</i> (Subgroup 4)	JGI 0001001-H03	0	0	0	0	5	0	0	6	2
<i>Acidobacteria</i>	<i>Blastocatellia</i> (Subgroup 4)	RB41	3	1	5	0	0	0	0	0	0
<i>Acidobacteria</i>	<i>Holophagae</i>	unknown Holophagae Subgroup 7 bacterium 1	0	0	0	5	0	0	1	2	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Acidobacteria</i>	<i>Holophagae</i>	<i>unknown Holophagae Subgroup 7 bacterium 2</i>	0	0	1	4	3	2	3	1	4
<i>Acidobacteria</i>	<i>Holophagae</i>	<i>unknown Holophagae Subgroup 7 bacterium 3</i>	0	0	0	0	3	0	2	8	4
<i>Acidobacteria</i>	<i>Holophagae</i>	<i>unknown Holophagae Subgroup 7 bacterium 4</i>	5	0	2	0	0	0	0	0	2
<i>Acidobacteria</i>	<i>Holophagae</i>	<i>unknown proteobacteriu m bacterium</i>	37	8	14	1	1	0	8	1	15
<i>Acidobacteria</i>	<i>Thermoanaerobaculia</i>	<i>Thermoanaerob aculaceae Subgroup 10 1</i>	320	204	112	286	85	254	191	3	258
<i>Acidobacteria</i>	<i>Thermoanaerobaculia</i>	<i>Thermoanaerob aculaceae Subgroup 10 2</i>	1	0	14	4	1	29	13	13	82
<i>Acidobacteria</i>	<i>Thermoanaerobaculia</i>	<i>Thermoanaerob aculaceae Subgroup 10 4</i>	3	0	1	0	0	0	1	0	2
<i>Acidobacteria</i>	<i>Thermoanaerobaculia</i>	<i>Thermoanaerob aculaceae Subgroup 10 6</i>	0	0	33	18	23	50	44	36	327
<i>Acidobacteria</i>	<i>Thermoanaerobaculia</i>	<i>Thermoanaerob aculaceae Subgroup 10 7</i>	1	0	13	4	14	42	27	33	47
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 15</i>	<i>unknown Acidobacteria Subgroup 15 bacterium 1</i>	7	14	10	3	1	4	12	4	5
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 15</i>	<i>unknown Acidobacteria Subgroup 15 bacterium 2</i>	1	7	0	0	0	0	3	0	1
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 15</i>	<i>unknown Acidobacteria Subgroup 15 bacterium 3</i>	0	0	2	1	0	1	1	0	4
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 15</i>	<i>unknown Acidobacteria Subgroup 15 bacterium 4</i>	6	1	3	1	0	1	1	0	0
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 15</i>	<i>unknown Acidobacteria Subgroup 15 bacterium 5</i>	0	9	0	1	0	0	2	0	0
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 15</i>	<i>unknown Acidobacteria Subgroup 15 bacterium 6</i>	0	3	1	0	0	3	2	0	3
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 5</i>	<i>unknown Acidobacteria Subgroup 5 bacterium 1</i>	20	33	40	7	0	12	6	4	28
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 5</i>	<i>unknown Acidobacteria Subgroup 5 bacterium 2</i>	73	31	65	17	0	40	15	2	38
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 5</i>	<i>unknown Acidobacteria Subgroup 5 bacterium 3</i>	1	0	3	0	0	0	1	0	2
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 5</i>	<i>unknown Acidobacteria Subgroup 5 bacterium 4</i>	3	2	5	1	1	6	2	1	15

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 5</i>	<i>unknown Acidobacteria Subgroup 5 bacterium 6</i>	31	11	42	16	1	16	12	0	29
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 5</i>	<i>unknown Acidobacteria Subgroup 5 bacterium 8</i>	40	12	47	18	2	26	9	4	26
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 6</i>	<i>unknown Acidobacteria Subgroup 6 bacterium 1</i>	2	6	13	0	2	3	6	5	30
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 6</i>	<i>unknown Acidobacteria Subgroup 6 bacterium 10</i>	48	14	18	1	0	1	11	2	7
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 6</i>	<i>unknown Acidobacteria Subgroup 6 bacterium 11</i>	19	3	13	0	0	1	6	5	9
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 6</i>	<i>unknown Acidobacteria Subgroup 6 bacterium 12</i>	1	0	1	0	0	0	2	0	5
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 6</i>	<i>unknown Acidobacteria Subgroup 6 bacterium 2</i>	11	2	4	0	0	1	1	0	1
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 6</i>	<i>unknown Acidobacteria Subgroup 6 bacterium 3</i>	1	1	3	0	0	0	1	1	5
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 6</i>	<i>unknown Acidobacteria Subgroup 6 bacterium 7</i>	4	1	2	0	0	0	1	0	4
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 6</i>	<i>unknown Acidobacteria Subgroup 6 bacterium 8</i>	3	0	1	0	0	0	1	0	1
<i>Acidobacteria</i>	<i>Acidobacteria Subgroup 6</i>	<i>unknown Acidobacteria Subgroup 6 bacterium 9</i>	43	10	40	1	4	6	19	7	35
<i>Actinobacteria</i>	<i>0319-7L14</i>	<i>unknown 0319-7L16 bacterium</i>	124	152	138	124	117	67	302	70	120
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiaceae</i>	35	3	68	66	1	102	20	1	37
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 1</i>	1	0	2	0	0	5	0	1	10
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 2</i>	0	0	16	0	1	9	0	1	13
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 3</i>	2	0	6	1	0	29	1	0	19
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 4</i>	0	0	13	9	15	2	5	16	2
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 5</i>	7	3	18	8	1	20	6	0	8
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 6</i>	2	11	13	15	5	15	19	17	17
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 7</i>	12	0	19	47	17	58	7	2	15
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 8</i>	21	58	30	12	24	29	24	27	32

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 9</i>	24	16	50	38	19	115	50	26	95
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 10</i>	153	93	77	127	14	86	132	31	94
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 11</i>	130	98	156	87	35	166	93	10	84
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 12</i>	276	149	337	311	123	416	918	82	466
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 13</i>	0	0	0	1	1	1	0	3	5
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 14</i>	1	0	1	5	1	7	0	0	4
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 15</i>	30	0	74	28	15	70	20	8	104
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 16</i>	0	0	175	0	4	94	2	1	164
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown IMCC26256 bacterium 17</i>	247	154	403	253	93	601	287	43	445
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>lamia 1</i>	0	0	7	4	3	6	1	1	4
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>lamia 2</i>	2	0	0	31	7	0	2	8	4
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>lamia 3</i>	0	0	2	3	1	0	0	0	0
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>lamia 5</i>	0	0	6	20	21	25	26	25	21
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>CL500-29 marine group 1</i>	0	0	2	6	1	0	0	0	1
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>CL500-29 marine group 2</i>	0	0	1	13	3	0	1	0	1
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>CL500-29 marine group 3</i>	0	0	1	12	1	2	1	1	2
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>CL500-29 marine group 4</i>	0	0	1	4	10	3	6	6	0
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Illumatobacteraceae 1</i>	0	0	1	54	16	1	28	4	0
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Illumatobacteraceae 2</i>	0	0	3	2	0	5	0	1	7
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Illumatobacteraceae 5</i>	0	0	3	0	0	7	1	0	6
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Illumatobacteraceae 6</i>	0	0	2	0	2	0	0	0	2
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichaceae 1</i>	0	0	1	5	4	2	1	6	3
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichaceae 2</i>	0	1	1	5	4	3	0	5	12
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichaceae 3</i>	1	0	0	9	13	1	8	0	1
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichales bacterium 1</i>	2	1	2	9	6	7	9	8	8
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichales bacterium 10</i>	1	0	1	5	3	0	0	4	1
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichales bacterium 12</i>	1	0	4	215	164	8	25	31	3
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichales bacterium 13</i>	4	2	1	26	21	16	7	14	13

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichales bacterium 14</i>	4	1	17	8	2	20	11	0	11
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichales bacterium 2</i>	1	0	32	70	31	30	27	17	20
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichales bacterium 3</i>	1	0	0	3	1	6	0	3	7
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichales bacterium 4</i>	0	0	1	2	2	0	0	1	1
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichales bacterium 5</i>	0	0	0	5	5	0	3	4	2
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichales bacterium 7</i>	0	0	0	1	4	1	0	0	1
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichales bacterium 8</i>	0	0	1	1	0	7	0	0	0
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Microtrichales bacterium 9</i>	0	0	3	15	8	2	2	0	5
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 1</i>	771	694	863	551	213	856	608	357	806
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 10</i>	0	0	7	0	1	15	0	2	21
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 11</i>	15	11	14	2	1	12	9	1	6
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 12</i>	0	0	0	2	8	0	4	11	0
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 13</i>	302	202	320	215	153	391	415	191	252
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 14</i>	60	41	52	34	4	65	38	5	74
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 15</i>	5	1	17	131	122	19	50	42	17
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 16</i>	6	3	5	11	4	16	2	0	9
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 17</i>	4	2	3	3	0	2	0	0	0
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 2</i>	7	55	18	409	1521	7	1508	1893	16
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 3</i>	236	184	268	204	156	431	147	111	236
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 4</i>	126	47	35	68	14	47	96	12	46
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 5</i>	1	0	43	2	0	20	10	3	13
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 6</i>	9	2	45	4	2	17	5	0	5
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 7</i>	0	0	1	31	25	6	4	1	1

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 8</i>	0	0	0	12	8	0	0	0	0
<i>Actinobacteria</i>	<i>Acidimicrobiia</i>	<i>unknown Acidimicrobiia bacterium 9</i>	8	1	6	12	7	3	16	4	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 1</i>	8	1	3	6	0	5	3	0	5
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 10</i>	6	2	1	7	1	27	9	0	5
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 11</i>	0	0	2	0	1	1	0	0	8
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 12</i>	3	3	0	2	0	1	1	0	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 14</i>	2	0	0	1	0	0	0	0	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 15</i>	0	0	0	0	0	3	0	0	28
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 2</i>	87	93	244	131	218	156	373	478	360
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 3</i>	43	457	34	6	6	9	15	326	22
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 4</i>	14	110	54	9	0	47	10	1	373
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 5</i>	51	0	60	81	1	34	30	0	51
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 6</i>	4	0	34	11	0	40	10	0	124
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 7</i>	0	0	10	0	0	27	0	0	64
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 8</i>	2	3	18	10	0	5	4	0	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinospica 9</i>	1	0	1	0	0	2	0	0	11
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Catenulispora 1</i>	73	17	45	74	24	58	50	31	62
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Catenulispora 2</i>	3	0	2	1	4	15	0	0	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Catenulispora 4</i>	0	0	2	1	0	0	0	0	7
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 1</i>	132	149	134	235	61	250	138	142	230
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 10</i>	1	1	1	0	14	21	4	9	29
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 11</i>	74	227	58	32	58	70	25	18	49
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 12</i>	6	7	10	21	4	16	31	3	11
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 13</i>	3	0	1	156	2	2	21	1	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 2</i>	36	37	29	42	17	148	54	45	73
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 3</i>	13	153	45	1	32	83	7	19	74
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 4</i>	21	6	32	22	20	63	25	23	46
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 5</i>	122	104	269	93	25	156	59	14	174
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 7</i>	990	1148	1482	599	279	1857	1225	548	1647
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 8</i>	204	438	426	84	68	629	171	146	506
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Mycobacterium 9</i>	11	17	20	68	38	28	16	40	46
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardia 1</i>	5	24	29	9	19	20	8	10	38
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardia 2</i>	5	8	13	3	10	13	5	20	11
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardia 3</i>	15	6	7	18	17	7	2	10	22
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardia 4</i>	6	0	3	5	0	1	1	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Rhodococcus 1</i>	1	0	0	8	49	1	1	2	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Rhodococcus 3</i>	1	1	7	0	2	3	1	1	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Tsukamurella</i>	0	0	0	0	7	0	2	0	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrmus 1</i>	5879	7335	4879	6028	4657	5365	5647	3169	6928
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrmus 10</i>	364	672	545	362	170	304	405	2347	626
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrmus 11</i>	666	427	391	455	369	555	585	80	552
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrmus 12</i>	25	118	29	25	6	54	29	22	241
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrmus 13</i>	128	53	70	221	102	218	111	66	102
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrmus 14</i>	2	75	36	0	0	52	3	3	193
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrmus 15</i>	5	4	26	9	10	12	11	43	51

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Plylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 16	675	5	59	323	75	14	102	14	32
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 17	271	184	146	169	38	45	73	52	72
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 18	28	29	20	62	17	34	53	19	35
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 19	103	63	138	89	36	73	66	33	184
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 2	3273	2584	3620	2764	2255	3940	2634	2135	4091
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 20	133	12	75	223	54	49	322	77	53
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 21	40	5	2	31	28	0	23	11	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 22	7	0	0	41	7	3	4	24	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 23	42	34	41	84	34	103	49	30	78
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 24	6	1	6	36	11	13	45	17	5
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 25	410	825	164	803	1587	97	1194	1108	127
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 26	11	1	1	17	5	1	18	5	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 27	7	8	10	5	6	14	8	1	8
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 28	0	1	5	0	3	0	0	1	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 29	5	2	24	2	0	14	4	1	18
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 3	1391	947	202	1589	3044	60	586	1445	92
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 30	4	9	58	11	3	8	1	32	17
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 31	3	0	1	4	2	0	0	3	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 32	1	2	3	1	0	1	1	2	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 33	4	5	5	12	2	5	6	5	8
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 34	7	5	3	22	3	17	8	1	9
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 35	13	9	3	10	17	0	4	8	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 37	5	0	0	13	2	21	6	0	9
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 38	6	0	14	0	0	7	2	0	20
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 39	587	185	194	1195	337	282	1386	415	207
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 4	664	77	176	1902	477	82	1628	720	111
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 40	25	10	14	49	21	56	21	13	23
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 41	855	1511	850	1337	1094	576	867	1765	1069
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 42	330	54	227	148	8	243	185	11	294
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 43	77	18	27	268	65	42	68	53	37
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 44	24	39	20	40	11	25	34	17	25
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 45	3	4	2	1	3	1	7	4	17
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 46	85	40	59	30	11	67	41	6	40
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 47	5	0	0	9	13	1	15	12	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 5	222	126	285	733	391	440	1430	431	547
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidotherrnus</i> 6	952	255	350	439	273	247	202	538	444

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidothermus 7</i>	170	231	141	159	51	444	96	71	377
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidothermus 8</i>	29	462	49	18	14	96	31	5	189
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidothermus 9</i>	136	267	253	54	31	276	49	51	163
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Cryptosporangium</i>	2	0	5	0	0	2	1	1	11
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Fodinicola</i>	0	0	1	1	3	0	1	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Cryptosporangia</i>	0	0	2	4	0	1	1	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Cryptosporangia bacterium</i>	17	1	4	165	221	26	268	185	15
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitan s 1</i>	2	6	36	61	71	91	44	57	63
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitan s 10</i>	1	1	8	13	17	7	11	28	7
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitan s 11</i>	0	0	0	9	7	8	4	3	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitan s 12</i>	0	0	0	0	0	1	0	1	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitan s 13</i>	10	15	50	97	62	141	139	74	85
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitan s 2</i>	1	7	57	66	42	233	21	23	103
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitan s 3</i>	0	8	4	25	66	17	55	62	20
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitan s 4</i>	11	1	24	179	268	37	319	165	31
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitan s 6</i>	2	5	125	52	61	321	46	30	279
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitan s 7</i>	6	1	37	231	81	313	65	63	61
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitan s 8</i>	6	7	15	15	33	29	29	62	59
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Jatrophihabitan s 9</i>	26	2	42	628	525	237	533	439	95
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Blastococcus 1</i>	96	3	40	899	881	133	877	378	97
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Blastococcus 2</i>	2	0	0	35	9	1	4	4	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Blastococcus 3</i>	2	2	3	44	39	21	16	4	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Modestobacter 1</i>	0	0	2	1	1	3	0	0	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Modestobacter 2</i>	19	0	11	538	572	6	213	187	8
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Modestobacter 3</i>	26	5	53	238	145	230	375	72	96
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Geodermatophilaceae bacterium</i>	2	0	9	11	3	9	4	2	19
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nakamurella 1</i>	0	0	39	25	8	72	4	6	70
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nakamurella 3</i>	2	2	8	15	36	47	13	30	15
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nakamurella 4</i>	0	0	1	9	304	0	23	29	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>hgcl clade</i>	2	0	0	230	3	0	54	6	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Sporichthyaceae bacterium 1</i>	3	6	2	35	26	18	12	23	8
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Sporichthyaceae bacterium 2</i>									

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Sporichthyaceae bacterium 5</i>	12	1	10	31	10	12	19	21	21
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 1</i>	0	0	1	21	39	4	13	11	22
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 10</i>	0	0	0	8	7	1	3	3	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 11</i>	55	0	0	931	1059	0	4007	1828	17
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 12</i>	2	0	0	11	2	4	9	3	8
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 13</i>	0	0	0	1	9	0	0	1	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 14</i>	0	0	4	1	4	2	1	1	5
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 16</i>	0	0	0	0	2	0	3	2	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 2</i>	4	0	0	0	0	0	0	0	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 3</i>	121	19	50	2065	1165	56	340	239	54
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 4</i>	2	0	15	27	10	52	18	18	33
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 5</i>	0	0	0	31	7	1	2	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 6</i>	0	2	35	41	5	37	34	47	73
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 7</i>	2	1	20	7	18	12	2	18	31
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 8</i>	10	1	10	11	0	3	5	0	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Frankiales bacterium 9</i>	5	9	2	2	1	9	3	1	11
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Kineosporia</i>	0	0	0	1	2	2	3	0	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown kineosporiaceae bacterium 1</i>	1	1	13	96	100	38	44	51	60
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown kineosporiaceae bacterium 2</i>	0	0	2	1	1	2	0	2	13
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Georgenia</i>	7	0	1	0	0	1	0	1	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Cellulomonas 1</i>	0	0	4	1	1	2	1	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Dermatophilaceae bacterium</i>	1	0	3	30	48	8	16	21	30
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Lapillicoccus</i>	19	0	310	72	166	178	270	100	258
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Phycococcus</i>	3	0	1	67	9	4	17	6	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Conyzicola</i>	21	4	0	4	12	1	0	5	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Curtobacterium</i>	69	144	2	24	75	2	29	5	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Frigoribacterium</i>	8	2	0	34	84	0	23	15	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Gryllotalpicola</i>	0	0	0	0	9	0	0	10	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Gryllotalpicola</i>	3	58	6	72	101	13	66	46	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Leifsonia 1</i>	13	13	32	260	380	117	272	241	78
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Leifsonia 2</i>	552	115	8	425	731	40	997	544	27
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Leifsonia 3</i>	26	5	0	41	33	3	32	11	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Leifsonia 4</i>	22	9	2	18	31	15	52	22	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Lysinimonas</i>	3	0	1	52	150	0	90	3	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Microbacterium</i> 3	4	0	0	1	9	0	0	2	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Parafriogibacterium</i> 1	2	4	1	7	3	1	0	14	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	unknown <i>Microbacteriaceae</i> bacterium 1	219	148	44	178	158	27	213	315	80
<i>Actinobacteria</i>	<i>Actinobacteria</i>	unknown <i>Microbacteriaceae</i> bacterium 2	1	0	0	54	41	13	13	33	20
<i>Actinobacteria</i>	<i>Actinobacteria</i>	unknown <i>Microbacteriaceae</i> bacterium 3	42	10	31	285	478	167	182	394	99
<i>Actinobacteria</i>	<i>Actinobacteria</i>	unknown <i>Microbacteriaceae</i> bacterium 4	0	1	4	0	0	21	1	0	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	unknown <i>Microbacteriaceae</i> bacterium 5	53	11	1	19	21	0	0	6	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Arthrobacter</i>	2	0	0	0	0	0	1	3	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Arthrobacter</i>	909	221	32	764	2365	79	1269	1135	86
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Glutamicibacter</i>	0	0	0	13	17	1	0	1	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Paeniglutamicibacter</i>	3	0	0	0	1	0	2	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudarthrobacter</i> 1	65	1	0	172	1475	4	51	441	10
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudarthrobacter</i> 2	212	18	110	768	1115	36	407	397	470
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudarthrobacter</i> 4	1	0	0	10	13	1	4	3	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Sinomonas</i>	2	1	14	7	2	11	26	0	10
<i>Actinobacteria</i>	<i>Actinobacteria</i>	unknown <i>Micrococcaceae</i> bacterium 1	138	4	13	1703	1149	11	175	392	21
<i>Actinobacteria</i>	<i>Actinobacteria</i>	unknown <i>Micrococcaceae</i> bacterium 2	98	1	1	252	622	8	76	97	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	unknown <i>Micrococcales</i> bacterium 1	0	0	13	16	8	8	5	4	9
<i>Actinobacteria</i>	<i>Actinobacteria</i>	unknown <i>Micrococcales</i> bacterium 2	0	0	0	2	0	0	0	7	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinoplanes</i>	0	0	1	3	1	4	2	2	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinoplanes</i>	1	0	9	1	2	7	2	0	25
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Dactylosporangium</i>	0	0	1	5	0	0	0	1	5
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Luedemannella</i>	46	0	7	9	1	0	2	2	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Micromonospora</i> 1	5	0	2	1	0	1	1	0	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Micromonospora</i> 2	23	0	0	20	0	0	127	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	unknown <i>Micromonosporaceae</i> bacterium 1	0	0	2	0	0	5	0	0	5
<i>Actinobacteria</i>	<i>Actinobacteria</i>	unknown <i>Micromonosporaceae</i> bacterium 3	7	2	32	50	18	37	26	20	97
<i>Actinobacteria</i>	<i>Actinobacteria</i>	unknown <i>Micromonosporaceae</i> bacterium 4	0	0	12	24	4	9	6	6	31

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Micromonosporaceae bacterium 5</i>	0	0	3	1	1	8	0	0	12
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Aeromicrobium</i>	1	0	0	11	1	0	0	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Kribbella 1</i>	0	0	4	5	17	0	0	8	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Marmoricola 1</i>	1	1	1	522	961	24	438	281	10
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Marmoricola 2</i>	0	1	0	48	24	32	52	15	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Marmoricola 4</i>	0	0	1	44	58	24	11	13	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 1</i>	0	0	3	4	6	9	3	1	13
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 10</i>	0	0	1	4	1	4	0	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 12</i>	1	0	0	4	0	1	1	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 13</i>	0	0	0	5	2	2	3	0	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 14</i>	0	0	1	0	0	4	1	0	4
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 15</i>	0	0	0	0	0	4	0	0	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 16</i>	0	1	0	1	10	0	1	3	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 18</i>	3	2	0	31	199	3	21	84	5
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 19</i>	3	0	0	24	2	0	1	1	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 2</i>	0	0	15	15	12	166	7	1	31
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 21</i>	1	0	0	23	7	1	1	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 23</i>	0	0	0	3	2	0	0	1	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 25</i>	1	0	4	6	0	0	0	0	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 26</i>	0	0	0	4	3	0	0	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 3</i>	0	0	1	44	10	12	4	1	11
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 4</i>	0	0	7	0	7	13	0	3	28
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 5</i>	0	0	0	4	0	8	0	1	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 6</i>	0	0	0	53	14	0	1	2	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 7</i>	0	0	0	42	0	4	4	0	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Nocardioideis 8</i>	0	0	5	5	1	28	2	2	12
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Cutibacterium</i>	16	17	14	2	5	2	1	0	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Friedmanniella</i>	0	0	2	3	0	8	2	2	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Microbunatus</i>	1	0	8	3	0	6	7	1	8
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetospora</i>	0	0	34	24	47	104	6	6	75
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinophytocola 3</i>	6	2	3	38	4	2	21	2	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Amycolatopsis 1</i>	1	29	3	54	513	6	69	223	12
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Amycolatopsis 2</i>	0	0	0	14	0	0	0	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Crossiella</i>	2	26	0	8	0	0	1	0	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Crossiella</i>	57	5	91	24	6	108	84	18	170
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Longimycelium 1</i>	9	24	91	6	13	65	9	6	131
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Longimycelium 2</i>	11	5	122	6	12	11	4	10	18
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Longimycelium 3</i>	15	9	63	62	34	62	93	46	87
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardia 1</i>	443	93	28	1926	1805	62	1187	1432	81
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardia 10</i>	9	0	8	8	0	18	5	2	14
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardia 2</i>	3	3	135	35	20	150	15	30	208
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardia 3</i>	0	2	1	11	8	9	4	14	15
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardia 4</i>	0	0	1	1	0	10	1	0	13

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardia</i> 5	0	0	0	6	1	0	2	2	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardia</i> 7	29	33	48	135	82	52	399	689	45
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardia</i> 8	3	0	0	22	12	0	4	4	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Pseudonocardia</i> 9	1	0	1	0	0	11	2	0	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	unknown <i>Pseudonocardia</i> <i>ceae bacterium</i> 1	2	3	34	13	14	17	42	12	31
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Kitasatospora</i> 1	14	6	14	28	0	6	7	0	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Kitasatospora</i> 2	9	1	19	0	0	0	0	0	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Kitasatospora</i> 3	4	1	1	1	0	0	0	0	11
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptacidiphilus</i> 1	98	14	38	74	97	20	20	16	18
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptacidiphilus</i> 2	8	3	68	39	20	62	24	79	72
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptacidiphilus</i> 3	12	3	62	5	4	11	10	24	176
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptacidiphilus</i> 4	2	1	1	1	4	3	2	1	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 1	2	1	7	1	0	32	3	0	8
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 10	19	0	0	1	0	1	0	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 11	1	2	1	4	3	0	2	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 13	1	0	1	0	0	1	0	0	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 14	1	0	1	0	0	6	0	0	3
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 15	0	0	0	0	0	0	0	0	14
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 16	3	5	0	0	0	0	0	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 17	2	0	0	2	0	4	0	0	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 19	7	1	1	0	0	1	0	0	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 2	2	0	1	0	0	16	0	0	6
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 27	1	0	1	0	0	2	1	0	5
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 3	1756	4505	47	371	1095	58	285	276	71
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 4	159	927	27	42	338	45	121	191	30
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 5	12	6	37	23	27	73	18	3	85
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 6	4	0	8	30	49	27	6	27	5
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 7	177	0	1	5	0	0	0	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 8	56	1	1	24	0	0	12	0	2
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptomyces</i> 9	4	0	0	1	0	49	0	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Microbispora</i> 1	3	0	0	0	1	2	2	2	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Streptosporangium</i> 3	18	1	1	1	0	3	0	1	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Motilibacter</i>	0	0	0	2	1	7	0	1	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinoallomurus</i> 1	239	92	9	484	4	9	895	15	19
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomadura</i> 1	3	1	5	9	0	5	9	0	1
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomadura</i> 2	12	0	1	3	0	0	8	1	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomadura</i> 3	0	1	1	1	0	2	0	1	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Thermomonas oraceae bacterium 2</i>	32	0	0	0	0	2	1	0	0
<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>unknown Actinobacteria bacterium 2</i>	0	0	0	1	5	0	14	0	0
<i>Actinobacteria</i>	<i>MB-A2-108</i>	<i>unknown MB-A2-110 bacterium</i>	0	0	2	0	0	3	0	0	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Gaiella 1</i>	0	0	111	246	213	100	74	87	89
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Gaiella 2</i>	0	0	0	5	2	2	0	0	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Gaiella 5</i>	0	0	15	0	0	4	0	1	17
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 1</i>	4	2	229	477	232	255	113	142	239
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 10</i>	30	9	106	15	1	88	6	1	124
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 11</i>	0	0	6	0	0	0	0	0	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 12</i>	4	0	93	9	4	49	3	1	104
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 13</i>	0	0	5	0	0	2	0	0	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 16</i>	8	0	43	11	0	29	3	1	22
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 18</i>	2	1	3	1	1	22	3	4	13
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 19</i>	0	0	1	1	0	4	1	0	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 2</i>	35	1	482	13	0	183	7	1	295
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 20</i>	20	0	6	2	0	8	2	0	4
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 21</i>	1	0	1	0	0	13	1	0	21
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 22</i>	1	1	9	0	0	4	0	0	10
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 23</i>	2	0	1	0	0	14	0	0	12
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 25</i>	0	0	0	0	0	15	0	0	7
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 28</i>	1	1	6	0	0	6	0	0	12
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 29</i>	2	0	2	0	0	12	0	0	6
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 3</i>	3	1	100	5	4	80	7	13	166
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 31</i>	0	0	0	3	2	1	6	1	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 32</i>	0	0	5	2	3	0	2	1	0
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 39</i>	0	0	7	0	0	1	0	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 4</i>	0	0	4	0	0	1	1	0	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 43</i>	1	0	33	10	1	39	15	2	46
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 5</i>	1	0	13	0	3	45	1	1	67
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 50</i>	1	0	5	1	0	1	0	0	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 51</i>	0	0	0	1	0	2	0	0	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 52</i>	2	0	0	2	2	6	4	0	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 57</i>	118	126	280	78	16	224	97	30	296
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 58</i>	26	9	95	7	0	45	18	3	64
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 59</i>	1	0	1	99	75	1	8	7	0
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 6</i>	0	0	21	40	16	21	15	8	20
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 60</i>	24	4	49	6	4	44	19	7	107
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 62</i>	3	0	13	1	1	9	0	0	12
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 63</i>	1	0	17	3	0	14	3	0	6
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 7</i>	2	0	9	25	23	43	19	28	48
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 8</i>	14	1	29	2	0	21	1	0	34
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Gaillales bacterium 9</i>	0	0	41	0	0	38	0	0	20
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 1</i>	0	0	1	2	0	2	0	0	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 2</i>	0	0	4	0	0	2	0	0	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 3</i>	0	0	2	1	0	2	1	0	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 4</i>	1	1	4	1	0	4	0	0	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 5</i>	0	0	4	5	0	6	0	0	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 6</i>	0	0	3	18	2	2	1	0	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 7</i>	7	0	6	6	0	9	1	0	4
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 8</i>	0	0	0	18	62	0	15	11	0
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 9</i>	12	2	44	26	3	45	4	2	31
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 10</i>	30	10	22	46	6	50	9	0	41
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 11</i>	1	1	42	36	28	79	11	21	62
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 12</i>	0	0	0	19	4	0	0	0	0
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 13</i>	0	0	0	17	4	0	1	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 14</i>	61	68	35	26	11	86	29	8	39
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 15</i>	43	39	76	127	57	138	144	52	67
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown 67-14 bacterium 16</i>	117	64	174	134	100	163	97	33	144
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 1</i>	4	1	4	54	27	22	10	2	20
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 10</i>	81	105	131	132	72	165	101	44	53
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 11</i>	0	5	3	2	0	7	0	0	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 12</i>	2	1	2	2	0	1	2	0	4
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 13</i>	6	9	1	3	1	2	2	1	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 2</i>	39	38	45	68	18	92	39	42	98
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 3</i>	1	0	29	114	34	48	14	5	14
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 4</i>	5	4	5	26	5	26	12	2	7
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 5</i>	0	0	0	13	3	0	0	0	0
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 6</i>	1	0	0	7	0	5	3	1	5
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 7</i>	7	2	14	10	5	27	10	2	3
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 8</i>	0	0	0	4	4	0	2	3	0
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Conexibacter 9</i>	2387	1402	2709	2985	1237	4415	2604	741	2811
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 1</i>	516	530	586	1037	796	707	2404	752	609
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 2</i>	142	89	156	109	53	131	159	24	155
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 3</i>	5	1	6	3	1	11	8	2	4
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 4</i>	2	0	1	5	0	0	2	0	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 5</i>	2	0	0	103	43	3	9	14	5
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 6</i>	2	0	0	32	18	18	6	3	2
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 7</i>	0	0	0	7	1	1	0	1	0
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>Solirubrobacter 8</i>	0	2	6	0	5	20	1	16	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Solirubrobacter aceae bacterium 1</i>	7	10	19	8	3	20	6	0	16
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Solirubrobacter aceae bacterium 2</i>	142	171	186	141	137	240	135	100	274
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Solirubrobacter aceae bacterium 3</i>	263	320	69	201	27	140	52	10	141
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Solirubrobacter aceae bacterium 4</i>	111	42	140	121	13	167	157	15	86
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Solirubrobacter aceae bacterium 5</i>	0	0	0	33	7	0	2	0	0
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Solirubrobacter aceae bacterium 6</i>	147	54	148	64	30	145	109	13	152
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Solirubrobacter aceae bacterium 7</i>	0	0	0	1	20	5	1	0	1
<i>Actinobacteria</i>	<i>Thermoleophilia</i>	<i>unknown Solirubrobacter aceae bacterium 8</i>	40	20	38	33	20	64	51	23	47
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown Armatimonadales bacterium 1</i>	25	163	20	10	11	7	53	97	51

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>10</i>	0	0	2	1	1	2	15	3	3
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>11</i>	1	5	1	0	3	8	17	1	2
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>12</i>	0	0	2	1	0	1	3	2	1
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>13</i>	1	1	1	0	0	0	2	2	1
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>14</i>	0	0	0	0	0	0	0	6	0
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>15</i>	2	4	2	2	0	3	4	8	9
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>16</i>	0	0	0	0	2	0	2	2	0
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>17</i>	3	0	1	0	0	0	3	0	1
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>18</i>	0	0	2	0	0	0	1	0	3
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>2</i>	40	88	31	14	17	28	81	43	87
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>20</i>	0	0	0	0	0	3	2	0	1
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>21</i>	0	1	0	1	0	3	0	0	2
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>22</i>	0	0	3	5	35	8	42	47	10
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>23</i>	7	32	15	1	1	6	4	1	23
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>24</i>	0	12	0	3	7	1	1	23	0
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>25</i>	24	3	9	2	4	5	9	12	4
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>26</i>	5	3	2	0	5	0	4	18	4
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>27</i>	2	3	3	1	1	11	3	0	1
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales bacterium</i> <i>3</i>	6	58	18	44	16	9	11	58	15

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales</i> <i>bacterium 4</i>	4	2	11	12	18	16	38	24	6
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales</i> <i>bacterium 5</i>	4	4	5	2	7	2	19	6	9
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales</i> <i>bacterium 6</i>	5	5	3	3	3	0	2	8	8
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales</i> <i>bacterium 7</i>	0	0	0	0	1	0	9	10	0
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales</i> <i>bacterium 8</i>	0	0	0	0	1	12	1	1	3
<i>Armatimonadetes</i>	<i>Armatimonadia</i>	<i>unknown</i> <i>Armatimonadales</i> <i>bacterium 9</i>	1	0	0	6	8	0	2	2	1
<i>Armatimonadetes</i>	<i>Chthonomonadetes</i>	<i>Chthonomonas</i> <i>1</i>	4	16	0	0	0	0	2	0	1
<i>Armatimonadetes</i>	<i>Chthonomonadetes</i>	<i>Chthonomonas</i> <i>2</i>	1	3	1	0	1	0	2	12	3
<i>Armatimonadetes</i>	<i>Chthonomonadetes</i>	<i>Chthonomonas</i> <i>3</i>	1	4	1	0	1	1	2	0	4
<i>Armatimonadetes</i>	<i>Chthonomonadetes</i>	<i>Chthonomonas</i> <i>6</i>	0	0	0	0	2	0	2	2	0
<i>Armatimonadetes</i>	<i>Chthonomonadetes</i>	<i>unknown</i> <i>Chthonomonadales</i> <i>bacterium 1</i>	0	0	0	0	0	0	0	11	0
<i>Armatimonadetes</i>	<i>Chthonomonadetes</i>	<i>unknown</i> <i>Chthonomonadales</i> <i>bacterium 2</i>	6	0	0	0	0	1	0	0	0
<i>Armatimonadetes</i>	<i>Chthonomonadetes</i>	<i>unknown</i> <i>Chthonomonadales</i> <i>bacterium 3</i>	1	1	1	0	0	0	4	0	0
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown</i> <i>Fimbriimonadaceae</i> <i>bacterium 1</i>	7	42	14	9	5	23	60	90	26
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown</i> <i>Fimbriimonadaceae</i> <i>bacterium 10</i>	0	0	0	2	1	5	16	3	2
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown</i> <i>Fimbriimonadaceae</i> <i>bacterium 11</i>	0	0	0	0	0	1	0	0	8
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown</i> <i>Fimbriimonadaceae</i> <i>bacterium 12</i>	1	3	8	0	3	6	11	15	2
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown</i> <i>Fimbriimonadaceae</i> <i>bacterium 13</i>	1	8	0	0	0	1	1	0	3
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown</i> <i>Fimbriimonadaceae</i> <i>bacterium 14</i>	2	2	3	0	3	0	2	0	6
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown</i> <i>Fimbriimonadaceae</i> <i>bacterium 17</i>	33	63	51	11	4	51	47	36	58
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown</i> <i>Fimbriimonadaceae</i> <i>bacterium 18</i>	17	68	13	1	0	10	26	6	38
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown</i> <i>Fimbriimonadaceae</i> <i>bacterium 19</i>	0	9	2	0	0	1	1	7	10

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown Fimbriimonadaceae bacterium 2</i>	21	48	37	21	15	14	60	44	53
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown Fimbriimonadaceae bacterium 20</i>	0	0	0	0	5	0	1	3	0
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown Fimbriimonadaceae bacterium 3</i>	0	7	10	9	3	13	95	45	5
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown Fimbriimonadaceae bacterium 4</i>	0	0	12	10	16	30	26	45	25
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown Fimbriimonadaceae bacterium 5</i>	3	41	1	1	11	0	10	32	2
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown Fimbriimonadaceae bacterium 6</i>	9	2	2	18	28	2	6	9	6
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown Fimbriimonadaceae bacterium 7</i>	3	26	2	2	4	1	2	27	6
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown Fimbriimonadaceae bacterium 8</i>	10	24	18	1	1	14	38	3	46
<i>Armatimonadetes</i>	<i>Fimbriimonadia</i>	<i>unknown Fimbriimonadaceae bacterium 9</i>	0	17	9	0	4	11	13	11	11
<i>Armatimonadetes</i>	<i>unknown Armatimonadetes</i>	<i>unknown Armatimonadetes bacterium 1</i>	3	9	12	0	1	1	15	1	9
<i>Armatimonadetes</i>	<i>unknown Armatimonadetes</i>	<i>unknown Armatimonadetes bacterium 2</i>	1	0	4	0	0	0	4	0	0
<i>Armatimonadetes</i>	<i>unknown Armatimonadetes</i>	<i>unknown Armatimonadetes bacterium 3</i>	0	0	3	0	1	0	8	5	1
<i>Armatimonadetes</i>	<i>unknown Armatimonadetes</i>	<i>unknown Armatimonadetes bacterium 4</i>	1	1	5	0	0	0	4	1	3
<i>Armatimonadetes</i>	<i>unknown Armatimonadetes</i>	<i>unknown Armatimonadetes bacterium 5</i>	0	0	3	0	2	0	3	0	1
<i>Armatimonadetes</i>	<i>unknown Armatimonadetes</i>	<i>unknown Armatimonadetes bacterium 8</i>	2	2	0	0	4	0	9	3	3
<i>Armatimonadetes</i>	<i>unknown Armatimonadetes</i>	<i>unknown Armatimonadetes bacterium 9</i>	3	2	1	0	0	0	1	0	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroides</i>	0	0	15	1	0	0	0	0	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Proteiniphilum</i>	0	3	0	0	4	0	2	0	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown 37-13 bacterium 1</i>	21	70	9	2	3	3	19	27	21
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown 37-13 bacterium 2</i>	122	228	44	9	16	6	116	170	41
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown 37-13 bacterium 3</i>	16	10	2	0	0	1	17	6	15
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Ferruginibacter 1</i>	0	5	0	0	1	0	0	1	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Ferruginibacter 2</i>	7	10	0	0	0	0	0	8	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Ferruginibacter 3</i>	7	2	3	0	0	1	2	16	4
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Ferruginibacter 4</i>	3	0	0	0	0	1	0	3	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Filimonas</i>	15	0	0	0	0	0	0	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Flavisolibacter 1</i>	5	2	7	2	17	1	14	30	6
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Flavisolibacter 2</i>	3	0	0	0	0	0	11	4	3
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Parafilimonas</i>	0	0	1	0	3	1	1	6	2
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Segetibacter 1</i>	10	5	0	8	105	0	21	36	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Segetibacter 3</i>	0	0	0	0	5	0	1	1	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 1</i>	18	1	19	1	0	0	3	2	14
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 10</i>	5	6	0	0	1	0	1	1	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 12</i>	1	3	2	0	0	0	0	0	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 13</i>	28	61	18	5	40	2	47	164	27
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 14</i>	15	1	2	1	0	0	1	0	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 15</i>	5	8	4	0	0	0	0	1	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 16</i>	1	0	0	0	4	1	0	4	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 17</i>	7	2	3	2	5	0	11	9	3
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 19</i>	4	2	1	0	1	0	0	0	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 2</i>	75	7	0	0	2	0	4	2	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 21</i>	1	6	3	3	6	0	5	34	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 22</i>	0	2	0	0	0	0	1	3	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 23</i>	1	6	0	0	8	0	1	5	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 3</i>	15	28	4	0	3	0	2	18	4
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 4</i>	2	0	3	2	1	0	2	3	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 5</i>	2	2	0	0	2	0	2	5	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 7</i>	1	0	2	0	1	0	0	3	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 8</i>	3	1	0	0	0	0	0	2	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagaceae bacterium 9</i>	0	0	0	0	2	0	3	2	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagales bacterium 1</i>	23	45	16	4	13	2	90	126	14
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagales bacterium 2</i>	7	5	3	0	2	1	5	6	11
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagales bacterium 5</i>	0	0	0	0	0	1	6	6	2
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagales bacterium 6</i>	8	1	0	1	0	0	3	2	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Chitinophagales bacterium 7</i>	0	3	1	0	0	1	0	1	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Cytophaga 1</i>	40	4	1	0	1	0	8	24	2
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Cytophaga 2</i>	1	8	1	0	0	0	1	0	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Sporocytophaga 1</i>	0	10	0	0	0	0	1	4	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Sporocytophaga 4</i>	0	0	1	0	0	0	2	7	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Adhaeribacter</i>	0	0	0	7	4	0	0	1	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Ohtaekwangia 5</i>	0	0	0	0	4	0	0	2	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 10</i>	0	0	0	2	6	0	4	1	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 12</i>	7	0	0	0	0	0	1	0	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 14</i>	0	0	0	1	4	0	0	1	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 5</i>	2	0	1	7	8	0	14	12	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown Microscillaceae bacterium 6</i>	7	0	2	1	0	7	3	16	3
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Spirosoma</i>	9	0	0	0	0	0	0	0	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Flavobacterium 1</i>	50	12	1	2	4	0	1	0	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Flavobacterium 2</i>	4	0	0	3	12	0	1	0	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Flavobacterium 4</i>	162	6	42	18	7	0	14	17	6
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Flavobacterium 5</i>	84	8	0	4	3	0	2	8	21
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Flavobacterium 6</i>	18	1	0	0	9	0	0	1	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Chryseobacterium 2</i>	0	0	0	0	33	0	2	0	20
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Chryseobacterium 3</i>	0	0	0	0	0	0	9	0	7
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown AKYH767 bacterium 1</i>	0	0	0	6	2	0	2	0	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown AKYH767 bacterium 2</i>	2	0	1	4	0	2	1	0	2
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown AKYH767 bacterium 3</i>	23	25	14	6	3	10	13	15	30
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown CWT CU03-E12 bacterium 1</i>	11	1	0	0	0	0	7	5	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown CWT CU03-E12 bacterium 2</i>	5	13	0	0	1	0	45	68	10
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown CWT CU03-E12 bacterium 3</i>	7	53	1	0	4	0	12	139	4

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown CWT CU03-E12 bacterium 4	63	34	5	0	0	0	330	196	16
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown CWT CU03-E12 bacterium 5	5	0	5	0	0	1	14	0	7
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown CWT CU03-E12 bacterium 6	13	29	4	19	8	0	72	18	19
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown CWT CU03-E12 bacterium 7	32	42	8	2	0	3	60	36	41
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 1	3	0	0	0	0	0	15	0	5
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 2	16	5	5	0	0	0	7	1	5
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 3	1	0	2	1	1	1	1	0	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 4	5	0	0	0	2	0	0	0	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 5	7	1	1	0	0	0	1	0	3
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 6	15	0	0	0	1	0	0	2	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 7	16	0	0	0	0	0	8	5	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 8	13	1	2	5	0	0	4	7	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 9	0	1	5	0	1	0	24	10	5
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 10	7	0	7	3	3	0	13	10	6
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 11	14	2	3	6	11	0	5	11	2
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 12	26	1	10	3	1	0	23	9	9
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 13	70	16	3	0	0	0	67	62	2
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 14	1	0	1	0	0	0	0	0	5
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 15	1	0	1	2	2	1	6	4	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 16	4	0	6	0	1	1	1	5	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 17	6	1	15	1	0	0	30	18	4
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown env.OPS 17 bacterium 18	20	1	11	1	8	0	17	31	6
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	uncultured bacterium	1	3	0	4	2	0	3	7	2
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	uncultured bacterium	0	0	0	14	2	0	4	3	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	uncultured bacterium	0	1	0	8	12	0	23	20	3
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	unknown KD3- 93 bacterium 1	27	4	3	2	1	0	6	8	6

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown KD3-93 bacterium 2</i>	5	0	1	1	0	0	4	5	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown LiUU-11-161 bacterium 1</i>	28	23	5	0	1	1	71	81	9
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown NS11-12 marine group bacterium 1</i>	2	0	0	0	1	0	3	1	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>unknown NS11-12 marine group bacterium 2</i>	9	0	0	0	0	0	0	1	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Mucilaginibacter 1</i>	93	32	1	1	13	0	10	52	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Mucilaginibacter 2</i>	34	3	0	0	2	0	4	10	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Mucilaginibacter 3</i>	2	1	1	0	2	0	2	10	1
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Mucilaginibacter 4</i>	19	6	0	0	1	0	3	10	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Pedobacter</i>	0	0	0	1	0	0	6	0	0
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Solitalea 1</i>	0	0	0	0	0	0	3	1	10
<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Solitalea 2</i>	0	5	1	0	0	0	1	0	0
<i>Bacteroidetes</i>	<i>Ignavibacteria</i>	<i>unknown OPB56 bacterium 1</i>	0	0	0	0	0	2	4	0	0
<i>Bacteroidetes</i>	<i>Ignavibacteria</i>	<i>unknown OPB56 bacterium 2</i>	3	0	0	0	0	2	2	0	0
<i>Bacteroidetes</i>	<i>Ignavibacteria</i>	<i>unknown OPB56 bacterium 3</i>	0	0	0	0	0	0	3	6	0
<i>Bacteroidetes</i>	<i>Ignavibacteria</i>	<i>unknown OPB56 bacterium 4</i>	1	2	2	1	0	2	0	0	1
<i>Bacteroidetes</i>	<i>Ignavibacteria</i>	<i>unknown OPB56 bacterium 5</i>	0	15	0	0	0	0	0	0	0
<i>Bacteroidetes</i>	<i>Ignavibacteria</i>	<i>unknown OPB56 bacterium 6</i>	1	1	3	7	6	2	21	25	4
<i>Bacteroidetes</i>	<i>Ignavibacteria</i>	<i>unknown OPB56 bacterium 7</i>	11	0	5	1	9	1	21	24	6
<i>Bacteroidetes</i>	<i>Ignavibacteria</i>	<i>unknown OPB56 bacterium 8</i>	13	26	21	3	0	2	24	9	14
<i>Bacteroidetes</i>	<i>Ignavibacteria</i>	<i>unknown OPB56 bacterium 9</i>	42	106	67	9	0	17	74	4	52
<i>Bacteroidetes</i>	<i>Ignavibacteria</i>	<i>unknown SJA-28 bacterium 1</i>	0	0	4	0	0	0	3	0	1
<i>Bacteroidetes</i>	<i>Ignavibacteria</i>	<i>unknown SJA-28 bacterium 2</i>	9	0	0	0	0	0	0	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Chlamydia</i>	0	2	1	0	0	2	2	0	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown cvE6 bacterium 1</i>	0	5	0	0	0	0	1	0	4
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown cvE6 bacterium 2</i>	5	2	2	2	0	1	1	0	3
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown cvE6 bacterium 3</i>	5	2	3	1	0	1	4	0	3
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown cvE6 bacterium 4</i>	6	6	0	0	0	0	2	1	6
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown cvE6 bacterium 5</i>	36	23	3	3	26	3	25	0	2
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown cvE6 bacterium 6</i>	0	0	0	0	0	0	2	5	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown cvE6 bacterium 7</i>	3	0	1	0	0	0	1	0	5

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown cvE6 bacterium 8</i>	1	8	0	0	0	0	1	8	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown cvE6 bacterium 9</i>	17	8	0	0	4	0	9	6	9
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Protochlamydia 10</i>	0	0	2	0	0	0	0	4	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Protochlamydia 11</i>	1	1	1	0	0	0	2	0	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Protochlamydia 2</i>	5	7	4	2	2	5	8	5	4
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Protochlamydia 3</i>	1	0	1	0	0	1	10	1	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Protochlamydia 4</i>	0	4	1	0	1	0	1	2	3
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Protochlamydia 5</i>	0	6	0	0	2	0	0	1	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Protochlamydia 7</i>	2	3	0	0	1	0	0	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Neochlamydia 1</i>	1	1	1	1	0	0	1	0	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Neochlamydia 14</i>	3	4	0	0	0	1	1	0	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Neochlamydia 20</i>	2	1	1	0	0	0	1	0	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Neochlamydia 21</i>	2	3	0	0	0	2	0	2	2
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Neochlamydia 4</i>	0	9	0	0	0	3	0	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Neochlamydia 7</i>	0	2	2	0	1	1	2	2	2
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Parachlamydiae bacterium 1</i>	7	3	9	3	1	9	9	2	7
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Parachlamydiae bacterium 14</i>	2	1	0	0	0	0	4	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Parachlamydiae bacterium 18</i>	2	0	1	2	1	0	2	0	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Parachlamydiae bacterium 2</i>	2	2	0	1	0	0	1	0	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Parachlamydiae bacterium 3</i>	8	0	0	1	0	0	6	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Parachlamydiae bacterium 4</i>	2	11	1	0	0	0	1	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Parachlamydiae bacterium 5</i>	0	7	1	0	0	1	2	0	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Parachlamydiae bacterium 6</i>	4	0	0	1	0	3	0	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Parachlamydiae bacterium 8</i>	3	0	0	1	1	0	2	2	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Rhabdochlamydia 1</i>	1	0	1	2	0	0	8	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Rhabdochlamydia 11</i>	6	0	0	1	0	0	2	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Rhabdochlamydia 15</i>	0	2	0	0	0	0	0	0	4
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Rhabdochlamydia 18</i>	1	0	1	0	0	0	4	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Rhabdochlamydia 2</i>	0	17	0	0	0	0	0	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Rhabdochlamydia 3</i>	4	5	0	1	4	0	2	2	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Rhabdochlamydia 4</i>	9	1	0	1	1	0	0	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Rhabdochlamydia 5</i>	0	5	0	0	1	0	1	1	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Rhabdochlamydia 6</i>	1	7	0	0	1	0	1	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Rhabdochlamydia 7</i>	0	0	0	0	0	1	4	0	2
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Rhabdochlamydia 8</i>	5	0	0	0	0	0	1	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>Candidatus Rhabdochlamydia 9</i>	2	0	2	0	4	0	0	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Simkaniaceae bacterium 1</i>	44	39	10	10	8	4	44	1	9
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Simkaniaceae bacterium 10</i>	1	8	0	0	0	0	0	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Simkaniaceae bacterium 12</i>	5	0	0	0	0	0	1	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Simkaniaceae bacterium 13</i>	7	0	0	0	0	0	0	0	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Simkaniaceae bacterium 2</i>	6	2	1	0	0	0	2	0	4
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Simkaniaceae bacterium 3</i>	4	5	0	1	0	0	4	0	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Simkaniaceae bacterium 5</i>	2	10	0	0	0	4	2	0	23
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Simkaniaceae bacterium 6</i>	0	3	1	0	11	1	5	2	0
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Simkaniaceae bacterium 8</i>	4	8	1	0	0	0	0	0	1
<i>Chlamydiae</i>	<i>Chlamydiae</i>	<i>unknown Simkaniaceae bacterium 9</i>	2	11	0	0	0	0	0	1	0
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 1</i>	0	0	1	0	0	4	0	0	4
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 2</i>	0	1	2	0	0	0	0	0	6
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 3</i>	0	0	0	2	4	1	12	0	2
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 4</i>	3	1	2	0	0	4	3	0	9

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 5</i>	1	0	7	5	0	2	0	0	9
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 6</i>	2	0	7	1	0	6	3	0	6
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 7</i>	7	4	6	0	2	1	4	0	6
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 8</i>	0	0	1	10	13	0	11	3	0
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 9</i>	7	15	8	3	3	2	1	0	0
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 10</i>	16	4	12	0	0	0	3	0	7
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 11</i>	0	0	0	11	0	0	34	1	0
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 12</i>	9	1	7	2	0	14	5	0	9
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 13</i>	5	0	3	10	2	2	27	0	4
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 14</i>	8	2	9	8	0	16	2	1	10
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 15</i>	2	2	24	5	0	5	0	0	27
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 16</i>	7	17	23	2	1	0	16	4	6
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 17</i>	11	1	4	29	0	17	7	0	11
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 18</i>	27	3	9	16	0	12	13	0	9
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 19</i>	12	5	10	30	0	12	9	0	20
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 20</i>	10	11	21	2	16	1	30	3	9
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 21</i>	51	10	57	1	1	1	2	1	5
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 22</i>	25	0	12	50	0	30	42	0	13
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 23</i>	6	1	65	5	1	34	4	0	74
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 24</i>	59	35	51	5	5	1	29	9	17
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 25</i>	38	7	31	28	1	38	52	0	27
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 26</i>	54	1	39	46	8	49	36	1	43
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 27</i>	53	34	42	63	0	63	17	5	49
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 28</i>	46	19	119	4	0	6	123	4	17
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 29</i>	75	4	40	28	0	140	3	0	111
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 30</i>	122	18	35	32	0	89	38	0	86
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 31</i>	101	88	146	3	11	3	104	6	122
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 32</i>	132	20	97	179	8	118	86	1	116
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 33</i>	77	71	40	198	0	176	45	28	158
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 34</i>	407	104	98	73	4	92	234	3	101
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 35</i>	339	97	116	225	15	135	163	2	122
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 36</i>	405	97	408	380	4	749	214	19	600
<i>Chloroflexi</i>	<i>AD3</i>	<i>unknown AD3 bacterium 37</i>	634	54	369	572	13	436	650	17	256
<i>Chloroflexi</i>	<i>Chloroflexia</i>	<i>unknown Roseiflexaceae bacterium 2</i>	1	0	20	14	8	16	7	1	19
<i>Chloroflexi</i>	<i>Chloroflexia</i>	<i>unknown Roseiflexaceae bacterium 3</i>	0	0	1	4	1	0	1	0	1

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Chloroflexi</i>	<i>Chloroflexia</i>	unknown <i>Roseiflexaceae</i> bacterium 5	0	0	7	0	0	1	1	0	2
<i>Chloroflexi</i>	<i>Chloroflexia</i>	unknown <i>Roseiflexaceae</i> bacterium 7	0	0	0	1	4	0	1	0	3
<i>Chloroflexi</i>	<i>Chloroflexia</i>	unknown AKIW781 bacterium	0	0	0	13	0	0	0	0	0
<i>Chloroflexi</i>	<i>Chloroflexia</i>	unknown JG30- KF-CM45 bacterium 1	5	0	0	0	3	0	1	1	0
<i>Chloroflexi</i>	<i>Chloroflexia</i>	unknown JG30- KF-CM45 bacterium 2	4	1	10	1	0	0	2	1	0
<i>Chloroflexi</i>	<i>Dehalococcoidia</i>	unknown S085 bacterium 1	0	0	0	3	0	0	2	0	2
<i>Chloroflexi</i>	<i>Dehalococcoidia</i>	unknown S085 bacterium 2	1	0	4	5	3	0	1	1	3
<i>Chloroflexi</i>	<i>Dehalococcoidia</i>	unknown S085 bacterium 3	5	0	5	2	0	2	4	0	4
<i>Chloroflexi</i>	<i>Dehalococcoidia</i>	unknown S085 bacterium 4	0	1	2	2	0	2	1	0	4
<i>Chloroflexi</i>	<i>Dehalococcoidia</i>	unknown S085 bacterium 5	7	1	6	1	0	6	4	1	5
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 1	0	0	5	2	0	2	6	7	6
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 2	7	10	17	2	0	8	4	0	16
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 3	1	0	0	3	0	2	0	0	1
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 4	1	1	1	0	0	0	1	0	4
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 5	0	0	1	0	0	3	3	0	2
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 6	5	0	2	1	0	1	0	0	0
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 7	0	3	2	0	0	4	0	0	2
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 8	4	1	0	1	0	3	3	0	1
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 9	4	1	4	1	0	3	0	0	5
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 10	0	0	11	0	0	5	0	0	2
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 11	2	2	3	7	0	3	2	0	0
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 12	3	1	5	3	1	2	1	0	4
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 13	3	0	7	5	0	4	2	0	4
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 14	3	0	5	1	0	6	1	1	9
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 15	0	2	6	1	0	11	2	0	6
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	unknown JG30- KF-CM66 bacterium 16	2	3	6	2	1	6	4	2	6

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	<i>unknown JG30-KF-CM66 bacterium 17</i>	2	8	9	2	1	2	7	1	4
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	<i>unknown JG30-KF-CM66 bacterium 18</i>	8	2	3	10	1	5	2	0	6
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	<i>unknown JG30-KF-CM66 bacterium 19</i>	4	3	13	1	1	2	4	3	12
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	<i>unknown JG30-KF-CM66 bacterium 20</i>	3	15	6	4	2	6	4	1	4
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	<i>unknown JG30-KF-CM66 bacterium 21</i>	7	5	9	7	0	8	3	0	9
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	<i>unknown JG30-KF-CM66 bacterium 22</i>	9	4	14	8	0	6	4	0	7
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	<i>unknown JG30-KF-CM66 bacterium 23</i>	10	1	10	6	0	8	10	0	9
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	<i>unknown JG30-KF-CM66 bacterium 24</i>	21	2	10	6	0	9	12	0	7
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	<i>unknown JG30-KF-CM66 bacterium 25</i>	67	61	35	34	4	34	45	0	14
<i>Chloroflexi</i>	<i>JG30-KF-CM66</i>	<i>unknown JG30-KF-CM66 bacterium 26</i>	5	3	11	2	1	8	7	2	20
<i>Chloroflexi</i>	<i>KD4-96</i>	<i>unknown KD4-98 bacterium</i>	9	1	6	0	0	1	0	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown B12-WMSP1 bacterium 1</i>	0	3	3	0	0	0	0	0	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown B12-WMSP1 bacterium 2</i>	0	3	2	0	0	0	1	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown B12-WMSP1 bacterium 3</i>	3	1	2	0	0	0	0	0	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown B12-WMSP1 bacterium 4</i>	1	3	2	0	0	0	1	1	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown B12-WMSP1 bacterium 5</i>	0	1	5	0	3	0	0	1	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown B12-WMSP1 bacterium 6</i>	0	4	6	0	0	0	2	1	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown B12-WMSP1 bacterium 7</i>	2	4	4	1	1	0	3	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown B12-WMSP1 bacterium 8</i>	3	7	3	1	0	0	1	0	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown B12-WMSP1 bacterium 9</i>	0	10	7	1	0	2	2	1	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown B12-WMSP1 bacterium 10</i>	4	3	14	0	0	0	3	0	4
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown C0119 bacterium 1</i>	3	0	4	0	0	0	0	0	5
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown C0119 bacterium 2</i>	0	0	1	0	0	0	0	0	17
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown C0119 bacterium 3</i>	0	0	1	7	4	2	4	2	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown C0119 bacterium 4</i>	1	0	3	12	25	4	6	1	2

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown C0119 bacterium 5</i>	1	3	1	18	31	1	0	2	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown C0119 bacterium 6</i>	17	0	2	59	47	10	22	13	5
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 1</i>	1	0	0	6	0	0	0	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 2</i>	1	0	1	0	0	8	0	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 3</i>	1	5	1	0	0	1	0	0	3
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 4</i>	11	0	6	0	0	1	1	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 5</i>	2	0	0	7	1	0	11	1	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 6</i>	0	0	12	1	0	6	0	0	9
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 7</i>	0	0	0	4	0	0	26	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 8</i>	1	3	11	4	0	2	16	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 9</i>	3	1	3	1	0	7	13	2	8
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 10</i>	22	11	12	10	2	8	16	11	10
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 11</i>	103	22	3	221	70	3	253	54	12
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 12</i>	2	0	1	0	0	2	0	0	5
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 13</i>	0	0	2	0	1	0	0	1	14
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 14</i>	15	10	9	2	3	2	4	1	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 15</i>	17	24	4	13	7	5	27	14	4
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 16</i>	5	26	0	22	23	2	27	20	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 17</i>	6	0	0	3	0	0	0	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 18</i>	1	0	13	0	0	6	0	0	5
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 19</i>	2	9	0	0	17	0	0	5	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 20</i>	3	1	0	15	0	0	104	1	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 21</i>	45	3	60	11	9	28	8	9	47
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown JG30-KF-AS9 bacterium 22</i>	118	33	5	247	190	1	409	23	5
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>I921-2 bacterium 1</i>	6	0	1	0	0	0	1	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 2</i>	6	0	0	1	1	0	1	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 3</i>	4	0	2	0	0	0	6	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 4</i>	3	0	3	0	0	0	1	4	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 5</i>	12	0	0	0	0	0	3	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 6</i>	11	1	2	1	0	0	2	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 7</i>	15	1	1	0	1	0	0	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 8</i>	10	1	2	1	3	0	0	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 9</i>	10	1	2	0	0	0	1	0	4
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 10</i>	7	2	8	0	1	1	0	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 11</i>	1	4	1	0	12	0	4	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 12</i>	17	0	4	0	0	0	5	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 13</i>	15	0	0	1	9	0	3	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 14</i>	10	0	2	0	17	0	1	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 15</i>	1	0	23	0	0	3	2	0	5
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 16</i>	0	12	1	0	14	0	8	4	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 17</i>	6	15	16	0	0	0	3	0	5
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 18</i>	9	3	24	0	0	0	7	0	8
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 19</i>	17	0	20	0	10	1	16	0	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 20</i>	59	0	7	0	0	0	11	1	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 21</i>	54	3	25	1	5	1	10	0	10
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 22</i>	103	0	3	1	1	0	18	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 23</i>	8	12	6	1	43	0	3	139	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 24</i>	1	3	3	6	0	0	2	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 25</i>	0	0	6	1	0	6	1	0	5
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 26</i>	2	0	1	14	0	0	3	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 27</i>	1	0	4	5	0	3	1	0	6
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 28</i>	5	1	7	22	0	2	6	1	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 29</i>	31	6	20	1	2	0	21	0	8
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 30</i>	12	8	9	63	3	2	14	0	8
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 31</i>	0	6	2	0	0	0	0	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 32</i>	7	8	1	2	3	0	0	2	3
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 33</i>	20	10	10	6	3	4	15	2	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>1921-2 bacterium 34</i>	9	18	0	8	21	1	6	8	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 1</i>	0	3	0	0	3	0	0	3	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 2</i>	0	0	0	0	2	0	9	2	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 3</i>	1	0	11	0	0	1	2	0	4

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 4</i>	1	2	2	0	15	0	3	1	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 5</i>	4	1	1	11	2	0	16	1	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 6</i>	4	11	11	0	11	1	22	22	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 7</i>	16	9	11	2	19	0	42	8	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 8</i>	10	1	1	16	14	0	72	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 9</i>	10	0	0	33	47	0	43	4	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 10</i>	12	8	33	1	23	1	57	41	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 11</i>	30	5	34	74	1	14	23	3	11
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 12</i>	87	14	1	1	37	0	43	36	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 13</i>	42	15	10	7	69	1	151	24	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 14</i>	82	1	5	54	8	1	237	3	3
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 15</i>	58	4	12	58	18	2	318	7	4
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 16</i>	49	7	5	185	33	2	383	17	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 17</i>	66	24	42	11	132	0	371	43	3
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 18</i>	155	10	19	265	46	8	571	29	6
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 19</i>	341	18	36	550	56	14	1132	59	17
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 20</i>	227	46	28	623	200	13	1427	74	16
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>FCPS473 bacterium 21</i>	308	76	0	883	239	0	2204	78	3
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>G12-WMSP1 bacterium</i>	0	0	175	12	1	58	54	3	58
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 1</i>	0	2	5	0	1	0	0	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 2</i>	3	2	2	1	0	0	0	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 3</i>	1	0	8	0	0	0	0	0	3
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 4</i>	4	0	5	0	0	0	2	0	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 5</i>	3	2	7	0	0	0	1	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 6</i>	4	9	2	1	0	0	1	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 7</i>	15	0	3	0	0	0	1	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 8</i>	16	0	0	0	0	1	3	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 9</i>	18	3	6	3	3	0	3	0	5
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 10</i>	23	0	13	0	0	0	13	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 11</i>	36	0	0	1	0	1	10	1	3
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 12</i>	2	21	18	0	9	0	0	7	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 13</i>	59	0	18	0	3	1	10	0	4
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 14</i>	51	8	17	1	5	0	9	0	4
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 15</i>	45	11	30	0	1	0	6	0	13
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 16</i>	159	0	2	4	0	0	8	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 17</i>	99	144	174	14	16	2	49	22	19

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>HSB OF53-F07 bacterium 18</i>	240	27	228	2	27	9	53	6	95
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 1</i>	3	1	0	0	0	0	2	0	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 2</i>	2	4	0	0	1	0	2	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 3</i>	7	1	0	0	0	1	3	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 4</i>	5	1	2	1	0	0	3	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 5</i>	2	0	26	0	0	0	0	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 6</i>	6	1	4	4	1	1	10	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 7</i>	3	4	21	0	0	0	2	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 8</i>	25	1	8	0	1	0	7	0	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 9</i>	3	0	0	15	0	0	29	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 10</i>	18	1	5	1	1	1	20	1	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 11</i>	18	3	22	0	1	1	3	0	6
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 12</i>	22	4	29	2	0	0	4	0	7
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 13</i>	15	6	43	0	4	0	8	0	5
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 14</i>	63	23	14	1	8	0	36	0	3
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 15</i>	32	5	104	2	2	1	17	0	15
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 16</i>	3	4	39	5	0	0	125	1	5
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>JG30a-KF-32 bacterium 17</i>	257	27	9	8	121	1	144	96	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>Ktedonobacter 1</i>	2	1	0	0	4	0	1	2	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>Ktedonobacter 2</i>	8	11	0	1	0	2	0	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>Ktedonobacter 3</i>	1	0	0	0	5	0	0	10	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>Ktedonobacter 4</i>	0	0	12	1	0	5	1	0	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>Thermosporothrix 1</i>	14	20	18	0	24	0	5	16	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>Thermosporothrix 2</i>	2	4	4	0	0	0	0	3	3
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>Thermosporothrix 3</i>	4	8	7	1	10	1	5	2	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteraceae bacterium 1</i>	161	268	70	480	526	45	542	376	20
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteraceae bacterium 10</i>	14	0	1	52	1	2	52	1	3
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteraceae bacterium 11</i>	28	4	16	1	3	19	5	1	20
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteraceae bacterium 12</i>	9	1	30	2	2	29	3	1	18
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteraceae bacterium 13</i>	9	38	18	2	1	0	5	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteraceae bacterium 14</i>	4	0	10	9	8	10	1	6	10

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 15</i>	17	13	16	21	1	15	12	2	8
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 16</i>	16	0	10	3	0	6	14	0	3
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 17</i>	16	24	2	2	0	2	0	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 18</i>	18	6	3	6	2	0	5	1	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 19</i>	3	5	6	1	3	8	3	2	13
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 2</i>	217	144	139	152	573	20	136	335	28
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 20</i>	9	14	0	0	0	0	4	2	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 21</i>	2	20	1	0	0	0	0	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 22</i>	10	2	0	1	4	1	1	1	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 23</i>	1	0	1	0	0	0	24	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 24</i>	3	1	0	7	0	0	4	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 25</i>	0	0	3	2	0	4	4	0	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 26</i>	0	14	4	0	1	1	2	3	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 27</i>	2	0	2	1	0	5	0	0	4
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 28</i>	2	2	1	0	2	0	2	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 29</i>	3	5	2	0	5	0	0	1	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 3</i>	49	37	95	56	332	17	70	105	12
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 30</i>	0	0	0	0	0	6	0	0	3

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 31</i>	1	0	4	0	0	10	0	0	6
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 32</i>	1	0	2	1	0	3	0	0	5
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 33</i>	2	1	3	0	1	0	1	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 34</i>	0	1	0	0	2	0	0	4	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 35</i>	3	4	2	0	0	0	0	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 37</i>	3	3	7	0	3	0	0	2	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 4</i>	36	163	15	22	429	15	85	181	7
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 40</i>	2	4	0	0	0	0	0	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 43</i>	3	1	2	1	0	0	0	1	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 46</i>	16	8	17	1	37	0	7	17	8
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 47</i>	2	7	8	0	11	0	1	5	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 48</i>	6	5	0	0	50	0	6	34	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 5</i>	54	28	54	28	97	11	35	85	10
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 50</i>	4	2	1	0	0	0	1	1	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 51</i>	2064	2805	1	1	571	0	334	263	1
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 52</i>	103	0	0	0	0	0	1	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 53</i>	15	3	2	1	0	2	9	0	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 54</i>	18	1	0	0	0	0	0	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 56</i>	13	0	1	0	4	0	4	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 57</i>	3	4	0	4	0	0	1	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 58</i>	6	0	0	0	0	0	0	0	0
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 6</i>	22	68	42	6	17	4	27	0	11
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 7</i>	10	61	27	1	75	0	0	10	3
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 8</i>	23	52	71	40	135	14	36	33	18
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacteria ceae bacterium 9</i>	18	5	7	3	93	2	2	6	2
<i>Chloroflexi</i>	<i>Ktedonobacteria</i>	<i>unknown Ktedonobacterial es bacterium</i>	13	33	87	0	19	1	6	11	2
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 1</i>	0	0	0	3	2	0	1	2	1
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 2</i>	0	0	3	0	0	0	2	2	0
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 3</i>	0	0	1	1	0	7	0	0	2
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 4</i>	0	0	0	0	0	1	0	0	12
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 5</i>	0	0	0	6	3	1	4	0	1
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 6</i>	0	0	1	1	0	8	3	0	2
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 7</i>	1	1	5	0	0	4	1	0	3
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 8</i>	1	9	2	0	0	1	2	0	4
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 9</i>	0	0	0	3	1	0	9	6	0
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 10</i>	0	0	0	5	10	0	1	3	0
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 11</i>	0	0	4	2	1	10	5	0	7
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 12</i>	5	1	8	9	0	9	5	0	5
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 13</i>	1	0	12	0	0	10	10	0	12
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 14</i>	3	0	10	2	0	7	21	1	13
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 15</i>	1	0	21	0	0	12	6	0	19
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 16</i>	31	1	35	18	9	55	19	4	43
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 17</i>	30	1	32	12	1	55	13	0	80
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 18</i>	23	22	44	20	3	54	22	2	55
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 19</i>	32	15	64	35	0	52	40	1	63
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 20</i>	0	0	0	38	147	0	107	85	0
<i>Chloroflexi</i>	<i>TK10</i>	<i>unkown TK10 bacterium 21</i>	24	45	49	55	26	27	73	36	68

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Chloroflexi</i>	<i>TK10</i>	<i>unknown TK10 bacterium 22</i>	0	0	1	8	1	2	2	0	1
<i>Chloroflexi</i>	<i>TK10</i>	<i>unknown TK10 bacterium 23</i>	3	2	3	0	0	5	1	0	10
<i>Chloroflexi</i>	<i>TK10</i>	<i>unknown TK10 bacterium 24</i>	0	0	0	12	16	0	0	2	0
<i>Chloroflexi</i>	<i>TK10</i>	<i>unknown TK10 bacterium 25</i>	59	28	152	95	9	106	99	11	171
<i>Cyanobacteria</i>	<i>Melainabacteria</i>	<i>unknown Obscuribacterales bacterium 1</i>	0	6	0	0	0	0	2	6	2
<i>Cyanobacteria</i>	<i>Melainabacteria</i>	<i>unknown Obscuribacterales bacterium 2</i>	2	1	1	0	1	0	0	0	5
<i>Cyanobacteria</i>	<i>Sericytochromatia</i>	<i>unknown Sericytochromatia bacterium 1</i>	0	0	0	4	6	0	1	6	0
<i>Cyanobacteria</i>	<i>Sericytochromatia</i>	<i>unknown Sericytochromatia bacterium 10</i>	0	0	0	0	0	5	9	0	0
<i>Cyanobacteria</i>	<i>Sericytochromatia</i>	<i>unknown Sericytochromatia bacterium 11</i>	1	0	0	2	0	1	0	2	0
<i>Cyanobacteria</i>	<i>Sericytochromatia</i>	<i>unknown Sericytochromatia bacterium 13</i>	0	0	0	7	3	0	0	0	0
<i>Cyanobacteria</i>	<i>Sericytochromatia</i>	<i>unknown Sericytochromatia bacterium 14</i>	0	0	0	0	0	0	5	1	3
<i>Cyanobacteria</i>	<i>Sericytochromatia</i>	<i>unknown Sericytochromatia bacterium 2</i>	2	1	0	0	1	0	3	2	1
<i>Cyanobacteria</i>	<i>Sericytochromatia</i>	<i>unknown Sericytochromatia bacterium 3</i>	6	1	1	4	17	5	3	3	0
<i>Cyanobacteria</i>	<i>Sericytochromatia</i>	<i>unknown Sericytochromatia bacterium 4</i>	1	0	0	16	3	0	5	1	0
<i>Cyanobacteria</i>	<i>Sericytochromatia</i>	<i>unknown Sericytochromatia bacterium 5</i>	0	0	0	4	7	0	1	3	0
<i>Cyanobacteria</i>	<i>Sericytochromatia</i>	<i>unknown Sericytochromatia bacterium 6</i>	0	0	0	6	2	0	1	0	0
<i>Cyanobacteria</i>	<i>Sericytochromatia</i>	<i>unknown Sericytochromatia bacterium 7</i>	0	0	3	0	0	0	8	0	2
<i>Cyanobacteria</i>	<i>Sericytochromatia</i>	<i>unknown Sericytochromatia bacterium 8</i>	0	0	2	0	0	0	5	1	0
<i>Cyanobacteria</i>	<i>Sericytochromatia</i>	<i>unknown Sericytochromatia bacterium 9</i>	1	2	2	11	5	0	2	1	0
<i>Deinococcus-Thermus</i>	<i>Deinococci</i>	<i>Deinococcus 1</i>	6	0	0	6	8	2	1	7	0
<i>Deinococcus-Thermus</i>	<i>Deinococci</i>	<i>Deinococcus 2</i>	0	0	0	6	1	0	0	2	0
<i>Deinococcus-Thermus</i>	<i>Deinococci</i>	<i>Deinococcus 3</i>	0	0	0	1	4	0	0	1	0
<i>Deinococcus-Thermus</i>	<i>Deinococci</i>	<i>Deinococcus 5</i>	0	0	0	18	12	1	6	8	0
<i>Deinococcus-Thermus</i>	<i>Deinococci</i>	<i>Deinococcus 6</i>	0	0	0	11	1	0	0	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliaceae bacterium 1</i>	1	0	1	0	0	0	4	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliaceae bacterium 2</i>	1	1	4	0	0	0	1	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliaceae bacterium 3</i>	0	0	2	0	0	1	1	0	3
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliaceae bacterium 6</i>	2	10	2	0	0	1	2	0	4
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliaceae bacterium 7</i>	1	2	0	0	1	0	1	0	1

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Babeliaceae</i> bacterium 8	0	5	1	0	1	0	1	0	1
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Babeliaceae</i> bacterium 9	2	0	1	0	0	2	1	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	unknown UBA12409 bacterium 1	0	3	0	0	0	0	3	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	unknown UBA12409 bacterium 2	1	0	0	0	0	0	5	3	7
<i>Dependentiae</i>	<i>Babeliae</i>	unknown UBA12409 bacterium 3	0	3	1	1	0	0	4	1	1
<i>Dependentiae</i>	<i>Babeliae</i>	unknown UBA12409 bacterium 4	0	0	0	0	0	0	4	8	0
<i>Dependentiae</i>	<i>Babeliae</i>	unknown UBA12409 bacterium 5	0	11	0	0	0	0	1	0	1
<i>Dependentiae</i>	<i>Babeliae</i>	unknown UBA12409 bacterium 6	13	7	6	7	2	3	3	0	9
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 1	3	0	6	11	38	0	5	18	3
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 10	0	0	0	0	0	0	0	14	0
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 11	5	6	5	2	1	0	2	1	0
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 12	6	3	0	3	0	2	4	1	2
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 13	0	0	0	0	0	0	0	0	17
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 14	7	0	1	0	0	2	2	0	5
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 15	7	2	0	3	0	3	1	0	1
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 16	4	9	1	0	0	0	10	0	1
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 17	4	5	0	0	0	0	3	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 18	1	1	6	0	1	0	1	4	0
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 19	4	1	0	0	0	1	1	0	5
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 2	2	4	0	0	0	0	0	1	1
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 20	1	7	0	0	3	0	1	0	2
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 21	3	10	1	2	0	1	0	1	4
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 22	0	4	5	0	0	0	0	3	1
<i>Dependentiae</i>	<i>Babeliae</i>	unknown <i>Vermiphilaceae</i> bacterium 23	2	0	4	0	0	1	1	0	1

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 24</i>	2	8	3	0	0	1	1	1	2
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 25</i>	2	3	1	0	0	0	0	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 26</i>	3	1	1	0	1	0	4	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 29</i>	0	4	0	0	0	0	1	0	2
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 3</i>	55	18	6	5	72	1	37	14	51
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 30</i>	0	3	3	1	0	0	0	1	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 32</i>	3	2	3	0	0	0	1	0	4
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 33</i>	2	0	0	0	0	7	1	0	6
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 36</i>	8	0	0	0	0	0	2	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 37</i>	2	4	0	0	0	1	0	0	2
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 38</i>	0	5	0	0	0	0	1	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 4</i>	50	13	2	1	0	1	15	0	1
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 40</i>	0	3	2	1	1	0	0	1	3
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 5</i>	0	46	1	1	0	0	2	0	2
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 58</i>	23	11	3	0	0	0	1	0	1
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 6</i>	2	42	0	0	0	0	0	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 7</i>	25	0	0	1	0	0	9	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 72</i>	0	2	2	0	2	0	0	0	1
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 74</i>	0	13	0	0	1	0	2	4	1
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 75</i>	5	0	1	2	0	0	5	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 76</i>	2	2	2	0	2	1	1	3	1
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 77</i>	9	1	0	1	0	0	0	0	1
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 78</i>	0	0	0	0	0	0	0	0	8
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 79</i>	1	5	0	0	1	0	1	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 8</i>	7	3	4	5	2	4	14	0	1
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Vermiphilaceae bacterium 9</i>	1	3	2	3	0	2	1	0	10
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 1</i>	7	0	0	0	0	0	4	54	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 10</i>	0	0	1	0	0	0	11	0	4
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 11</i>	0	9	0	0	0	0	0	1	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 13</i>	0	2	0	0	2	1	0	0	1
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 19</i>	0	0	0	0	0	0	3	4	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 2</i>	25	1	0	1	0	0	12	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 28</i>	0	0	2	0	0	2	4	2	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 3</i>	9	16	1	1	0	0	5	0	2
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 4</i>	11	15	0	0	0	1	4	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 5</i>	20	0	0	0	0	0	2	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 6</i>	3	6	4	1	0	0	2	1	1
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 7</i>	4	0	0	0	0	3	2	0	0
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 8</i>	8	1	0	1	0	2	3	0	1
<i>Dependentiae</i>	<i>Babeliae</i>	<i>unknown Babeliales bacterium 9</i>	0	6	0	0	0	0	0	2	0
<i>Elusimicrobia</i>	<i>Elusimicrobia</i>	<i>unknown FCPU454 bacterium</i>	7	7	7	0	0	1	0	0	9
<i>Elusimicrobia</i>	<i>Elusimicrobia</i>	<i>unknown Lineage IV bacterium 1</i>	59	159	69	13	46	12	169	153	66
<i>Elusimicrobia</i>	<i>Elusimicrobia</i>	<i>unknown Lineage IV bacterium 2</i>	18	7	28	6	6	9	55	47	58
<i>Elusimicrobia</i>	<i>Elusimicrobia</i>	<i>unknown Lineage IV bacterium 3</i>	2	1	3	0	0	1	4	0	8
<i>Elusimicrobia</i>	<i>Elusimicrobia</i>	<i>unknown Lineage IV bacterium 4</i>	0	1	1	0	0	0	4	0	6
<i>Elusimicrobia</i>	<i>Elusimicrobia</i>	<i>unknown Lineage IV bacterium 7</i>	1	0	2	0	0	3	1	0	1
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unknown Lineage Iia bacterium 1</i>	36	26	21	4	6	13	23	2	35
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unknown Lineage Iia bacterium 10</i>	11	1	0	0	0	1	4	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unkonwn Lineage Iia bacterium 11</i>	0	0	0	0	0	1	1	1	6
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unkonwn Lineage Iia bacterium 12</i>	23	11	8	1	0	10	25	2	18
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unkonwn Lineage Iia bacterium 13</i>	26	8	1	2	1	6	8	2	7
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unkonwn Lineage Iia bacterium 14</i>	5	3	2	0	0	2	3	0	3
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unkonwn Lineage Iia bacterium 15</i>	5	0	3	0	0	0	0	0	1
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unkonwn Lineage Iia bacterium 2</i>	53	2	6	5	2	12	32	0	11
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unkonwn Lineage Iia bacterium 3</i>	34	2	2	1	1	8	6	0	1
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unkonwn Lineage Iia bacterium 4</i>	20	3	4	2	0	5	6	0	13
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unkonwn Lineage Iia bacterium 5</i>	1	8	5	2	1	0	1	14	18
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unkonwn Lineage Iia bacterium 6</i>	15	5	0	0	0	6	5	0	5
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unkonwn Lineage Iia bacterium 7</i>	0	1	0	0	2	0	2	18	2
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unkonwn Lineage Iia bacterium 8</i>	5	6	13	0	0	2	2	0	14
<i>Elusimicrobia</i>	<i>Lineage IIa</i>	<i>unkonwn Lineage Iia bacterium 9</i>	1	1	1	0	0	0	1	0	3
<i>Elusimicrobia</i>	<i>Lineage IIb</i>	<i>unkonwn Lineage Iib bacterium 1</i>	0	0	5	1	6	4	15	20	22
<i>Elusimicrobia</i>	<i>Lineage IIb</i>	<i>unkonwn Lineage Iib bacterium 10</i>	1	0	10	7	6	2	17	7	33
<i>Elusimicrobia</i>	<i>Lineage IIb</i>	<i>unkonwn Lineage Iib bacterium 11</i>	0	0	5	2	2	0	6	2	1
<i>Elusimicrobia</i>	<i>Lineage IIb</i>	<i>unkonwn Lineage Iib bacterium 2</i>	5	0	4	0	0	2	12	0	3
<i>Elusimicrobia</i>	<i>Lineage IIb</i>	<i>unkonwn Lineage Iib bacterium 3</i>	3	1	3	0	0	3	2	0	6
<i>Elusimicrobia</i>	<i>Lineage IIb</i>	<i>unkonwn Lineage Iib bacterium 4</i>	3	1	3	0	0	1	1	0	5
<i>Elusimicrobia</i>	<i>Lineage IIb</i>	<i>unkonwn Lineage Iib bacterium 7</i>	1	0	2	0	0	0	1	0	3
<i>Elusimicrobia</i>	<i>Lineage IIb</i>	<i>unkonwn Lineage Iib bacterium 8</i>	1	4	7	2	0	1	1	0	1
<i>Epsilonbacteraeota</i>	<i>Campylobacteria</i>	<i>Arcobacter</i>	0	1	0	2	1	4	0	0	0
<i>FBP</i>	<i>unknown FBP</i>	<i>unknown FBP bacterium 1</i>	0	0	0	1	7	1	3	1	1
<i>FBP</i>	<i>unknown FBP</i>	<i>unknown FBP bacterium 2</i>	0	0	0	0	0	1	1	0	5
<i>FBP</i>	<i>unknown FBP</i>	<i>unknown FBP bacterium 3</i>	0	2	0	0	0	2	1	0	2
<i>FBP</i>	<i>unknown FBP</i>	<i>unknown FBP bacterium 4</i>	0	0	0	2	0	0	7	2	0
<i>FBP</i>	<i>unknown FBP</i>	<i>unknown FBP bacterium 5</i>	0	0	0	0	8	0	1	2	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>FBP</i>	<i>unknown FBP</i>	<i>unknown FBP bacterium 6</i>	0	0	6	2	1	5	29	7	3
<i>FBP</i>	<i>unknown FBP</i>	<i>unknown FBP bacterium 7</i>	0	0	0	3	74	6	18	19	3
<i>FBP</i>	<i>unknown FBP</i>	<i>unknown FBP bacterium 8</i>	0	2	2	0	0	2	3	0	9
<i>FCPU426</i>	<i>unknown FCPU426</i>	<i>unknown FCPU426 bacterium 1</i>	14	10	3	0	0	0	12	1	2
<i>FCPU426</i>	<i>unknown FCPU427</i>	<i>unknown FCPU426 bacterium 2</i>	5	3	15	0	0	0	27	16	5
<i>FCPU426</i>	<i>unknown FCPU428</i>	<i>unknown FCPU426 bacterium 3</i>	6	32	1	0	0	0	2	1	2
<i>FCPU426</i>	<i>unknown FCPU429</i>	<i>unknown FCPU426 bacterium 4</i>	7	38	0	0	0	0	19	19	7
<i>Fibrobacteres</i>	<i>Fibrobacteria</i>	<i>unknown Fibrobacteracea e bacterium 1</i>	0	0	1	2	1	0	1	0	1
<i>Fibrobacteres</i>	<i>Fibrobacteria</i>	<i>unknown Fibrobacteracea e bacterium 2</i>	0	0	2	2	0	0	0	7	0
<i>Fibrobacteres</i>	<i>Fibrobacteria</i>	<i>unknown Fibrobacteracea e bacterium 5</i>	2	4	1	0	0	0	2	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Acidibacillus</i>	82	17	0	2	1	0	1	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Alcyclobacillus 1</i>	15	1	0	3	1	0	3	1	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Alcyclobacillus 10</i>	91	5	0	6	5	0	7	4	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Alcyclobacillus 11</i>	22	18	0	1	0	0	0	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Alcyclobacillus 12</i>	3	0	0	6	1	0	0	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Alcyclobacillus 13</i>	21	73	4	7	3	0	5	3	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Alcyclobacillus 3</i>	279	327	6	365	199	0	179	120	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Alcyclobacillus 4</i>	619	164	0	14	4	0	49	12	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Alcyclobacillus 5</i>	363	183	0	8	3	0	25	2	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Alcyclobacillus 6</i>	79	0	0	0	1	0	3	1	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Alcyclobacillus 7</i>	79	2	0	0	0	0	0	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Alcyclobacillus 8</i>	75	1	0	0	0	0	0	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Alcyclobacillus 9</i>	19	2	2	0	0	0	4	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Tumebacillus 1</i>	23	8	6	7	0	5	8	0	4
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Tumebacillus 2</i>	167	15	2	0	1	0	6	5	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Tumebacillus 3</i>	137	13	0	2	0	0	9	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Tumebacillus 5</i>	43	7	0	1	2	0	7	16	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Tumebacillus 6</i>	2	2	0	6	5	0	3	4	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Tumebacillus 7</i>	20	55	0	3	6	0	4	3	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 1</i>	4	7	23	5	4	9	15	1	13
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 10</i>	3	2	2	2	3	1	1	1	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 11</i>	150	23	9	35	17	5	15	17	7
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 12</i>	391	121	116	143	97	63	43	79	79
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 14</i>	625	130	54	166	109	53	89	130	57
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 18</i>	3	0	1	0	0	2	0	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 2</i>	2	1	1	0	0	3	0	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 4</i>	13	6	5	19	18	1	8	22	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 6</i>	30	12	6	17	15	9	3	3	12
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 8</i>	11	2	3	12	5	8	1	0	3
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Bacillus 9</i>	144	54	29	54	58	24	23	42	43
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Oceanobacillus</i>	37	1	1	2	3	3	0	3	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>unknown Bacillaceae bacterium 1</i>	27	18	1	35	0	1	26	1	2

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Ammoniphilus</i>	6	2	0	3	4	0	1	1	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Cohnella 1</i>	1	1	2	0	1	1	2	5	2
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Cohnella 2</i>	6	3	2	0	2	1	4	6	3
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Cohnella 3</i>	5	2	2	0	7	0	1	5	2
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Cohnella 4</i>	4	1	0	7	7	0	3	4	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Cohnella 5</i>	3	0	0	2	1	0	4	1	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Cohnella 6</i>	4	0	0	1	1	0	3	1	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 1</i>	160	22	2	20	84	1	15	13	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 10</i>	1	0	0	1	4	0	0	1	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 12</i>	4	0	1	4	0	0	0	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 14</i>	0	0	1	1	2	0	3	0	5
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 2</i>	2	0	1	3	3	0	1	2	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 20</i>	159	40	2	46	98	0	44	43	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 21</i>	2	1	3	9	6	0	2	5	2
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 22</i>	0	0	0	2	2	1	3	0	3
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 23</i>	1	1	1	3	2	0	3	2	3
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 24</i>	64	6	2	10	17	0	10	5	2
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 26</i>	17	4	1	13	23	0	4	18	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 27</i>	5	0	3	0	4	2	2	4	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 28</i>	21	2	0	11	18	0	3	10	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 29</i>	18	4	0	3	9	0	3	1	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 31</i>	1	1	1	2	5	2	7	0	3
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 32</i>	11	1	0	9	13	0	4	12	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 33</i>	0	1	1	1	2	1	2	0	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 36</i>	0	2	1	0	5	1	1	1	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 4</i>	78	2	1	47	236	0	48	140	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 41</i>	3	1	0	3	6	0	1	1	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 42</i>	0	5	0	0	0	0	1	0	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 43</i>	3	1	0	0	0	0	0	3	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 46</i>	2	0	1	4	3	0	2	3	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 47</i>	2	1	0	3	2	0	2	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 49</i>	3	0	0	0	3	0	2	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 5</i>	5	0	0	8	11	1	11	6	4
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 50</i>	5	0	0	0	1	0	2	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 51</i>	2	0	0	0	4	0	1	1	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 53</i>	2	0	0	2	5	0	1	1	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 54</i>	2	2	1	0	1	0	1	0	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 58</i>	4	4	3	0	2	0	2	0	2
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 6</i>	0	2	4	1	1	1	2	2	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Paenibacillus 8</i>	14	3	0	1	3	0	1	1	1
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Domibacillus</i>	27	1	3	477	99	0	51	72	3
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Lysinibacillus</i>	35	2	5	8	6	3	3	0	7
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Rummeliibacillus</i>	3	1	4	1	2	0	1	1	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Solibacillus</i>	3	0	0	9	7	0	3	1	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Sporosarcina 2</i>	56	5	9	16	6	4	9	2	11
<i>Firmicutes</i>	<i>Bacilli</i>	<i>unknown Planococcaceae bacterium</i>	3	0	0	23	3	0	4	0	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>unknown Thermoactinomyces bacterium 1</i>	6	2	0	7	13	0	0	9	0
<i>Firmicutes</i>	<i>Bacilli</i>	<i>Carnobacterium</i>	0	0	0	0	2	0	0	6	0
<i>Firmicutes</i>	<i>Erysipelotrichia</i>	<i>Turicibacter 1</i>	2	0	0	3	0	1	0	0	0
<i>GAL15</i>	<i>unknown GAL15</i>	<i>unknown GAL18 bacterium</i>	21	14	11	3	4	1	0	1	2
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 11</i>	1	1	10	0	0	4	0	0	11
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 12</i>	0	0	2	0	1	0	0	0	8
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 13</i>	0	0	1	0	2	0	6	8	1
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 14</i>	0	0	3	2	1	0	2	5	1
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 19</i>	2	0	2	0	0	1	0	0	2
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 2</i>	10	8	14	29	84	21	230	220	54
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 21</i>	1	0	7	1	0	0	1	0	12
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 22</i>	0	0	3	1	0	2	4	5	2
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 23</i>	2	0	2	5	0	0	19	21	1
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 24</i>	0	0	0	2	4	3	2	3	5
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 25</i>	11	1	5	33	37	10	88	113	12
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 26</i>	0	0	5	22	27	4	96	61	11
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 27</i>	0	0	1	13	67	4	57	83	6
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 28</i>	42	30	17	10	0	15	16	0	21
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 29</i>	5	1	4	1	3	4	73	32	11
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 3</i>	3	0	3	34	3	16	224	19	61
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 30</i>	4	1	0	6	11	0	15	22	21
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 31</i>	17	1	0	15	4	0	38	6	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 32</i>	10	0	3	2	5	1	20	8	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 33</i>	5	0	4	5	10	8	20	20	17
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 34</i>	0	0	0	3	5	2	16	22	3
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 35</i>	0	0	1	4	3	0	5	7	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 36</i>	0	0	21	0	0	1	0	0	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 37</i>	5	1	0	1	3	2	24	15	4
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 38</i>	0	0	0	0	2	3	5	4	1
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 39</i>	0	1	2	2	1	1	3	0	8
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 4</i>	17	1	62	2	0	20	2	1	24
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 40</i>	4	1	0	1	0	1	0	0	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas 41</i>	4	0	0	0	1	0	1	1	3

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 42	0	0	0	0	3	0	2	4	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 43	0	0	1	2	0	3	1	0	5
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 5	28	12	16	11	1	10	14	1	24
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 6	0	11	12	2	0	5	26	4	7
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 7	13	4	16	2	6	18	17	9	29
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 8	1	1	0	4	3	0	2	1	3
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatimonas</i> 9	6	0	1	1	0	0	0	0	2
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatirosa</i> 1	0	0	0	3	21	2	8	20	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatirosa</i> 2	1	0	0	1	2	1	1	5	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatirosa</i> 3	0	0	0	3	6	1	0	4	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatirosa</i> 4	73	187	60	1	16	10	31	1	23
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatirosa</i> 5	50	80	38	18	17	14	99	13	58
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatirosa</i> 6	1	3	4	3	0	0	36	6	1
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatirosa</i> 7	7	8	6	3	1	7	4	1	8
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatirosa</i> 8	0	10	0	0	3	1	3	13	2
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>Gemmatirosa</i> 9	0	0	0	2	4	0	0	1	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 1	20	0	61	5	0	62	4	0	61
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 11	0	0	1	0	0	3	6	0	1
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 13	0	0	5	0	0	3	1	0	2
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 15	7	1	7	1	0	4	0	0	8
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 16	0	0	14	1	0	10	2	0	21
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 17	1	0	1	4	30	5	186	81	1
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 18	0	0	6	0	0	1	0	0	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 19	17	4	6	7	0	4	10	0	5
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 2	74	28	15	9	13	19	26	23	35
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 20	4	8	1	1	0	4	10	5	8
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 21	0	0	0	3	7	0	0	2	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	unknown <i>Gemmatimonadaceae</i> bacterium 22	0	0	2	0	1	2	2	3	4

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>unknown Gemmatimonadaceae bacterium 3</i>	28	1	0	0	0	3	0	0	0
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>unknown Gemmatimonadaceae bacterium 4</i>	71	9	7	0	0	6	3	0	2
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>unknown Gemmatimonadaceae bacterium 6</i>	0	0	5	0	1	0	1	2	2
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>unknown Gemmatimonadaceae bacterium 7</i>	0	0	33	1	0	9	1	0	4
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>unknown Gemmatimonadaceae bacterium 8</i>	5	0	11	1	5	7	4	4	16
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes</i>	<i>unknown Gemmatimonadaceae bacterium 9</i>	0	0	12	0	0	0	1	0	2
<i>Gemmatimonadetes</i>	<i>unknown Gemmatimonadetes</i>	<i>unknown Gemmatimonadetes bacterium</i>	2	0	0	0	1	1	0	2	4
<i>Nitrospirae</i>	<i>Nitrospira</i>	<i>Nitrospira 1</i>	0	0	3	0	2	2	3	1	2
<i>Nitrospirae</i>	<i>Nitrospira</i>	<i>Nitrospira 2</i>	0	0	7	0	0	1	1	0	0
<i>Nitrospirae</i>	<i>Nitrospira</i>	<i>Nitrospira 3</i>	0	0	2	0	0	4	0	0	0
<i>Nitrospirae</i>	<i>Nitrospira</i>	<i>Nitrospira 4</i>	0	0	0	5	7	0	6	3	1
<i>Nitrospirae</i>	<i>Nitrospira</i>	<i>Nitrospira 5</i>	7	2	1	0	0	4	1	0	3
<i>Patescibacteria</i>	<i>Berkelbacteria</i>	<i>unknown Berkelbacteria bacterium 2</i>	0	0	1	0	2	0	0	4	0
<i>Patescibacteria</i>	<i>Berkelbacteria</i>	<i>unknown Berkelbacteria bacterium 3</i>	1	1	0	0	1	0	6	4	1
<i>Patescibacteria</i>	<i>Berkelbacteria</i>	<i>unknown Berkelbacteria bacterium 4</i>	0	0	0	0	0	0	4	2	0
<i>Patescibacteria</i>	<i>Microgenomatia</i>	<i>unknown Microgenomatia bacterium</i>	5	0	7	2	0	7	6	0	1
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown Candidatus Adlerbacteria bacterium 1</i>	2	11	4	0	2	0	16	32	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown Candidatus Adlerbacteria bacterium 10</i>	2	0	0	0	0	0	8	6	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown Candidatus Adlerbacteria bacterium 11</i>	12	1	0	0	0	0	0	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown Candidatus Adlerbacteria bacterium 12</i>	0	1	1	0	0	0	10	0	1
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown Candidatus Adlerbacteria bacterium 14</i>	0	0	4	0	0	0	2	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown Candidatus Adlerbacteria bacterium 15</i>	1	4	0	0	0	0	2	2	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown Candidatus Adlerbacteria bacterium 2</i>	0	7	0	0	0	0	6	7	1

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Adlerbacteria</i> <i>bacterium 21</i>	2	6	0	0	0	0	3	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Adlerbacteria</i> <i>bacterium 22</i>	0	0	0	0	0	0	3	3	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Adlerbacteria</i> <i>bacterium 3</i>	0	0	0	0	3	0	4	11	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Adlerbacteria</i> <i>bacterium 4</i>	0	0	1	0	3	0	5	9	1
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Adlerbacteria</i> <i>bacterium 5</i>	0	0	0	0	0	0	0	12	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Adlerbacteria</i> <i>bacterium 6</i>	0	9	0	0	0	0	0	5	1
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Adlerbacteria</i> <i>bacterium 7</i>	0	0	3	0	0	0	10	4	1
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Adlerbacteria</i> <i>bacterium 8</i>	0	0	2	0	0	0	1	3	1
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Adlerbacteria</i> <i>bacterium 9</i>	29	3	0	0	0	0	1	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 1</i>	2	18	4	0	2	0	69	61	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 10</i>	1	0	0	1	1	0	18	6	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 11</i>	0	0	0	0	0	0	18	7	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 12</i>	1	14	4	0	0	0	1	1	4
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 13</i>	11	27	4	0	1	0	24	19	1
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 14</i>	0	5	3	0	0	0	2	11	1
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 15</i>	6	0	0	0	4	0	1	5	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 16</i>	2	11	0	0	0	0	0	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 17</i>	12	0	0	0	0	0	0	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 19</i>	0	4	0	0	0	0	5	2	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 2</i>	2	2	0	0	0	0	7	54	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 20</i>	0	0	3	0	0	0	0	6	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 22</i>	5	0	1	0	0	0	0	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 25</i>	3	0	0	0	0	0	4	1	1
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 27</i>	10	0	1	1	1	0	255	40	2
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 28</i>	0	3	0	0	1	0	31	41	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 29</i>	10	1	3	0	0	0	9	0	7
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 3</i>	0	0	6	0	0	0	70	5	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 30</i>	8	11	0	0	0	0	0	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 31</i>	0	0	0	0	0	0	6	3	1
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 32</i>	0	0	8	0	0	0	0	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 33</i>	0	0	0	0	0	0	8	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 34</i>	0	0	4	0	0	0	0	0	2
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 39</i>	2	6	0	0	0	0	0	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 4</i>	18	0	0	0	4	0	48	6	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 40</i>	0	0	0	0	0	0	0	10	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 5</i>	13	26	18	0	0	0	1	14	1

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 6</i>	3	0	0	0	0	0	29	29	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 7</i>	2	3	0	0	0	0	34	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 8</i>	0	17	0	0	0	0	8	12	3
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Kaiserbacteria</i> <i>bacterium 9</i>	2	35	2	0	0	0	12	36	3
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Candidatus</i> <i>Nomurabacteria</i> <i>bacterium 1</i>	0	0	3	0	0	0	3	5	2
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Parcubacteria</i> <i>bacterium 1</i>	0	19	1	0	0	0	0	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Parcubacteria</i> <i>bacterium 2</i>	6	11	0	0	0	0	1	1	5
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Parcubacteria</i> <i>bacterium 3</i>	1	0	0	0	0	0	15	1	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Parcubacteria</i> <i>bacterium 4</i>	6	4	1	0	0	0	2	0	2
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Parcubacteria</i> <i>bacterium 5</i>	0	12	1	0	0	0	0	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Parcubacteria</i> <i>bacterium 6</i>	7	6	2	0	0	0	2	0	3
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Parcubacteria</i> <i>bacterium 7</i>	0	4	2	0	0	0	0	0	0
<i>Patescibacteria</i>	<i>Parcubacteria</i>	<i>unknown</i> <i>Parcubacteria</i> <i>bacterium 8</i>	0	6	0	0	0	0	0	0	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown</i> <i>Saccharimonad</i> <i>ales bacterium</i> <i>1</i>	48	148	64	4	10	6	203	83	26
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown</i> <i>Saccharimonad</i> <i>ales bacterium</i> <i>10</i>	1	0	0	0	15	0	26	63	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown</i> <i>Saccharimonad</i> <i>ales bacterium</i> <i>102</i>	2	5	1	0	2	0	0	0	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown</i> <i>Saccharimonad</i> <i>ales bacterium</i> <i>11</i>	15	58	8	0	4	1	6	2	6
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown</i> <i>Saccharimonad</i> <i>ales bacterium</i> <i>12</i>	0	1	0	0	0	0	1	83	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown</i> <i>Saccharimonad</i> <i>ales bacterium</i> <i>13</i>	8	17	8	0	0	0	28	3	4
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown</i> <i>Saccharimonad</i> <i>ales bacterium</i> <i>14</i>	0	0	0	0	28	0	5	25	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 15</i>	0	0	1	0	0	0	38	3	9
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 16</i>	0	0	2	0	0	0	11	17	13
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 17</i>	6	1	0	6	0	0	29	0	2
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 18</i>	17	8	1	1	0	0	14	0	3
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 19</i>	0	0	0	0	0	0	41	11	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 2</i>	58	102	28	4	6	2	60	61	14
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 20</i>	6	36	5	0	0	0	2	0	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 21</i>	3	2	12	1	0	0	18	0	14
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 22</i>	0	0	2	1	0	1	32	3	2
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 23</i>	30	2	2	0	3	0	13	3	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 24</i>	0	3	3	0	2	1	33	2	4
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 25</i>	1	0	0	0	0	0	26	7	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 26</i>	0	0	3	0	0	0	24	0	4
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 27</i>	1	19	5	1	0	2	2	6	8
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 28</i>	0	6	3	0	5	0	4	23	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 29</i>	0	0	17	0	1	0	22	18	13
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 3</i>	3	13	21	8	0	0	223	27	28
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 30</i>	0	0	0	0	0	1	7	22	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 31</i>	0	1	0	0	13	0	2	12	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 32</i>	0	1	0	0	0	0	20	0	5
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 33</i>	6	32	8	1	1	0	23	0	19
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 34</i>	0	0	0	0	1	0	18	4	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 35</i>	17	0	0	0	0	0	0	0	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 36</i>	0	2	0	0	0	0	1	14	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 37</i>	0	0	0	7	10	0	0	0	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 38</i>	1	4	4	0	0	0	0	0	14
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 39</i>	0	0	0	0	0	0	12	0	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 4</i>	8	0	11	7	13	4	48	106	16
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 40</i>	0	0	0	0	1	0	0	9	3
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 41</i>	1	0	2	0	0	0	10	0	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 42</i>	0	0	1	0	0	0	1	10	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 43</i>	0	0	0	0	0	0	12	0	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 44</i>	5	0	0	0	0	0	6	0	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 45</i>	0	0	1	0	0	0	9	0	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 46</i>	5	0	3	0	0	1	3	0	4
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 47</i>	0	1	1	0	0	0	11	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 48</i>	5	3	0	0	5	0	3	3	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 49</i>	0	1	0	0	0	1	1	12	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 5</i>	194	11	0	0	0	0	18	3	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 50</i>	0	5	0	0	0	0	2	0	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 51</i>	0	0	1	0	0	0	7	0	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 52</i>	6	0	0	0	0	0	2	0	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 53</i>	1	1	7	2	0	1	3	0	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 54</i>	0	0	2	0	0	0	4	0	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 57</i>	0	0	1	0	0	0	0	0	6
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 58</i>	0	23	11	0	1	0	1	0	3
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 59</i>	0	0	0	1	1	0	4	8	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 6</i>	34	86	22	0	5	0	7	27	25
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 60</i>	1	3	2	0	0	0	1	0	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 61</i>	0	0	1	0	0	0	15	2	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 67</i>	0	8	0	0	0	0	1	0	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 68</i>	0	0	0	0	0	0	2	5	2
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 7</i>	1	63	25	0	11	0	47	101	7
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 70</i>	1	0	3	0	0	1	3	0	2

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 72</i>	0	7	1	0	0	0	1	1	2
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 73</i>	0	2	1	0	0	0	5	4	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 8</i>	0	2	0	0	11	0	101	16	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 81</i>	27	104	31	2	5	3	67	37	6
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 85</i>	4	2	0	0	0	0	1	0	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 86</i>	2	3	2	0	0	0	0	0	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 87</i>	2	4	10	0	0	0	5	2	12
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 88</i>	1	1	0	0	0	0	2	0	17
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 9</i>	5	26	11	0	5	0	66	17	13
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 91</i>	6	4	4	1	3	0	2	0	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 92</i>	0	0	0	0	0	0	0	0	8
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 93</i>	0	0	1	0	0	1	0	0	5
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 94</i>	0	0	1	14	8	0	50	5	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 95</i>	0	0	0	14	0	0	10	22	0
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 97</i>	0	0	1	0	0	0	17	0	1
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 98</i>	0	1	2	0	0	2	2	0	5
<i>Patescibacteria</i>	<i>Saccharimonadia</i>	<i>unknown Saccharimonad ales bacterium 99</i>	0	1	2	0	0	0	1	1	1
<i>Patescibacteria</i>	<i>WWE3</i>	<i>unknown WWE5 bacterium</i>	0	0	0	0	0	0	0	10	0
<i>Planctomycetes</i>	<i>BD7-11</i>	<i>unknown BD7- 11 bacterium 1</i>	2	1	5	0	0	0	0	0	5
<i>Planctomycetes</i>	<i>BD7-11</i>	<i>unknown BD7- 11 bacterium 2</i>	5	0	1	0	0	0	4	1	2

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Planctomycetes</i>	<i>BD7-11</i>	<i>unknown BD7-11 bacterium 3</i>	8	1	2	0	0	0	3	0	0
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>Phycisphaera</i>	3	4	3	0	0	0	0	0	0
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>SM1A02 bacterium 1</i>	2	1	1	0	0	0	0	1	2
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>SM1A02 bacterium 2</i>	0	0	0	0	0	1	0	0	6
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>SM1A02 bacterium 3</i>	0	0	3	0	1	1	4	0	3
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>SM1A02 bacterium 4</i>	0	0	4	1	5	0	12	11	9
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown Phycisphaerae bacterium 2</i>	7	10	1	0	1	0	0	2	6
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown CPla-3 termite group bacterium 1</i>	7	0	9	0	0	0	1	2	19
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown CPla-3 termite group bacterium 2</i>	9	17	11	0	2	0	7	7	21
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown CPla-3 termite group bacterium 3</i>	2	11	0	0	0	0	0	0	1
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown CPla-3 termite group bacterium 4</i>	0	0	1	0	0	0	3	1	10
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown CPla-3 termite group bacterium 5</i>	10	14	4	0	2	0	8	14	14
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown WD2101 soil group bacterium 1</i>	0	0	0	0	3	0	1	2	0
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown WD2101 soil group bacterium 2</i>	5	0	0	1	2	0	0	0	0
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown WD2101 soil group bacterium 3</i>	1	1	5	0	0	0	0	0	2
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown WD2101 soil group bacterium 4</i>	0	0	1	0	0	0	1	0	7
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown WD2101 soil group bacterium 5</i>	0	2	2	0	1	0	0	4	1
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown WD2101 soil group bacterium 6</i>	3	5	1	0	1	0	0	0	2
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown WD2101 soil group bacterium 7</i>	0	5	3	0	1	0	2	0	1
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown WD2101 soil group bacterium 8</i>	2	5	0	0	0	0	0	0	7
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown WD2101 soil group bacterium 9</i>	3	4	2	0	1	0	0	0	4
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown WD2101 soil group bacterium 10</i>	0	3	6	0	0	1	1	3	3
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	<i>unknown WD2101 soil group bacterium 11</i>	1	2	3	0	1	0	4	2	4

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	unknown WD2101 soil group bacterium 12	4	2	5	0	0	1	1	3	6
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	unknown WD2101 soil group bacterium 13	3	8	0	0	0	0	0	1	10
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	unknown WD2101 soil group bacterium 14	4	5	4	0	1	0	1	2	7
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	unknown WD2101 soil group bacterium 15	3	4	1	0	3	0	8	10	1
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	unknown WD2101 soil group bacterium 16	2	3	2	0	16	0	4	12	1
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	unknown WD2101 soil group bacterium 17	3	12	8	0	9	1	6	0	5
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	unknown WD2101 soil group bacterium 18	5	25	6	0	2	0	2	1	3
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	unknown WD2101 soil group bacterium 19	3	3	6	0	6	0	20	13	8
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	unknown WD2101 soil group bacterium 20	6	30	9	0	4	0	4	17	1
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	unknown WD2101 soil group bacterium 21	11	7	8	2	4	0	40	11	0
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	unknown WD2101 soil group bacterium 22	12	33	16	0	3	0	9	14	20
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	unknown WD2101 soil group bacterium 23	59	84	87	2	33	3	62	31	39
<i>Planctomycetes</i>	<i>Phycisphaerae</i>	unknown WD2101 soil group bacterium 24	6	4	6	0	2	1	58	2	5
<i>Planctomycetes</i>	<i>Pla4 lineage</i>	unknown Pla4 lineage 1	8	0	5	0	0	4	0	0	12
<i>Planctomycetes</i>	<i>Pla4 lineage</i>	unknown Pla4 lineage 2	58	28	18	5	0	10	7	0	42
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Fimbrigliobus</i> 1	4	0	1	0	0	0	3	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Fimbrigliobus</i> 2	0	0	0	0	1	0	3	2	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Fimbrigliobus</i> 4	0	0	0	0	2	0	2	6	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Fimbrigliobus</i> 5	1	0	1	1	7	0	2	3	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Gemmata</i> 1	8	15	1	0	0	0	4	0	12
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Gemmata</i> 10	2	5	0	0	0	0	1	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Gemmata</i> 11	1	0	0	1	6	0	2	2	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Gemmata</i> 2	2	0	0	1	18	0	2	7	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Gemmata</i> 3	0	3	1	0	3	0	8	15	4
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Gemmata</i> 4	0	0	3	0	0	0	2	0	7
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Gemmata</i> 5	0	0	0	0	4	0	0	3	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Gemmata</i> 6	0	0	2	0	0	0	1	0	4
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Gemmata</i> 7	0	3	3	0	0	0	0	0	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Gemmata</i> 8	2	2	1	0	6	0	9	13	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Gemmata</i> 9	0	0	1	0	0	0	7	1	1

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 1</i>	108	103	78	1	23	1	38	3	27
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 10</i>	26	19	23	0	7	0	6	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 100</i>	1	3	1	0	1	0	1	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 105</i>	118	70	76	1	8	5	29	1	36
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 106</i>	10	15	39	0	1	1	4	0	7
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 107</i>	17	26	13	0	10	0	10	2	10
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 108</i>	11	13	14	0	7	0	3	0	4
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 109</i>	19	0	8	0	0	0	1	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 11</i>	24	17	12	1	6	0	3	0	8
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 110</i>	1	1	4	1	4	0	7	1	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 111</i>	16	10	13	0	0	0	3	0	7
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 112</i>	1	6	6	0	0	0	2	1	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 113</i>	2	6	0	0	1	0	2	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 114</i>	5	7	3	0	2	0	2	0	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 115</i>	4	2	11	0	0	0	2	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 116</i>	5	3	8	0	5	0	11	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 117</i>	1	4	4	0	2	0	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 118</i>	0	6	2	0	2	1	0	0	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 119</i>	2	4	1	0	0	0	1	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 12</i>	10	11	12	0	2	0	4	0	11
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 120</i>	4	5	1	1	0	0	0	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 121</i>	4	1	2	0	1	0	0	0	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 122</i>	0	6	0	0	4	0	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 123</i>	0	1	6	1	1	0	0	0	2

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 124</i>	16	12	9	0	0	0	1	0	7
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 126</i>	6	1	4	0	0	0	0	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 127</i>	1	5	3	0	0	0	0	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 128</i>	1	2	4	0	0	0	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 129</i>	13	26	5	2	3	0	7	2	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 13</i>	0	3	3	2	18	0	36	34	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 130</i>	8	10	16	0	0	0	6	0	10
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 131</i>	7	7	6	0	0	0	3	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 132</i>	8	6	16	0	0	1	3	2	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 133</i>	11	5	10	0	1	0	5	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 134</i>	8	3	2	0	2	0	0	0	5
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 135</i>	6	5	0	0	1	0	1	1	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 136</i>	8	2	5	0	2	0	2	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 137</i>	2	3	5	0	0	0	0	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 138</i>	5	5	6	0	1	0	1	0	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 139</i>	6	3	2	0	0	0	0	0	6
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 14</i>	8	25	19	0	10	0	10	0	15
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 140</i>	0	2	3	0	0	0	1	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 15</i>	17	18	20	0	2	0	2	0	10
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 16</i>	43	5	17	2	0	0	3	0	13
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 17</i>	19	6	17	0	8	0	4	0	9
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 18</i>	1	24	1	0	15	0	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 19</i>	14	3	12	0	3	0	10	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 2</i>	70	102	51	0	26	0	36	3	8

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 20</i>	3	5	66	0	1	0	8	0	13
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 21</i>	18	10	16	0	3	0	1	0	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 22</i>	10	5	7	0	2	0	7	0	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 23</i>	20	4	15	0	7	1	4	0	5
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 24</i>	12	5	26	0	6	0	4	0	7
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 25</i>	9	3	7	0	3	0	3	0	5
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 26</i>	10	9	8	0	1	0	2	0	7
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 27</i>	4	5	6	0	4	0	6	0	5
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 28</i>	3	9	17	0	1	1	3	0	7
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 29</i>	9	13	8	0	5	0	2	0	4
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 3</i>	25	69	26	0	34	2	7	0	11
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 30</i>	2	1	7	0	0	0	2	1	23
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 31</i>	11	8	11	0	0	0	3	0	9
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 32</i>	7	3	5	0	1	0	3	1	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 33</i>	9	0	6	0	3	0	1	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 34</i>	0	14	5	0	2	0	1	1	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 35</i>	0	0	0	0	0	0	12	4	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 36</i>	4	2	3	0	8	0	6	1	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 37</i>	17	4	8	0	0	0	1	0	4
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 38</i>	12	3	4	0	0	0	0	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 39</i>	7	21	5	0	3	0	4	1	5
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 4</i>	16	85	43	0	17	0	3	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 40</i>	6	1	2	0	1	1	6	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 41</i>	1	2	9	0	7	1	3	0	2

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 42</i>	3	4	6	0	2	0	4	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 43</i>	6	6	5	0	1	0	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 44</i>	6	5	3	0	0	0	1	0	6
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 45</i>	7	21	9	0	8	0	3	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 46</i>	3	3	6	0	0	0	0	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 47</i>	7	5	5	0	1	0	6	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 48</i>	5	3	1	0	0	0	4	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 49</i>	11	10	8	0	1	0	3	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 5</i>	10	22	7	0	35	0	4	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 50</i>	2	6	1	0	3	0	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 51</i>	3	1	0	0	0	0	1	0	5
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 52</i>	17	27	16	0	9	0	15	0	6
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 53</i>	5	11	12	0	2	0	0	0	8
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 54</i>	4	3	5	0	1	0	0	0	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 55</i>	2	3	8	0	0	0	0	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 56</i>	2	4	3	0	0	0	4	0	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 57</i>	0	5	0	0	0	0	2	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 58</i>	2	5	2	0	0	0	1	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 59</i>	0	1	4	0	0	0	1	1	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 6</i>	29	46	5	1	26	0	11	0	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 60</i>	2	3	0	0	5	0	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 61</i>	2	3	0	0	0	0	1	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 62</i>	6	2	2	0	1	1	0	0	4
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 63</i>	0	5	1	0	2	0	2	0	1

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 64</i>	1	3	4	0	0	0	3	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 65</i>	1	2	2	0	2	0	0	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 67</i>	3	5	2	0	1	0	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 68</i>	1	6	3	1	1	0	0	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 7</i>	16	10	24	0	6	1	18	1	9
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 70</i>	1	0	1	0	2	0	2	3	4
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 71</i>	4	0	3	0	0	1	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 74</i>	3	0	2	0	0	0	0	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 75</i>	0	2	4	0	1	0	0	0	6
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 76</i>	0	3	0	0	1	0	2	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 78</i>	1	0	2	1	2	0	0	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 8</i>	4	4	2	0	32	0	1	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 80</i>	0	0	3	0	4	0	0	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 83</i>	2	1	3	0	2	0	1	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 85</i>	0	0	8	0	0	1	0	0	4
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 87</i>	3	0	2	0	0	0	0	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 89</i>	1	3	2	0	0	0	1	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 9</i>	5	55	9	0	3	0	0	0	9
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 92</i>	7	0	1	0	0	0	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 93</i>	2	2	4	0	0	0	1	0	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 95</i>	2	2	1	0	1	0	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 97</i>	9	13	11	0	2	0	2	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gemmataceae bacterium 98</i>	3	0	9	0	0	0	0	0	15
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Candidatus Nostocoida 1</i>	38	76	94	0	44	0	223	64	50
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Candidatus Nostocoida 2</i>	13	27	6	0	52	0	16	74	8

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 1	10	29	18	0	15	0	21	28	30
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 10	1	1	2	0	8	0	13	11	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 11	5	5	1	0	15	0	16	4	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 12	1	6	2	0	7	0	4	0	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 13	0	4	2	0	6	0	0	0	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 14	9	1	0	0	0	0	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 15	0	5	4	0	5	0	8	6	6
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 16	2	0	3	0	22	0	10	10	3
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 2	12	0	0	0	6	0	15	12	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 3	0	0	1	0	17	0	2	6	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 4	12	3	0	0	30	0	31	35	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 5	0	1	1	1	1	0	5	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 6	0	1	0	0	0	0	5	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 7	61	130	109	0	49	0	55	10	19
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 8	15	19	15	0	36	1	35	43	17
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Singulisphaera</i> 9	0	0	0	0	5	0	51	1	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	unknown <i>Isosphaeraceae</i> bacterium 1	0	3	3	0	1	1	0	0	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	unknown <i>Isosphaeraceae</i> bacterium 2	11	18	30	1	21	0	17	7	5
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Pir4 lineage</i> bacterium 1	3	2	1	0	0	0	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Pir4 lineage</i> bacterium 2	0	1	6	0	3	0	3	0	18
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Pirellula</i> 2	0	0	0	0	1	0	2	2	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	unknown <i>Pirellulaceae</i> bacterium 1	7	8	5	0	3	1	18	22	11
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	unknown <i>Pirellulaceae</i> bacterium 10	16	33	5	0	1	0	3	0	10
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	unknown <i>Pirellulaceae</i> bacterium 11	6	0	2	0	0	0	0	0	40
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	unknown <i>Pirellulaceae</i> bacterium 12	13	14	5	0	1	1	1	2	21
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	unknown <i>Pirellulaceae</i> bacterium 13	3	25	9	0	1	0	4	1	15
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	unknown <i>Pirellulaceae</i> bacterium 14	13	18	13	0	0	0	2	0	14
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	unknown <i>Pirellulaceae</i> bacterium 15	1	17	5	0	0	1	3	0	9
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	unknown <i>Pirellulaceae</i> bacterium 16	3	16	5	0	2	0	1	0	5
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	unknown <i>Pirellulaceae</i> bacterium 17	2	13	5	0	3	0	2	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	unknown <i>Pirellulaceae</i> bacterium 18	3	7	3	0	0	0	0	0	10

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 19</i>	15	18	4	1	2	1	3	0	16
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 2</i>	6	2	5	0	0	0	0	1	4
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 21</i>	5	0	2	0	0	0	1	0	7
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 22</i>	2	3	1	0	0	0	0	0	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 23</i>	1	1	2	0	0	0	1	0	2
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 4</i>	4	0	0	0	0	0	0	2	0
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 5</i>	69	39	29	1	22	3	9	6	64
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 6</i>	48	50	92	0	2	0	19	0	15
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 7</i>	35	40	21	0	2	1	10	0	30
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 8</i>	60	12	21	0	0	2	13	0	11
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Pirellulaceae bacterium 9</i>	10	15	14	1	3	0	5	0	12
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>unknown Gimesiaceae bacterium</i>	37	66	30	0	0	0	10	0	30
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Schlesneria 1</i>	32	18	5	0	10	0	22	45	1
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Schlesneria 2</i>	24	33	15	0	13	1	42	74	23
<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Schlesneria 3</i>	5	24	2	0	4	0	6	32	9
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 1</i>	0	1	2	0	0	6	9	8	12
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 2</i>	0	2	4	1	4	0	13	4	36
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 3</i>	0	1	6	7	13	10	8	20	22
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 4</i>	5	0	0	0	1	0	1	0	0
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 5</i>	2	0	0	0	4	0	1	0	0
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 6</i>	5	1	2	0	0	0	0	0	0
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 7</i>	1	0	0	0	0	0	14	0	1
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 8</i>	6	0	1	0	1	0	1	6	1
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 9</i>	0	1	6	0	0	0	9	1	2
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 10</i>	0	0	2	0	0	0	11	13	3
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 11</i>	1	6	5	0	0	1	4	3	15

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 12</i>	2	0	6	1	1	2	10	5	11
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 13</i>	0	0	3	0	3	0	19	4	9
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 14</i>	5	35	0	0	0	0	2	0	9
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 15</i>	2	12	6	0	0	0	16	19	3
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 16</i>	14	2	6	0	0	0	6	24	12
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 17</i>	3	40	21	0	1	1	47	74	22
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 18</i>	16	13	43	12	18	13	76	45	68
<i>Planctomycetes</i>	<i>vadinHA49</i>	<i>unknown vadinHA49 bacterium 19</i>	2	34	10	0	0	0	20	21	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acetobacter</i>	0	0	0	0	106	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidocaldus 1</i>	35	16	63	12	2	69	33	2	79
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidocaldus 2</i>	14	0	0	7	0	2	6	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidocaldus 3</i>	4	3	5	0	1	2	2	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidocaldus 4</i>	15	2	10	6	0	17	3	0	21
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 1</i>	112	23	0	0	15	0	0	14	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 10</i>	0	0	4	3	2	8	5	5	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 11</i>	0	1	2	2	13	0	6	11	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 12</i>	8	0	4	0	0	5	2	0	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 13</i>	1	0	1	0	2	11	1	1	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 14</i>	1	0	1	1	6	14	4	3	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 15</i>	0	2	0	0	7	4	3	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 16</i>	0	0	0	1	1	2	2	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 17</i>	1	0	0	1	1	1	1	0	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 2</i>	19	4	1	13	18	1	19	7	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 3</i>	4	14	31	20	122	157	79	74	92
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 4</i>	0	5	4	7	16	21	31	43	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 5</i>	0	2	4	8	13	41	26	7	15
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 6</i>	0	0	2	0	4	18	2	1	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 7</i>	1	4	3	6	4	15	9	7	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 8</i>	1	0	3	7	18	12	9	17	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidiphilium 9</i>	5	1	10	0	0	6	1	0	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidisoma 1</i>	156	84	5	61	446	15	46	149	20
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidisoma 2</i>	97	2	0	0	1	0	4	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidisoma 3</i>	0	1	0	0	0	0	2	0	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidisphaera</i>	24	1	14	7	1	25	15	0	42
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidocella 1</i>	12	0	316	0	1	0	3	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidocella 2</i>	0	0	0	11	0	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidocella 3</i>	40	48	574	5	6	38	2	4	21
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidocella 4</i>	0	7	1	5	179	0	13	84	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidocella 5</i>	1	8	5	2	12	10	1	10	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidocella 6</i>	4	8	6	1	65	0	13	7	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Acidocella 7</i>	3	24	16	3	13	0	12	49	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Endobacter</i>	0	30	24	6	13	49	23	12	52
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Gluconobacter</i>	0	0	0	0	232	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodopila</i>	34	3	67	10	9	63	23	3	79
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodovastum 1</i>	15	0	2	15	3	5	9	12	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodovastum 2</i>	33	12	1	10	12	7	14	28	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodovastum 3</i>	7	13	28	7	5	13	5	7	11
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodovastum 4</i>	4	1	1	38	17	0	8	6	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodovastum 5</i>	91	168	290	91	102	73	83	160	122
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodovastum 6</i>	40	86	72	69	121	45	78	54	54

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodovastum</i> 7	25	8	51	25	53	17	41	92	40
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodovastum</i> 8	6	0	1	17	9	0	5	10	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodovastum</i> 9	0	2	4	0	4	3	1	1	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Roseococcus</i>	10	0	0	8	9	0	2	7	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Roseomonas</i> 1	1	1	0	1	10	0	2	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Roseomonas</i> 2	1	0	2	11	16	0	1	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Roseomonas</i> 3	0	0	0	0	1	7	1	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Roseomonas</i> 4	0	0	0	13	3	0	0	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Roseomonas</i> 5	0	0	0	5	4	0	1	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 1	34	8	208	33	10	107	47	12	154
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 10	5	62	100	2	0	24	3	18	73
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 11	14	128	16	4	1	9	13	0	38
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 12	52	4	0	6	22	0	17	31	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 13	4	14	27	2	5	18	13	9	27
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 14	5	10	29	1	8	5	1	49	27
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 15	13	25	33	2	0	16	9	10	21
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 16	4	11	61	6	0	15	4	2	42
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 17	3	0	30	3	3	12	15	1	26
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 18	4	1	14	3	2	3	23	0	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 19	0	1	31	17	12	2	10	12	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 2	3	11	22	6	14	8	10	19	15
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 20	0	9	0	0	0	5	1	0	24
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 21	0	0	0	6	8	2	4	11	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 22	20	32	12	48	56	10	116	108	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Acetobacteraceae</i> <i>bacterium</i> 23	2	1	2	52	37	1	55	28	1

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 24</i>	0	9	1	22	23	0	34	31	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 25</i>	17	26	7	6	0	10	4	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 26</i>	2	9	13	7	8	0	29	14	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 27</i>	0	3	5	0	0	1	0	0	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 28</i>	2	1	19	0	0	2	2	0	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 29</i>	0	0	0	3	8	1	1	5	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 3</i>	13	19	155	4	5	61	17	24	112
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 30</i>	1	6	5	22	9	4	2	1	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 31</i>	5	0	3	1	0	4	1	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 32</i>	0	0	5	0	3	9	3	3	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 33</i>	0	5	3	0	0	0	1	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 34</i>	6	0	7	0	12	2	1	7	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 35</i>	2	1	1	1	0	2	1	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 36</i>	34	1	23	5	0	11	8	0	15
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 37</i>	2	5	9	0	0	3	2	1	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 39</i>	0	0	9	3	1	0	0	2	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 4</i>	0	2	7	5	0	0	0	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 40</i>	0	5	0	0	0	0	0	3	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 41</i>	0	1	0	1	1	5	1	0	3

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 42</i>	0	1	3	0	0	1	0	5	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 43</i>	1	0	2	1	0	0	0	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 44</i>	141	162	439	73	35	201	112	8	328
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 45</i>	43	2	6	52	59	5	62	69	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 46</i>	6	8	93	40	30	65	37	64	116
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 47</i>	1	26	124	12	7	14	13	22	60
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 48</i>	83	71	130	117	201	105	372	256	220
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 49</i>	24	9	33	15	10	32	12	6	22
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 50</i>	1	38	133	119	12	2	6	55	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 51</i>	1	0	1	14	66	7	6	7	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 52</i>	90	22	49	60	80	82	46	83	67
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 53</i>	2	9	60	33	37	27	36	38	60
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 54</i>	13	2	10	12	14	18	11	9	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 55</i>	1	0	1	3	8	4	8	3	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 56</i>	0	0	0	0	0	0	0	0	11
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 57</i>	0	2	1	0	0	0	0	7	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 58</i>	0	0	0	5	7	0	1	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 59</i>	7	2	4	11	8	3	4	10	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 59</i>	2	0	7	7	2	14	5	4	4

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 6</i>	1	4	0	0	1	0	0	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 60</i>	1	0	2	1	0	1	1	1	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 61</i>	82	112	96	309	480	101	660	533	129
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 62</i>	101	153	57	145	147	22	72	497	20
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 63</i>	28	177	56	20	5	19	26	0	77
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 64</i>	8	2	121	9	1	133	14	1	170
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 65</i>	2	54	39	4	4	36	5	9	45
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 66</i>	15	36	49	7	1	17	2	0	31
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 67</i>	10	5	8	22	10	12	35	22	14
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 68</i>	9	3	36	4	0	22	10	0	21
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 69</i>	13	13	29	8	0	27	19	3	24
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 7</i>	190	75	369	203	19	192	241	19	285
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 70</i>	0	10	9	0	3	9	1	6	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 71</i>	5	2	13	2	1	9	2	0	13
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 72</i>	0	21	2	5	2	8	7	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 73</i>	2	4	3	9	12	4	1	4	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 74</i>	11	1	1	6	1	2	13	2	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 75</i>	0	11	29	1	1	15	1	2	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 76</i>	1	2	6	0	0	1	11	0	4

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 77</i>	6	0	5	3	0	6	2	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 78</i>	6	2	4	0	0	4	1	0	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 79</i>	0	0	4	0	0	9	2	0	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 8</i>	126	45	210	38	4	142	61	0	121
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 80</i>	2	5	1	2	31	0	0	5	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 81</i>	1	0	2	0	0	2	0	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 82</i>	3	0	8	2	0	2	14	0	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 83</i>	0	0	3	3	8	0	1	1	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 84</i>	1	0	3	0	1	0	0	3	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 85</i>	2	1	1	2	0	1	1	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 86</i>	1	2	4	4	2	1	4	4	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 88</i>	2	0	3	0	0	3	1	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 89</i>	6	0	0	0	0	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 9</i>	40	20	71	25	0	37	32	0	93
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Acetobacteraceae bacterium 90</i>	3	0	0	1	4	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Azospirillum 1</i>	5	30	0	3	28	0	9	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Azospirillum 2</i>	0	3	0	0	9	0	4	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Azospirillum 3</i>	0	0	0	4	2	0	0	3	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Nitrospirillum</i>	0	0	1	0	0	0	3	2	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Skermanella 1</i>	0	0	2	0	0	9	5	1	12
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Inquilinus 1</i>	71	28	9	18	57	10	76	135	24
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Inquilinus 2</i>	19	10	2	5	28	1	33	112	12
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Inquilinus 3</i>	14	17	8	1	1	2	9	8	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Inquilinus 4</i>	3	4	8	0	0	1	5	0	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Inquilinus 5</i>	1	3	2	1	1	2	5	9	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Inquilinus 6</i>	1	7	1	0	0	0	1	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Caedibacter</i>	1	1	1	0	1	1	3	2	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Asticcacaulis 1</i>	8	1	1	5	3	1	0	5	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Asticcacaulis 2</i>	61	51	8	10	20	0	78	65	12

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Brevundimonas</i> 1	0	0	0	1	8	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Brevundimonas</i> 2	0	0	0	1	1	0	0	0	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Caulobacter</i> 1	16	2	1	2	7	0	14	11	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Caulobacter</i> 2	224	189	108	186	434	54	577	722	165
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Caulobacter</i> 3	21	20	7	8	9	3	30	50	11
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Phenylobacteriu</i> m 1	112	93	241	313	423	136	914	826	293
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Phenylobacteriu</i> m 2	77	70	94	42	37	72	135	104	86
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Phenylobacteriu</i> m 3	42	36	16	62	88	6	59	254	33
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 1	6	23	2	23	24	2	18	25	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 10	0	0	8	3	0	1	8	0	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 11	0	0	0	0	5	1	1	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 13	182	211	195	63	75	123	215	186	345
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 14	124	77	43	89	77	9	163	156	34
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 15	71	171	74	17	24	17	24	15	17
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 16	130	80	50	25	32	16	53	78	79
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 17	41	35	16	12	6	15	51	10	28
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 18	35	44	109	30	55	53	66	54	116
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 19	9	2	1	12	37	3	36	68	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 2	17	29	19	17	31	14	73	115	29
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 20	2	8	0	4	1	12	6	1	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 21	75	58	24	48	65	12	86	133	22
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	unknown <i>Caulobacterace</i> ae bacterium 22	3	16	23	9	4	6	62	19	13

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 3</i>	25	10	7	37	37	10	55	100	22
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 4</i>	3	16	47	17	5	14	47	35	39
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 5</i>	9	0	5	8	9	0	10	44	20
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 6</i>	11	30	27	8	1	7	11	6	45
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 7</i>	1	0	3	14	13	3	31	34	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 8</i>	7	5	20	35	23	10	57	51	25
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Caulobacteraceae bacterium 9</i>	10	0	0	3	15	0	12	9	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Hirschia 2</i>	0	0	0	3	2	1	1	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Dongia 1</i>	0	0	4	0	1	2	1	5	18
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Dongia 2</i>	0	0	0	0	0	1	0	0	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Aliidongia 1</i>	0	0	0	0	0	0	32	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Aliidongia 2</i>	4	19	2	1	0	1	1	0	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteraceae bacterium 1</i>	14	48	27	0	0	6	6	0	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteraceae bacterium 10</i>	23	42	5	38	279	5	235	480	11
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteraceae bacterium 11</i>	10	18	0	3	13	0	5	41	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteraceae bacterium 12</i>	0	2	1	1	2	0	15	4	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteraceae bacterium 13</i>	3	13	0	0	3	0	1	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteraceae bacterium 14</i>	1	0	0	0	0	0	1	6	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteraceae bacterium 2</i>	0	0	12	1	0	15	2	3	27
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteraceae bacterium 3</i>	1	0	6	1	0	2	0	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteraceae bacterium 4</i>	5	1	9	6	47	11	88	140	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteraceae bacterium 5</i>	7	7	12	0	0	5	8	1	30
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteraceae bacterium 6</i>	8	2	19	7	1	3	35	3	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteraceae bacterium 7</i>	0	0	0	2	9	0	0	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsteraceae bacterium 8</i>	0	4	0	0	0	1	0	5	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown URHD0088 bacterium</i>	0	0	13	0	0	6	0	0	15
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 1</i>	7	11	25	7	2	39	13	2	45

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 10</i>	3	17	35	1	0	2	5	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 100</i>	7	0	1	1	0	0	7	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 101</i>	0	5	5	0	0	0	1	1	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 102</i>	0	0	0	2	8	0	0	2	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 103</i>	0	2	0	0	0	1	3	2	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 104</i>	0	0	0	0	0	2	3	1	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 11</i>	42	3	15	3	1	3	30	0	18
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 12</i>	4	0	8	0	0	5	6	0	11
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 13</i>	3	8	0	0	0	0	1	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 14</i>	0	0	1	0	0	2	1	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 15</i>	2267	4777	2832	1626	1882	2508	1218	505	2393
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 16</i>	49	169	74	33	2	45	80	3	77
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 17</i>	123	31	84	33	0	84	124	2	82
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 18</i>	62	130	38	26	0	20	66	1	67
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 19</i>	30	103	80	24	79	50	19	6	67
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 2</i>	2	3	31	0	19	37	24	44	57
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 20</i>	147	127	78	57	192	65	82	35	53
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 21</i>	58	87	24	41	65	23	11	4	16
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 22</i>	13	70	22	36	50	21	7	1	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 23</i>	19	1	53	12	0	37	8	2	67
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 24</i>	18	128	11	3	0	11	17	0	23
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 25</i>	28	82	44	11	0	52	36	1	126
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 26</i>	50	28	37	5	0	30	9	0	13
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 27</i>	18	4	40	6	1	24	40	4	42

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 28</i>	47	49	40	24	0	17	34	0	15
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 29</i>	9	12	58	17	2	45	10	4	88
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 3</i>	0	2	1	1	2	0	12	9	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 30</i>	2	3	0	23	17	0	35	37	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 31</i>	24	6	15	10	28	3	7	10	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 32</i>	35	51	32	22	38	41	35	5	32
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 33</i>	30	0	4	9	0	12	13	1	17
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 34</i>	7	42	10	1	0	11	1	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 35</i>	438	64	239	284	91	221	244	18	180
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 36</i>	7	0	0	1	0	8	26	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 37</i>	1	5	1	2	6	0	10	23	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 38</i>	7	8	6	6	0	4	1	3	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 39</i>	9	7	4	6	4	6	6	2	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 4</i>	185	35	180	184	19	89	367	8	124
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 40</i>	1	1	3	3	1	1	7	8	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 41</i>	2	1	0	7	3	0	7	12	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 42</i>	9	2	32	6	0	25	12	0	52
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 43</i>	8	24	44	7	1	36	10	3	41
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 44</i>	8	34	15	10	10	9	4	3	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 45</i>	1	0	14	3	0	4	2	0	15
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 46</i>	0	15	3	0	0	2	0	0	15
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 47</i>	3	2	6	0	0	4	2	0	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 48</i>	2	3	6	1	2	5	0	0	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 49</i>	2	12	7	2	0	8	1	0	22

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 5</i>	198	99	60	41	12	70	149	0	77
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 50</i>	0	7	0	0	1	2	0	1	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 51</i>	0	0	0	4	4	0	6	3	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 52</i>	1	3	2	1	0	0	2	0	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 53</i>	8	14	16	2	1	28	0	0	13
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 54</i>	0	0	0	0	0	0	2	11	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 55</i>	0	11	0	0	0	0	0	0	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 56</i>	1	6	2	0	0	0	0	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 57</i>	3	0	4	0	0	4	12	1	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 58</i>	4	0	0	2	0	1	0	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 59</i>	32	14	2	3	1	1	1	1	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 6</i>	228	47	36	62	6	67	213	4	50
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 60</i>	1	0	18	0	0	8	3	0	27
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 61</i>	3	1	2	0	0	0	1	1	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 62</i>	1	0	2	3	0	0	2	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 63</i>	3	1	0	0	1	0	0	0	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 64</i>	8	4	4	2	3	0	2	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 65</i>	1	0	0	0	3	0	3	4	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 67</i>	2	0	5	0	0	5	2	0	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 68</i>	0	1	0	0	0	0	1	5	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 69</i>	1	2	1	1	0	0	0	6	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 7</i>	22	77	92	24	9	14	182	3	34
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 71</i>	0	0	1	0	5	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 74</i>	0	1	0	0	0	0	1	4	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 76</i>	0	2	4	0	0	1	2	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 77</i>	0	0	2	0	0	1	2	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 8</i>	59	57	8	38	33	23	100	8	15
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 82</i>	224	120	195	58	27	149	165	45	196
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 84</i>	32	11	1	101	300	3	180	178	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 85</i>	56	52	43	24	67	25	75	75	18
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 86</i>	27	87	127	20	3	35	37	2	25
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 87</i>	27	124	40	2	1	26	18	3	63
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 88</i>	3	2	3	7	10	1	33	43	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 89</i>	4	12	24	5	2	17	17	17	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 9</i>	18	20	15	6	2	8	17	0	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 90</i>	3	32	18	0	1	8	4	0	12
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 91</i>	6	1	7	4	0	13	12	0	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 92</i>	6	16	8	2	3	11	1	0	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 93</i>	3	11	5	2	8	0	19	39	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 94</i>	6	17	9	0	0	2	4	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 95</i>	5	0	1	0	0	3	1	0	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 96</i>	2	6	1	7	5	0	9	8	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 97</i>	7	9	9	1	0	4	5	0	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 98</i>	0	0	1	0	0	8	4	0	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Elsterales bacterium 99</i>	2	1	1	2	0	5	2	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Holosporaceae bacterium 2</i>	1	0	3	0	0	0	2	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Holosporaceae bacterium 3</i>	4	7	0	0	0	2	3	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micavibrionaceae bacterium 1</i>	0	1	10	0	1	2	9	22	5

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micavibrionales bacterium 1</i>	0	0	0	0	2	0	1	104	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Micropepsis</i>	4	20	11	3	7	4	7	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 1</i>	36	28	14	41	25	4	37	110	16
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 10</i>	14	37	7	0	1	11	12	2	27
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 11</i>	0	0	14	2	7	15	8	12	25
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 12</i>	0	6	5	2	2	4	0	16	50
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 13</i>	0	35	4	0	0	1	4	5	25
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 14</i>	7	5	6	2	1	0	1	14	18
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 15</i>	5	9	9	0	7	3	0	1	15
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 16</i>	22	9	12	25	12	6	19	31	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 17</i>	2	6	1	1	0	2	6	3	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 18</i>	2	13	4	0	0	2	6	0	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 19</i>	33	4	5	8	6	13	14	15	17
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 2</i>	10	8	2	13	13	0	13	22	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 20</i>	0	0	0	2	2	0	0	1	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 21</i>	43	25	28	11	1	22	22	2	23
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 22</i>	35	40	0	5	0	0	14	32	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 23</i>	0	2	0	2	1	0	26	1	20
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 24</i>	2	2	3	0	1	3	0	0	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 25</i>	0	0	0	3	0	0	3	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 3</i>	13	40	24	3	1	15	14	5	35
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 4</i>	2	26	9	0	0	2	3	1	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 5</i>	1652	937	702	526	835	319	1472	2117	931
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 6</i>	183	154	103	65	2	102	233	2	157
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 7</i>	313	241	229	222	346	84	698	564	412

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 8</i>	2	0	5	11	20	6	38	27	50
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Micropepsaceae bacterium 9</i>	36	12	4	13	27	3	39	42	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Candidatus Captivus 2</i>	0	3	0	0	2	0	1	4	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Candidatus Captivus 3</i>	0	0	2	0	0	0	1	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Candidatus Finniella</i>	0	0	0	0	0	0	0	6	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Candidatus Paracaedibacter 1</i>	0	5	0	0	0	0	0	11	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Candidatus Paracaedibacter 2</i>	4	12	4	2	5	2	3	9	12
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Candidatus Paracaedibacter 3</i>	0	2	1	0	2	0	0	9	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Candidatus Paracaedibacter 7</i>	0	0	0	0	0	0	1	11	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Paracaedibacter aceae bacterium 1</i>	1	7	0	0	0	0	5	8	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Paracaedibacter aceae bacterium 2</i>	2	1	1	2	2	0	2	6	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Paracaedibacter aceae bacterium 4</i>	6	0	0	0	0	0	0	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Paracaedibacter aceae bacterium 5</i>	0	1	0	0	1	1	0	3	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Parvibaculum</i>	30	0	2	2	1	0	8	5	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Reyranella 1</i>	12	21	15	3	4	31	20	1	20
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Reyranella 2</i>	24	5	77	32	38	100	23	37	126
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Reyranella 3</i>	1	0	1	1	0	2	3	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Reyranella 4</i>	120	60	177	79	111	81	184	350	139
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Reyranella 5</i>	2	0	0	3	14	0	3	11	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Reyranellaceae bacterium</i>	0	0	3	0	2	0	1	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown A0839 bacterium</i>	0	0	30	0	0	6	0	1	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>1174-901-12 bacterium 1</i>	0	0	0	0	4	0	1	3	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>1174-901-12 bacterium 2</i>	1	0	0	6	3	1	0	1	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>1174-901-12 bacterium 3</i>	1	0	1	1	7	2	3	5	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>1174-901-12 bacterium 4</i>	1	0	0	6	0	0	24	2	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>1174-901-12 bacterium 5</i>	2	2	1	10	13	16	5	7	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>1174-901-12 bacterium 6</i>	3	0	9	11	19	22	11	22	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>1174-901-12 bacterium 7</i>	6	1	4	42	71	11	105	72	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>alpal cluster 1</i>	75	3	5	49	73	11	174	91	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>alpal cluster 2</i>	18	21	12	16	24	11	33	41	12
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>alpal cluster 3</i>	0	0	0	5	2	0	2	1	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>alpal cluster 5</i>	0	0	2	2	1	0	0	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>alpal cluster 6</i>	0	0	2	2	9	1	1	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>alpal cluster 7</i>	383	567	549	208	204	471	317	63	369

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bosea 1</i>	1	0	0	1	22	0	0	7	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bosea 2</i>	21	1	0	3	4	0	1	2	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Methylobacterium 1</i>	0	0	1	14	6	0	0	2	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Methylobacterium 2</i>	1	0	9	20	34	34	4	15	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Methylobacterium 3</i>	1	0	3	5	15	13	2	4	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Methylobacterium 4</i>	0	0	0	0	0	0	0	0	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Methylocella 1</i>	13	5	19	2	2	31	6	1	39
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Methylocella 2</i>	19	90	4	0	59	1	8	33	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Methylosula 1</i>	128	6	12	141	252	34	100	51	13
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Methylosinus</i>	104	206	286	34	14	108	74	15	128
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Microvira</i>	76	15	14	81	135	19	75	46	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Microvira 1</i>	7	5	4	27	70	15	28	32	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Microvira 2</i>	1	0	0	34	7	0	0	6	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Psychroglaciella</i>	14	1	1	45	118	32	15	9	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodoblastus 1</i>	0	0	1	0	0	4	0	3	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodoblastus 2</i>	1	1	0	2	1	1	2	14	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Roseiarcus 1</i>	630	1170	776	394	515	703	722	838	1295
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Roseiarcus 2</i>	10	18	25	9	3	53	32	17	114
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Roseiarcus 3</i>	1	4	2	3	0	4	1	0	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 1</i>	142	160	210	92	101	127	151	104	435
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 10</i>	24	4	6	67	94	22	85	115	15
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 11</i>	31	32	47	28	27	35	41	31	31
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 12</i>	15	11	3	9	8	3	46	44	11
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 13</i>	38	20	0	15	26	4	17	52	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 14</i>	0	0	2	40	30	3	3	6	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 15</i>	8	2	0	6	8	0	3	13	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 16</i>	22	1	0	0	2	0	0	6	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 17</i>	1	0	2	1	0	2	1	5	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 18</i>	0	0	2	0	0	3	0	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 2</i>	1	9	1	20	54	2	44	67	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 21</i>	0	0	2	1	0	0	0	0	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 3</i>	4	0	1	6	7	0	1	19	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 4</i>	232	254	208	102	96	139	180	2	275
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 5</i>	2	5	8	16	16	42	17	28	27
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 6</i>	1	0	0	18	0	1	0	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 7</i>	0	5	2	1	7	1	1	1	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 8</i>	1	0	0	6	2	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unkown Beijerinckiaceae bacterium 9</i>	5	7	0	33	108	2	119	118	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Arsenicitalea</i>	0	2	0	0	0	0	3	26	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Devosia 1</i>	9	1	28	32	25	13	56	54	60
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Devosia 2</i>	30	3	4	32	22	2	11	32	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Devosia 4</i>	5	0	0	1	1	0	2	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Devosiaceae bacterium</i>	103	50	16	86	99	20	217	353	46
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Hyphomicrobium 1</i>	1	0	0	4	12	0	3	2	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Hyphomicrobium 2</i>	20	1	26	138	48	43	45	22	30
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Hyphomicrobium 3</i>	7	1	26	30	27	14	14	10	33
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Hyphomicrobium 4</i>	2	0	5	1	3	4	1	6	15
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Hyphomicrobium 5</i>	0	0	1	0	1	1	0	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pedomicrobium 1</i>	1	0	2	9	6	6	2	3	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pedomicrobium 2</i>	16	4	23	4	0	16	6	0	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pedomicrobium 3</i>	8	0	30	18	7	29	5	4	13
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Hyphomicrobiaceae bacterium</i>	0	0	1	0	0	1	0	0	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Kaistia</i>	27	0	2	26	31	0	2	19	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown KF-JG30-B3 bacterium 1</i>	11	5	23	2	1	15	2	2	19
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown KF-JG30-B3 bacterium 2</i>	50	19	19	11	1	17	24	5	13
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown KF-JG30-B3 bacterium 3</i>	165	89	231	94	21	103	190	34	257
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Labrys 1</i>	84	22	17	43	67	26	94	151	61
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Labrys 2</i>	0	0	8	0	0	1	7	5	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Methylobacteriaceae bacterium 1</i>	1	2	1	0	0	1	0	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Methylobacteriaceae bacterium 2</i>	1	0	3	0	0	1	1	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Pleomorphomonadaceae bacterium 1</i>	1	3	0	0	3	0	4	10	12
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Pleomorphomonadaceae bacterium 2</i>	0	0	2	3	0	2	0	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium 1</i>	104	6	0	48	72	0	92	98	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium 2</i>	9	0	1	0	0	1	1	1	13
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium 3</i>	5	0	0	8	10	0	0	3	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Allorhizobium- Neorhizobium- Pararhizobium- Rhizobium 4</i>	5	0	1	0	0	0	2	5	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Allorhizobium- Neorhizobium- Pararhizobium- Rhizobium 5</i>	10	0	1	1	2	0	2	1	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Allorhizobium- Neorhizobium- Pararhizobium- Rhizobium 6</i>	13	0	0	2	2	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Allorhizobium- Neorhizobium- Pararhizobium- Rhizobium 7</i>	2	0	0	5	4	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Allorhizobium- Neorhizobium- Pararhizobium- Rhizobium 8</i>	1	1	0	1	2	0	0	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Mesorhizobium 2</i>	10	0	0	0	1	1	1	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Mesorhizobium 3</i>	170	17	8	122	136	8	322	511	21
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Mesorhizobium 4</i>	34	1	39	4	6	20	9	5	79
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Ochrobactrum</i>	0	1	0	0	0	18	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bauldia 1</i>	76	0	7	1	1	3	1	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bauldia 2</i>	0	0	0	0	0	0	1	7	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bauldia 3</i>	4	0	1	0	3	1	1	1	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bauldia 5</i>	4	0	1	6	1	0	5	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bauldia 6</i>	105	39	96	43	15	102	60	5	92
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhizobiales Incertae Sedis bacterium 1</i>	2	0	16	14	18	10	69	77	54
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhizobiales Incertae Sedis bacterium 2</i>	0	0	2	14	13	0	6	4	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhizobiales Incertae Sedis bacterium 3</i>	0	0	0	0	0	0	4	11	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodomicrobium</i>	9	4	3	0	1	8	4	1	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pannonibacter</i>	0	0	0	0	8	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Afipia 1</i>	15	0	5	27	25	3	32	40	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Afipia 2</i>	2	0	0	0	3	0	7	4	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bradyrhizobium 1</i>	519	524	990	638	1256	987	2154	1920	1821
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bradyrhizobium 2</i>	2200	1908	2585	1529	1280	2188	3912	1903	3312
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bradyrhizobium 3</i>	0	0	0	2	15	0	4	9	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Bradyrhizobium 4</i>	0	0	0	0	2	0	2	1	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pseudolabrys 1</i>	12	7	21	753	953	8	1303	1141	20
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pseudolabrys 2</i>	26	1	37	13	0	31	63	6	90
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pseudolabrys 3</i>	18	26	4	5	5	8	28	60	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pseudolabrys 4</i>	1	2	0	2	0	5	1	1	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pseudolabrys 6</i>	5	0	0	0	1	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pseudolabrys 7</i>	55	5	14	47	30	16	97	75	31
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pseudolabrys 8</i>	5	3	47	4	5	40	35	20	46
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodoplanes 1</i>	1	3	8	14	8	1	32	97	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodoplanes 2</i>	0	0	4	1	0	4	4	1	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodoplanes 3</i>	0	0	22	0	0	3	3	1	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodopseudomonas</i>	78	6	2	22	26	0	61	96	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Tardiphaga</i>	93	3	5	19	35	0	7	8	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacteraceae bacterium 1</i>	15	1	0	4	12	0	1	12	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 10</i>	78	65	103	28	20	77	88	51	94
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 11</i>	70	17	72	27	5	69	15	5	68
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 12</i>	55	18	70	69	5	144	33	2	55
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 13</i>	5	23	47	6	0	11	6	24	84
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 14</i>	84	50	117	38	8	50	40	0	74
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 15</i>	18	1	23	18	0	20	6	0	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 16</i>	27	23	39	12	1	28	15	1	35
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 17</i>	7	0	14	4	0	11	4	0	14
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 18</i>	3	11	16	0	0	3	2	0	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 19</i>	56	101	69	14	6	44	22	1	96
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 2</i>	2	3	3	11	6	0	5	3	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 20</i>	0	4	0	0	0	2	6	6	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 21</i>	1	1	0	4	4	0	3	8	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 22</i>	14	1	3	0	0	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 23</i>	1	0	1	1	0	0	6	3	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 24</i>	9	0	0	2	1	0	2	2	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 25</i>	0	0	0	5	1	0	2	1	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 26</i>	46	12	50	35	8	43	14	3	36

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 27</i>	15	10	27	2	0	15	7	1	20
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 28</i>	41	9	53	39	20	40	26	2	27
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 29</i>	1	2	2	0	4	2	3	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 3</i>	12	25	17	7	12	15	30	32	31
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 30</i>	11	7	0	1	2	4	4	0	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 31</i>	4	0	4	2	0	2	1	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 32</i>	791	391	626	603	139	999	367	28	722
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 33</i>	121	103	198	53	24	197	68	6	250
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 34</i>	27	8	44	15	5	52	32	22	57
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 35</i>	15	15	2	7	5	0	19	3	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 36</i>	0	0	5	4	0	5	0	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 37</i>	2	0	5	4	0	6	2	2	24
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 38</i>	37	2	65	44	34	37	29	10	43
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 39</i>	7	0	17	9	13	12	31	26	23
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 4</i>	1704	1080	2083	1027	417	1180	1330	77	1206
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 40</i>	4	2	0	27	3	0	45	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 41</i>	51	58	141	18	3	28	18	7	124
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 42</i>	5	2	8	33	27	15	18	17	6

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 43</i>	16	0	4	2	1	3	1	1	13
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 44</i>	13	5	0	0	2	0	2	3	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 45</i>	0	0	4	1	0	0	2	4	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 47</i>	1	1	0	1	0	1	1	0	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 5</i>	1604	838	1910	898	371	1439	701	79	1406
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 6</i>	428	662	724	318	413	715	138	91	613
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 7</i>	29	19	329	165	68	143	188	177	332
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 8</i>	657	639	1084	383	297	910	446	95	857
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Xanthobacterac eae bacterium 9</i>	467	341	524	394	139	519	487	56	380
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhizobiales bacterium 1</i>	21	15	111	150	104	89	159	162	167
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhizobiales bacterium 4</i>	8	0	6	1	0	1	5	0	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhizobiales bacterium 5</i>	5	0	6	9	0	3	5	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Pseudorhodoba cter</i>	1	0	0	2	6	0	0	4	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Telmatospirillu m 2</i>	0	1	4	0	0	0	1	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Telmatospirillu m 3</i>	0	3	0	0	1	0	2	4	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Magnetospiillac eae bacterium 1</i>	0	2	1	7	37	0	3	11	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Magnetospiillac eae bacterium 10</i>	17	11	8	1	0	6	1	0	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Magnetospiillac eae bacterium 11</i>	1	5	3	0	0	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Magnetospiillac eae bacterium 2</i>	5	8	0	3	1	0	10	14	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Magnetospiillac eae bacterium 3</i>	3	10	3	0	1	1	1	1	6

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Magnetospirillaceae bacterium 4</i>	0	9	2	0	0	0	1	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Magnetospirillaceae bacterium 6</i>	58	59	3	4	9	0	2	16	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Magnetospirillaceae bacterium 7</i>	171	51	4	3	30	0	60	90	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Magnetospirillaceae bacterium 9</i>	96	14	7	26	77	0	56	49	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillaceae bacterium 1</i>	20	28	58	13	12	23	41	50	52
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillaceae bacterium 2</i>	13	46	29	8	15	5	40	58	19
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillaceae bacterium 3</i>	12	1	6	1	2	1	10	4	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillaceae bacterium 4</i>	0	0	3	0	0	0	1	2	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillaceae bacterium 5</i>	1	0	0	1	2	0	6	5	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillaceae bacterium 7</i>	3	0	0	1	2	0	2	2	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 1</i>	0	2	7	0	1	1	13	8	15
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 10</i>	3	8	2	0	0	1	0	9	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 11</i>	1	13	8	0	0	0	0	0	9
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 12</i>	1	9	1	0	0	0	1	5	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 13</i>	3	15	0	0	0	0	0	8	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 14</i>	2	11	0	1	2	0	4	5	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 15</i>	6	3	0	0	0	0	7	6	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 16</i>	0	5	3	0	0	0	3	0	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 17</i>	0	9	0	0	0	0	1	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 18</i>	2	9	5	0	0	0	0	0	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 19</i>	3	3	2	1	1	2	6	11	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 20</i>	0	1	0	0	0	0	0	8	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 21</i>	2	0	0	0	1	0	0	6	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 22</i>	3	2	3	0	0	0	4	0	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 23</i>	2	0	1	0	0	0	4	5	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 24</i>	0	0	0	0	0	1	2	1	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 25</i>	0	6	2	0	0	1	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 3</i>	46	220	38	5	3	3	148	99	32
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 32</i>	0	14	6	0	0	1	1	2	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 33</i>	1	3	1	0	0	1	1	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 35</i>	1	3	1	0	0	0	0	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 36</i>	12	0	0	0	0	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 37</i>	0	11	0	0	0	0	0	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 38</i>	1	3	1	0	0	0	2	3	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 39</i>	0	3	6	0	0	2	4	0	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 4</i>	2	23	1	0	4	0	32	32	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 5</i>	11	13	12	5	0	7	16	3	36
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 6</i>	2	21	9	0	0	2	5	0	28
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 7</i>	6	20	5	0	0	3	6	1	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 8</i>	10	4	5	0	0	5	6	0	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rhodospirillales bacterium 9</i>	1	0	0	4	14	0	11	4	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Candidatus Jidaibacter 1</i>	1	3	0	0	0	0	3	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Candidatus Megaira</i>	0	0	0	0	1	0	6	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 1</i>	0	0	0	0	0	0	7	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 2</i>	0	0	0	1	0	0	7	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 3</i>	0	1	1	0	1	0	2	6	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 4</i>	0	6	2	0	0	0	2	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 5</i>	0	0	0	0	0	0	5	9	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 6</i>	1	0	0	0	0	0	9	5	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 7</i>	0	0	0	0	0	0	4	13	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 8</i>	6	0	1	1	0	0	0	8	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 9</i>	5	0	7	0	0	1	1	3	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 10</i>	1	5	3	1	0	0	5	6	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 11</i>	3	0	0	2	0	0	10	18	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 12</i>	0	0	1	0	1	0	35	24	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 13</i>	2	20	1	0	0	0	67	3	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 14</i>	3	9	9	1	2	0	62	19	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 15</i>	0	0	0	0	0	0	6	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 16</i>	0	17	0	0	0	0	1	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 17</i>	5	0	5	0	0	2	0	0	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 18</i>	4	0	0	0	0	0	0	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 19</i>	0	3	4	0	0	0	0	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 20</i>	0	2	1	1	0	0	1	0	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 21</i>	1	0	4	0	0	2	0	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 22</i>	2	2	0	2	0	1	0	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 23</i>	0	1	2	0	0	0	4	0	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 24</i>	0	0	3	0	0	1	10	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 25</i>	6	8	7	2	0	5	3	0	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 26</i>	7	11	2	0	0	0	19	17	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 27</i>	9	17	2	0	1	3	25	8	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 28</i>	41	64	35	3	1	6	75	7	50
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 29</i>	1	0	0	0	1	0	4	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Plylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 31</i>	0	0	0	0	0	0	9	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 32</i>	0	0	1	0	0	0	5	5	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 33</i>	3	2	3	0	0	0	4	1	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 34</i>	3	2	0	0	0	0	6	0	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 35</i>	3	0	5	0	2	0	5	4	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 36</i>	3	5	2	1	0	0	4	3	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 37</i>	0	0	0	1	0	0	6	16	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 38</i>	3	8	1	0	0	1	3	3	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 39</i>	0	21	0	0	0	0	1	2	2
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 40</i>	0	5	0	0	14	0	1	6	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 41</i>	3	10	5	0	0	0	5	6	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 42</i>	4	13	3	4	1	1	3	7	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 43</i>	3	34	1	0	0	1	4	0	8
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 44</i>	1	5	4	0	18	1	0	25	5
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 45</i>	5	38	4	0	3	1	1	17	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown SM2D12 bacterium 46</i>	20	1	1	0	0	1	15	32	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Rickettsiales bacterium</i>	0	0	0	0	0	0	80	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Altererythrobacter 1</i>	0	0	5	15	27	10	29	35	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Altererythrobacter 2</i>	1	0	0	2	21	1	0	31	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Ellin6055 1</i>	0	0	0	0	0	1	3	0	4
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Ellin6055 2</i>	0	0	7	1	6	4	28	14	30
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Ellin6055 3</i>	8	1	4	150	172	10	121	162	50
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Novosphingobium 1</i>	7	2	0	0	14	0	0	10	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Novosphingobium 2</i>	571	113	6	17	48	9	49	148	48
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Novosphingobium 3</i>	4	0	1	6	10	7	18	20	10
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Novosphingobium 4</i>	8	0	6	8	26	1	30	49	21
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Novosphingobium 5</i>	6	7	2	3	3	1	2	9	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Novosphingobium 6</i>	5	0	1	3	1	0	2	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Novosphingobium 7</i>	0	0	1	0	1	0	1	1	5

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingobium 1</i>	0	0	0	0	2	0	0	12	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingobium 2</i>	3	0	4	3	2	0	1	1	6
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingobium 3</i>	0	4	1	2	0	1	2	9	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingobium 4</i>	4	0	1	1	2	0	1	9	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingobium 5</i>	1	0	0	0	2	0	1	4	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 10</i>	123	9	14	55	99	9	140	440	30
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 11</i>	1	0	69	34	15	51	160	90	133
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 12</i>	35	10	5	8	15	6	53	92	42
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 13</i>	16	40	1	2	25	3	2	33	11
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 14</i>	16	5	0	2	5	27	2	2	14
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 15</i>	40	9	0	0	6	0	0	4	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 16</i>	0	0	4	0	0	2	2	2	41
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 2</i>	10	33	389	29	12	153	334	139	514
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 3</i>	8	8	8	12	13	13	88	65	42
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 4</i>	47	3	1	0	1	0	4	15	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 5</i>	12	1	1	20	34	1	14	30	7
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 6</i>	45	1	1	3	3	0	12	24	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 7</i>	0	0	0	0	5	0	0	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 8</i>	0	0	0	1	10	0	1	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonas 9</i>	0	0	1	1	0	2	4	2	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingorhabdus</i>	5	0	0	2	7	0	5	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Alphaproteobacteria bacterium 1</i>	15	0	34	72	387	5	71	130	40
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Alphaproteobacteria bacterium 10</i>	0	0	4	0	0	7	1	0	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Alphaproteobacteria bacterium 12</i>	1	0	17	15	14	8	18	15	11
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Alphaproteobacteria bacterium 13</i>	1	5	0	0	0	0	1	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Alphaproteobacteria bacterium 15</i>	10	2	0	1	1	0	0	6	1
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Alphaproteobacteria bacterium 16</i>	0	11	0	1	1	0	7	2	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Alphaproteobacteria bacterium 17</i>	0	3	1	0	2	0	3	17	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Alphaproteobacteria bacterium 2</i>	1	0	0	3	1	0	2	1	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown Alphaproteobacteria bacterium 3</i>	11	0	24	3	8	22	9	23	19

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Alphaproteobact</i> <i>eria bacterium</i> 4	2	15	14	1	4	15	1	0	27
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Alphaproteobact</i> <i>eria bacterium</i> 5	32	1	0	10	8	0	27	12	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Alphaproteobact</i> <i>eria bacterium</i> 6	15	21	13	2	0	2	16	0	3
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Alphaproteobact</i> <i>eria bacterium</i> 7	9	11	24	6	0	3	9	0	0
<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>unknown</i> <i>Alphaproteobact</i> <i>eria bacterium</i> 9	3	4	9	1	0	1	2	0	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bacteriovorax</i> 1	39	0	0	1	16	0	2	10	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bacteriovorax</i> 2	9	0	0	4	6	0	0	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bacteriovorax</i> 3	16	1	1	2	3	0	2	5	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Peredibacter</i> 1	2	1	0	3	7	0	1	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Peredibacter</i> 2	3	4	0	0	0	0	1	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Peredibacter</i> 3	1	1	0	0	4	0	1	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Peredibacter</i> 4	14	0	0	0	0	0	1	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 1	4	0	1	6	9	0	4	4	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 10	1	2	8	0	0	1	13	7	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 11	1	0	3	4	2	0	6	12	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 12	11	7	2	0	0	1	2	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 13	2	3	1	0	1	0	4	8	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 14	1	1	1	0	0	0	8	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 15	4	2	2	0	0	3	1	2	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 16	1	4	5	0	1	1	3	1	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 17	3	1	1	2	3	1	2	6	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 18	6	0	0	1	1	0	1	2	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 19	0	0	3	0	0	1	0	0	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 2	14	25	24	2	5	9	49	29	20
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 20	11	6	3	0	0	0	4	4	10
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 21	1	2	1	0	2	2	2	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 22	4	0	1	0	1	0	0	4	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 23	1	0	2	0	0	0	1	0	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 24	1	2	0	0	0	0	4	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 25	0	0	3	2	0	0	1	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 28	4	5	1	1	0	0	2	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 3	9	36	13	1	2	0	41	0	21
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 30	1	1	3	0	0	0	1	0	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 31	9	0	1	0	0	0	2	1	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 32	1	4	2	0	0	0	3	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 34	5	2	1	1	0	2	6	2	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 36	25	5	2	11	16	0	5	15	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 37	5	1	0	0	11	1	0	3	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 38	7	2	3	3	1	0	5	4	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 39	12	1	1	0	0	0	2	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 4	10	33	26	1	1	4	15	5	29
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 40	1	0	1	1	4	0	3	8	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 5	16	35	14	0	3	2	9	5	22
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 6	7	16	6	1	0	3	4	0	20
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 7	7	6	2	3	5	2	28	17	9
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 8	8	27	10	0	0	2	6	0	16
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Bdellovibrio</i> 9	1	3	6	1	0	1	19	15	12
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Geobacter</i>	11	0	2	0	0	1	0	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobac</i> <i>ter</i> 1	1	2	106	45	30	40	168	153	187
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobac</i> <i>ter</i> 10	17	0	0	0	0	2	0	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobac</i> <i>ter</i> 11	0	16	1	0	0	0	0	2	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobac</i> <i>ter</i> 12	7	10	4	0	0	4	1	0	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobac</i> <i>ter</i> 13	3	0	1	2	0	0	1	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 14</i>	3	8	4	1	1	0	6	1	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 15</i>	5	5	0	0	0	0	1	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 16</i>	2	0	0	0	3	0	3	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 18</i>	0	5	1	0	0	0	0	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 19</i>	0	0	0	0	0	1	6	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 2</i>	2	11	2	10	4	2	31	49	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 20</i>	1	0	5	0	0	1	1	0	8
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 21</i>	1	5	0	0	0	0	2	3	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 23</i>	0	1	4	0	0	0	1	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 24</i>	1	0	7	1	1	2	5	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 27</i>	1	0	0	5	0	0	2	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 29</i>	1	0	14	5	5	11	25	55	43
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 3</i>	0	0	15	0	0	9	0	0	9
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 30</i>	0	0	14	2	3	11	19	7	66
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 31</i>	9	10	11	2	8	3	15	7	9
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 33</i>	0	2	1	2	0	0	3	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 4</i>	13	0	6	2	0	7	7	0	14
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 5</i>	16	29	6	1	1	0	6	7	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 6</i>	1	0	11	2	1	4	10	1	9
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 7</i>	11	15	2	0	1	0	1	6	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 8</i>	1	1	16	2	3	20	38	34	21
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Anaeromyxobacter 9</i>	1	11	1	1	1	0	2	7	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Archangiaceae bacterium</i>	0	0	0	0	0	2	5	1	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Biri41 bacterium 1</i>	5	1	3	6	2	1	2	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Biri41 bacterium 2</i>	22	1	29	8	0	2	49	15	41
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Biri41 bacterium 3</i>	0	0	2	0	0	2	0	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Biri41 bacterium 4</i>	1	0	0	3	0	0	2	0	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Biri41 bacterium 5</i>	0	0	9	1	0	0	4	0	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Biri41 bacterium 6</i>	1	0	1	0	0	0	0	0	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Blfdi19 bacterium 1</i>	0	0	6	0	0	2	0	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Blfdi19 bacterium 2</i>	5	4	1	0	0	0	4	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Bldi19 bacterium 3</i>	1	5	4	2	1	3	6	0	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Bldi19 bacterium 4</i>	0	0	2	0	1	1	14	20	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Bldi19 bacterium 5</i>	4	1	1	7	5	1	9	11	12
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Eel-36e1D6bacterium 1</i>	0	0	9	0	0	0	0	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 1</i>	3	1	6	0	4	3	8	4	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 10</i>	0	0	3	3	1	5	2	8	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 12</i>	1	0	0	1	0	4	2	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 13</i>	0	2	1	3	1	3	1	0	11
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 14</i>	1	1	1	2	1	4	2	0	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 15</i>	1	0	6	0	0	2	1	0	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 16</i>	6	2	1	0	0	4	3	0	8
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 17</i>	5	1	2	0	0	1	3	0	7
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 18</i>	2	1	7	1	2	2	3	2	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 19</i>	0	0	5	0	0	4	0	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 2</i>	32	18	101	15	1	38	51	10	281
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 20</i>	0	0	1	0	0	3	1	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 21</i>	1	0	8	0	0	1	1	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 22</i>	0	0	11	0	0	1	0	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 23</i>	2	0	10	3	0	4	0	0	14
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 24</i>	0	0	0	0	0	7	1	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 25</i>	4	0	0	0	0	0	2	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 28</i>	0	0	2	0	0	3	1	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 3</i>	32	20	83	3	1	14	18	3	155
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 30</i>	0	0	0	0	0	2	3	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 31</i>	0	0	2	1	0	2	0	0	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 32</i>	0	0	2	0	1	2	2	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 35</i>	6	1	42	1	1	8	7	18	19
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 37</i>	1	0	0	9	0	0	1	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 38</i>	0	0	0	0	0	0	5	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 4</i>	11	1	49	24	2	34	49	1	54
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 40</i>	0	0	5	0	0	0	0	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 43</i>	1	0	0	2	0	4	0	0	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 5</i>	0	3	8	8	10	5	8	9	26
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 6</i>	10	4	8	15	0	10	22	5	26
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 7</i>	5	0	6	21	11	3	13	12	7
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 8</i>	0	0	16	0	0	3	0	0	26
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Haliangium 9</i>	0	0	32	1	3	5	10	7	15
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown KD3-10 bacterium 1</i>	0	0	5	0	0	0	2	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown KD3-10 bacterium 2</i>	1	0	5	0	0	0	3	5	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown mle1-27 bacterium 1</i>	0	0	2	1	2	1	6	3	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown mle1-27 bacterium 2</i>	0	0	3	0	5	2	5	9	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown mle1-27 bacterium 3</i>	2	10	4	3	0	1	12	6	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown mle1-27 bacterium 4</i>	0	0	0	2	1	1	1	4	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown mle1-27 bacterium 5</i>	2	0	1	3	0	0	3	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown mle1-27 bacterium 6</i>	2	0	2	2	1	0	4	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown mle1-27 bacterium 7</i>	3	0	2	0	0	0	4	0	10
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P30B-42 bacterium 1</i>	1	0	0	0	0	0	5	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P30B-42 bacterium 2</i>	0	0	0	0	0	7	0	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P30B-42 bacterium 3</i>	0	0	2	0	0	0	2	1	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P30B-42 bacterium 4</i>	1	1	1	0	0	1	6	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P30B-42 bacterium 5</i>	4	0	0	5	9	0	1	1	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P3OB-42 bacterium 6</i>	1	0	13	1	2	2	1	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P3OB-42 bacterium 7</i>	2	4	3	0	1	0	5	3	7
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P3OB-42 bacterium 8</i>	2	5	1	0	3	0	5	9	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P3OB-42 bacterium 9</i>	0	0	0	3	18	0	0	9	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P3OB-42 bacterium 10</i>	1	2	13	5	14	2	20	12	13
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P3OB-42 bacterium 11</i>	15	59	9	0	0	12	8	4	32
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P3OB-42 bacterium 12</i>	40	17	53	4	6	38	48	4	35
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown P3OB-42 bacterium 13</i>	1	1	2	2	0	4	3	0	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Phaselocystis 1</i>	0	0	1	0	0	8	3	1	11
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Phaselocystis 2</i>	2	1	2	0	2	1	6	3	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Phaselocystis 3</i>	1	1	1	1	1	1	2	1	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Minicystis</i>	15	6	20	2	6	5	8	27	33
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 1</i>	136	89	72	36	3	103	148	3	137
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 10</i>	0	1	0	0	2	1	10	0	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 11</i>	16	3	1	3	2	15	19	1	18
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 12</i>	0	0	2	0	0	3	4	5	11
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 13</i>	0	0	0	4	5	3	5	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 14</i>	0	0	0	0	0	6	0	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 15</i>	9	20	28	1	2	11	13	7	38
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 16</i>	4	0	4	4	7	4	6	5	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 17</i>	27	1	0	3	0	0	29	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 2</i>	36	39	34	24	49	34	142	133	117
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 3</i>	22	44	31	9	17	14	78	45	61
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 4</i>	13	78	17	5	0	26	37	2	83
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 5</i>	25	0	3	12	0	5	39	0	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 6</i>	50	66	45	26	17	48	128	23	76
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 7</i>	0	2	2	5	1	2	10	0	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 8</i>	0	0	0	2	2	0	10	5	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Pajaroellobacter 9</i>	2	1	0	2	4	3	2	7	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Polyangiaceae bacterium 1</i>	30	51	35	7	4	16	52	14	75
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Polyangiaceae bacterium 2</i>	0	0	1	0	1	1	1	2	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Polyangiaceae bacterium 3</i>	2	0	2	13	7	3	7	9	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Polyangiaceae bacterium 4</i>	2	1	3	7	1	5	9	2	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Polyangiaceae bacterium 5</i>	1	1	1	0	3	0	2	1	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Polyangiaceae bacterium 6</i>	6	0	3	1	0	0	0	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Sandaracinaceae bacterium 1</i>	0	0	2	1	1	1	0	2	10
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Sandaracinaceae bacterium 3</i>	0	0	0	0	2	1	1	0	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Sandaracinaceae bacterium 4</i>	0	0	0	5	0	0	3	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown UASB-TL25 bacterium</i>	2	0	0	1	0	5	1	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Myxococcales bacterium 1</i>	9	7	6	1	0	3	5	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Myxococcales bacterium 2</i>	3	3	1	1	0	6	1	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Myxococcales bacterium 3</i>	1	0	17	11	17	3	3	7	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Myxococcales bacterium 4</i>	3	0	24	0	0	3	2	3	18
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Myxococcales bacterium 5</i>	0	0	8	0	0	0	0	1	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Myxococcales bacterium 6</i>	14	8	7	4	1	4	3	1	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 1</i>	1	0	4	1	0	1	2	2	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 2</i>	0	0	1	1	1	0	7	8	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 3</i>	2	43	31	7	0	8	5	0	15
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 4</i>	34	27	18	3	9	6	66	101	26
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 5</i>	0	6	0	0	0	0	0	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 6</i>	0	3	0	0	0	0	3	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 7</i>	0	0	2	1	0	0	0	0	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 8</i>	0	0	1	0	0	0	4	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 9</i>	0	0	0	0	0	0	3	2	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 10</i>	1	2	1	0	0	0	2	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 11</i>	2	0	1	0	0	2	0	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 12</i>	1	0	2	0	1	0	2	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 13</i>	0	0	4	0	0	0	0	0	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 14</i>	1	1	0	0	0	1	1	3	1

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 15</i>	1	1	2	1	0	0	5	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 16</i>	0	0	0	0	0	0	4	7	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 17</i>	0	0	0	2	0	0	2	7	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 18</i>	4	0	0	0	0	0	4	3	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 19</i>	0	0	1	2	0	0	6	3	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 20</i>	5	0	0	0	4	1	1	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 21</i>	0	3	2	0	0	1	1	2	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 22</i>	0	3	3	0	0	0	0	6	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 23</i>	3	0	0	1	1	2	1	6	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 24</i>	4	3	3	0	0	0	3	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 25</i>	1	1	5	1	1	0	0	4	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 26</i>	0	0	0	0	0	0	1	14	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 27</i>	0	1	2	1	1	1	2	3	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 28</i>	2	4	1	0	0	0	0	1	7
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 29</i>	0	4	2	0	1	0	3	3	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 30</i>	0	0	0	0	0	0	13	5	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 31</i>	12	0	1	1	1	0	1	1	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 32</i>	1	0	6	0	5	1	3	1	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 33</i>	0	2	0	0	0	2	3	13	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 34</i>	3	9	3	0	0	0	1	0	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 35</i>	2	1	2	1	0	1	10	1	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 36</i>	1	1	9	0	1	0	3	0	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 37</i>	0	0	0	5	4	0	4	8	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 38</i>	2	12	0	0	0	0	2	2	3

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 39</i>	3	9	6	1	0	1	2	1	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 40</i>	1	8	3	0	0	1	6	2	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 41</i>	4	5	4	1	2	1	4	0	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 42</i>	0	3	1	4	11	0	5	2	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 43</i>	2	3	4	3	0	3	2	4	8
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 44</i>	2	2	5	0	0	0	4	14	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 45</i>	4	2	1	1	0	2	13	4	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 46</i>	1	16	10	0	0	2	2	1	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 47</i>	6	12	4	0	0	0	5	0	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 48</i>	1	0	1	0	2	2	9	3	15
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 49</i>	1	1	0	0	0	0	4	27	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 50</i>	0	3	4	0	0	2	10	9	7
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 51</i>	7	9	4	2	0	3	0	0	10
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 52</i>	5	26	5	0	0	0	2	0	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 53</i>	2	6	11	0	2	1	10	1	9
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 54</i>	9	10	8	0	0	1	6	2	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 55</i>	0	1	0	0	1	2	14	18	9
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 56</i>	4	25	0	1	0	0	12	5	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 57</i>	12	15	8	0	0	1	6	0	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 58</i>	4	6	11	1	1	3	7	2	14
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 59</i>	2	6	3	4	2	2	14	7	10
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 60</i>	3	17	6	1	0	3	9	6	10
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 61</i>	23	15	1	0	2	0	6	7	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 62</i>	5	13	13	0	0	3	11	2	12

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 63</i>	6	13	19	1	1	3	7	3	11
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 64</i>	7	7	5	2	8	2	15	11	13
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 65</i>	1	7	9	1	1	3	17	16	17
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 66</i>	0	0	4	6	7	2	26	25	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 67</i>	14	6	8	3	15	0	20	10	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 68</i>	8	40	17	1	2	1	31	5	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 69</i>	15	42	16	3	0	3	22	22	15
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 70</i>	11	33	39	2	3	8	21	9	50
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 71</i>	66	117	80	11	19	16	79	41	34
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 72</i>	0	0	3	1	0	0	0	2	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 73</i>	0	0	1	0	0	0	4	2	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 74</i>	0	0	3	0	0	0	2	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 75</i>	1	0	4	0	1	0	3	6	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 76</i>	0	10	3	0	1	0	4	0	11
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 77</i>	0	3	0	0	0	0	1	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 78</i>	0	0	0	1	0	0	2	2	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 79</i>	1	0	3	0	0	0	1	2	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 80</i>	0	0	0	0	0	1	2	4	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 81</i>	0	1	0	0	0	1	1	0	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 82</i>	0	1	0	0	0	2	3	1	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 83</i>	5	2	0	0	0	2	1	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 84</i>	0	4	3	1	2	1	4	1	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 85</i>	2	4	1	0	0	1	1	5	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 86</i>	1	1	1	0	0	0	16	0	5

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 87</i>	3	0	4	3	2	0	4	7	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 88</i>	0	0	0	1	1	1	7	14	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 89</i>	6	2	5	0	0	2	12	2	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 90</i>	0	2	0	2	1	0	32	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 91</i>	3	6	4	1	0	2	14	6	6
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 92</i>	4	1	4	0	0	2	16	0	18
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 93</i>	19	5	7	1	3	0	15	9	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 94</i>	15	9	3	3	2	4	21	14	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 95</i>	12	26	13	3	8	4	17	18	29
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 96</i>	1	2	6	2	11	3	90	31	13
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 97</i>	53	20	3	4	6	0	33	51	11
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown 0319-6G20 bacterium 98</i>	28	41	46	3	6	14	57	39	43
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Oligoflexus 1</i>	1	1	0	1	12	0	2	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Silvanigrella 1</i>	4	2	1	0	0	0	1	1	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Silvanigrella 3</i>	4	13	0	0	1	0	6	3	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Silvanigrella 4</i>	2	7	4	1	4	0	8	6	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Silvanigrella 7</i>	0	2	2	0	0	0	5	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Oligoflexaceae bacterium 1</i>	0	0	6	0	0	0	6	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Oligoflexaceae bacterium 10</i>	4	3	6	0	4	0	19	15	4
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Oligoflexaceae bacterium 11</i>	12	0	2	6	14	0	2	7	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Oligoflexaceae bacterium 12</i>	5	1	1	0	0	0	0	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Oligoflexaceae bacterium 14</i>	2	2	2	0	0	0	1	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Oligoflexaceae bacterium 2</i>	3	0	1	1	5	0	2	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Oligoflexaceae bacterium 4</i>	2	1	2	1	0	0	11	2	5
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Oligoflexaceae bacterium 5</i>	9	0	0	0	1	0	0	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Oligoflexaceae bacterium 6</i>	1	0	1	1	1	1	6	9	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Oligoflexaceae bacterium 7</i>	1	1	0	0	3	0	2	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Oligoflexaceae bacterium 8</i>	8	36	6	4	1	2	19	5	4

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown Oligoflexaceae bacterium 9</i>	1	2	4	0	0	0	41	10	3
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown RCP2-54 bacterium 1</i>	2	0	1	3	0	0	0	0	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown RCP2-54 bacterium 2</i>	1	6	2	1	2	0	3	0	1
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown RCP2-54 bacterium 3</i>	1	0	4	0	0	2	1	0	10
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown RCP2-54 bacterium 4</i>	1	7	3	0	1	0	5	0	2
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown RCP2-54 bacterium 5</i>	8	1	5	5	2	6	12	2	0
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown RCP2-54 bacterium 6</i>	5	10	12	2	2	13	4	3	34
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown RCP2-54 bacterium 7</i>	15	8	68	2	0	13	9	0	10
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown RCP2-54 bacterium 8</i>	7	66	5	2	27	2	6	3	11
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown RCP2-54 bacterium 9</i>	50	67	49	26	49	29	37	10	46
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown RCP2-54 bacterium 10</i>	140	250	115	34	14	62	121	4	77
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown RCP2-54 bacterium 11</i>	115	331	39	52	117	23	79	45	28
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown RCP2-54 bacterium 12</i>	124	298	69	106	198	48	160	109	78
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown RCP2-54 bacterium 13</i>	20	26	23	5	1	26	17	0	45
<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>unknown SAR324 clade(Marine group B) bacterium</i>	0	0	4	0	0	0	0	1	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Aeromonas 1</i>	5	3	4	0	0	0	0	0	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Aeromonas 2</i>	3	7	4	0	0	2	0	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 1</i>	2	1	4	7	0	7	0	0	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 2</i>	0	0	7	0	1	8	2	1	29
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 3</i>	0	1	23	0	0	17	0	0	13
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 4</i>	0	0	6	12	2	2	22	14	16
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 5</i>	4	0	23	12	3	10	16	9	27
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 6</i>	5	0	25	0	0	7	5	1	68
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 7</i>	3	0	18	32	3	18	31	19	32
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 8</i>	8	0	11	3	0	95	1	0	41
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 9</i>	47	8	212	14	0	165	23	7	303
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 10</i>	285	145	144	81	39	105	167	2	127
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 11</i>	0	0	0	2	0	0	9	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 12</i>	55	3	44	8	0	96	0	0	111
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown A21b bacterium 13</i>	5	1	225	5	1	93	20	15	130
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown B1- 7BS bacterium 1</i>	2	0	2	11	60	1	6	6	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown B1- 7BS bacterium 2</i>	103	45	172	20	0	42	55	0	20
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>AAP99 bacterium</i>	7	9	5	8	18	0	36	33	15
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Aquabacterium 1</i>	27	12	33	96	56	21	96	112	98
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Aquabacterium 2</i>	1	22	0	11	10	0	9	108	25
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Bordetella</i>	116	135	0	27	85	0	50	32	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 1</i>	80	373	137	26	91	77	60	147	102
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 10</i>	219	103	35	135	280	52	258	434	153
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 11</i>	715	62	5	249	585	6	798	627	20
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 12</i>	301	133	149	184	245	117	547	718	543
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 13</i>	252	399	17	108	127	8	134	605	122
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 14</i>	5	1	1	21	38	1	2	19	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 15</i>	0	0	0	8	16	0	2	2	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 16</i>	2	3	0	0	2	0	3	6	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 17</i>	0	0	0	0	0	0	0	0	7
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 18</i>	0	3	0	1	0	0	1	0	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 2</i>	769	124	14	370	953	51	721	493	104
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 20</i>	2	4	1	5	17	2	4	12	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 3</i>	227	16	2	147	204	1	279	329	6
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia- Caballeronia- Paraburkholderi a 4</i>	2708	1456	143	536	1507	127	1844	4173	569

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia-Caballeronia-Paraburkholderia 5</i>	567	1272	139	3415	3704	122	5069	2468	272
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia-Caballeronia-Paraburkholderia 6</i>	880	1297	231	461	1439	131	1387	3266	607
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia-Caballeronia-Paraburkholderia 7</i>	149	70	244	249	1113	385	651	1244	1059
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia-Caballeronia-Paraburkholderia 8</i>	680	294	29	308	427	35	504	674	94
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Burkholderia-Caballeronia-Paraburkholderia 9</i>	77	164	169	61	59	114	92	109	348
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Caenimonas 1</i>	346	30	59	636	758	60	691	830	164
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Caenimonas 2</i>	120	11	38	188	105	8	1062	266	43
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Caenimonas 3</i>	0	0	0	6	1	0	0	1	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Cupriavidus 1</i>	33	1	7	21	24	2	22	28	21
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Cupriavidus 2</i>	0	0	10	0	12	1	0	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Delftia</i>	2	0	0	0	5	0	0	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Herbaspirillum</i>	2782	126	103	58	86	10	490	911	248
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Hermiimonas</i>	0	0	1	0	0	0	4	0	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Lautropia 1</i>	0	0	0	3	0	0	0	6	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Lautropia 2</i>	0	0	0	2	4	0	1	4	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Limnobacter 1</i>	2	0	5	9	20	34	28	12	42
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Limnobacter 2</i>	0	0	0	7	6	1	3	4	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Massilia 1</i>	487	86	47	745	1424	74	682	460	71
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Massilia 2</i>	99	16	2	888	1474	4	245	531	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Massilia 3</i>	185	12	7	854	513	3	210	242	13
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Massilia 4</i>	135	8	30	120	190	23	219	34	20
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Massilia 5</i>	50	20	2	219	264	15	122	59	13
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Massilia 6</i>	22	3	30	4	16	1	105	71	16
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Massilia 7</i>	1	0	1	15	18	4	8	5	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Massilia 8</i>	960	157	15	147	187	11	88	123	19
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 38</i>	0	0	2	0	0	0	0	0	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Noviherbaspirillum 1</i>	57	2	3	456	268	3	47	91	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Noviherbaspirillum 2</i>	47	8	9	62	60	8	64	69	11
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Noviherbaspirillum 3</i>	0	2	0	2	1	2	24	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pandoraea 1</i>	825	962	8	38	188	3	289	872	6
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pandoraea 2</i>	31	1	2	20	42	0	17	38	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Polaromonas</i>	63	2	5	25	10	3	50	28	8
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Polynucleobacter 1</i>	0	0	0	0	0	0	0	12	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Polynucleobacter 2</i>	2	0	2	0	0	0	3	2	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ralstonia</i>	4	4	10	4	4	0	22	5	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ramlibacter 1</i>	3	0	40	58	32	13	64	49	56
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ramlibacter 2</i>	12	0	6	3	3	3	30	20	20
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ramlibacter 3</i>	2	0	10	4	4	1	2	1	13
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Rhizobacter</i>	32	6	33	142	166	50	254	289	127
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Rhodoferrax 1</i>	31	3	6	97	129	2	84	59	6
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Rhodoferrax 2</i>	8	0	2	8	11	0	12	2	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Variovorax</i>	48	14	22	93	69	7	128	84	21
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 10</i>	223	1	7	3	6	0	13	63	12
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 11</i>	34	4	8	48	50	35	57	47	11
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 12</i>	439	53	1	164	616	3	164	177	4

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 13</i>	156	71	0	83	81	0	86	247	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 14</i>	15	0	3	6	1	1	17	50	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 15</i>	72	1	12	80	58	6	59	37	10
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 16</i>	6	10	1	5	3	0	3	4	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 17</i>	29	1	0	5	5	0	1	5	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 18</i>	27	16	0	26	54	0	74	98	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 19</i>	4	1	2	6	6	3	6	5	8
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 2</i>	716	66	16	664	1277	10	556	485	25
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 20</i>	0	0	0	12	12	1	3	1	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 21</i>	4	0	1	10	2	0	5	0	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 22</i>	5	0	0	8	0	0	0	0	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 23</i>	4	2	0	60	26	0	13	16	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 24</i>	2	1	0	31	50	2	10	9	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 25</i>	11	2	2	179	199	30	35	92	20
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 26</i>	14	1	3	67	86	0	25	41	11
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 27</i>	0	0	0	0	0	0	7	0	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 28</i>	35	143	17	0	3	5	43	104	51
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 29</i>	2	0	0	11	10	1	6	6	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 3</i>	516	111	109	187	9	143	239	15	65
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 30</i>	44	176	22	5	6	5	60	101	40
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 31</i>	2	11	0	1	1	0	5	2	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 32</i>	5	1	1	22	32	0	10	11	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 34</i>	0	1	0	1	5	0	0	6	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 35</i>	5	0	0	7	2	0	4	10	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 37</i>	1	0	0	0	0	0	4	3	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 4</i>	78	128	2	0	6	3	36	63	17
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 5</i>	0	0	0	2	0	0	0	0	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 6</i>	296	191	159	132	160	118	877	1252	626
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 7</i>	339	65	118	289	389	88	284	440	245
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 8</i>	159	40	0	13	52	0	51	80	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Burkholderiaceae bacterium 9</i>	2	340	1	0	1	1	0	18	6
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Chitinibacteraceae bacterium</i>	1	3	0	0	0	0	0	2	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Chitinimonas 2</i>	2	0	0	0	0	0	2	4	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Crenobacter</i>	0	0	0	0	0	0	1	8	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Gallionella</i>	4	1	1	157	445	0	117	537	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Sideroxydans</i>	23	0	1	52	73	0	31	87	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Gallionellaceae bacterium</i>	10	3	0	1	11	0	27	4	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Hydrogenophila ceae bacterium 1</i>	5	1	7	7	0	0	6	2	6
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Methylophilus</i>	13	0	3	1	1	0	2	2	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Methylothera</i>	9	0	0	0	0	0	2	1	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>OM43 clade bacterium</i>	59	1	0	8	21	0	1	4	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Neisseriaceae bacterium 12</i>	4	3	3	0	0	0	10	5	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Neisseriaceae bacterium 13</i>	0	3	0	1	0	0	2	11	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Neisseriaceae bacterium 2</i>	0	0	0	0	0	0	0	17	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Neisseriaceae bacterium 3</i>	3	0	1	0	0	0	1	16	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Neisseriaceae bacterium 4</i>	0	0	0	0	0	0	21	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Neisseriaceae bacterium 5</i>	2	5	3	0	1	0	3	15	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Neisseriaceae bacterium 6</i>	0	6	0	0	0	0	0	1	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ellin6067 bacterium 1</i>	0	0	3	1	0	1	1	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ellin6067 bacterium 2</i>	0	0	0	0	8	0	0	2	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ellin6067 bacterium 3</i>	0	0	4	0	1	1	0	2	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ellin6067 bacterium 4</i>	0	0	0	8	0	0	7	2	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ellin6067 bacterium 5</i>	3	0	52	30	9	16	60	87	40
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ellin6067 bacterium 6</i>	3	0	97	40	9	20	57	22	73
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ellin6067 bacterium 7</i>	3	0	360	39	8	41	106	62	284

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Ellin6067 bacterium 8</i>	12	0	306	52	27	185	258	147	503
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>IS-44 bacterium 1</i>	0	0	11	0	0	3	0	0	6
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>IS-44 bacterium 2</i>	4	0	129	50	31	38	95	25	70
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 bacterium 1</i>	0	0	0	3	8	0	1	2	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 bacterium 2</i>	1	0	2	3	19	0	2	0	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 bacterium 3</i>	2	0	0	2	7	0	11	8	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 bacterium 4</i>	2	0	1	8	2	0	5	15	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 bacterium 5</i>	0	0	19	0	0	19	4	5	21
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 bacterium 6</i>	0	0	0	19	63	0	5	4	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 bacterium 7</i>	0	0	3	23	21	2	22	31	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 bacterium 8</i>	13	0	77	18	52	24	37	16	29
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>MND1 bacterium 9</i>	21	0	14	36	97	9	55	20	22
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Nitrospira</i>	4	0	2	278	424	5	331	198	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Nitrosomonada ceae bacterium 1</i>	4	0	2	1	0	0	6	2	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Nitrosomonada ceae bacterium 3</i>	5	8	15	9	7	2	41	29	22
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Uliginosibacteri um</i>	11	0	1	2	0	0	1	2	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Rhodocyclaceae bacterium 1</i>	20	1	11	1	3	0	2	60	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Rhodocyclaceae bacterium 2</i>	2	11	6	4	2	1	17	6	16
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I- 84 bacterium 1</i>	1	0	3	0	0	4	0	1	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I- 84 bacterium 2</i>	1	0	5	5	0	8	0	1	12
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I- 84 bacterium 3</i>	0	0	19	24	3	3	31	2	11
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I- 84 bacterium 4</i>	5	0	14	35	10	10	23	25	41
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I- 84 bacterium 5</i>	2	1	79	55	25	60	65	74	115
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown SC-I- 84 bacterium 6</i>	3	0	18	12	0	9	3	0	9
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Feritrophicum</i>	5	15	5	0	0	3	1	0	15
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown TRA3-20 bacterium 1</i>	0	0	0	3	1	0	1	1	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown TRA3-20 bacterium 2</i>	18	3	47	42	39	22	118	105	69
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown TRA3-20 bacterium 3</i>	7	0	7	201	129	8	47	55	13
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown TRA3-20 bacterium 4</i>	0	0	8	4	2	0	0	3	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Betaproteobact eriales bacterium 1</i>	0	4	1	0	0	1	3	0	7

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Betaproteobacterales bacterium 10</i>	5	1	8	2	2	4	11	12	15
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Betaproteobacterales bacterium 2</i>	176	473	13	17	10	24	172	7	9
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Betaproteobacterales bacterium 3</i>	317	264	0	11	11	0	39	3	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Betaproteobacterales bacterium 4</i>	3	25	3	6	3	45	35	0	9
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Betaproteobacterales bacterium 5</i>	158	25	3	51	108	11	272	16	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Betaproteobacterales bacterium 6</i>	1	5	0	0	0	5	6	1	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Betaproteobacterales bacterium 7</i>	30	1	0	24	79	0	3	19	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Betaproteobacterales bacterium 9</i>	11	3	0	0	0	0	1	1	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown CCD25 bacterium</i>	0	0	0	1	0	0	4	4	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Cellvibrio</i>	35	13	3	4	4	0	2	15	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Coxiella 1</i>	2	14	1	2	6	6	8	0	7
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Aquicella 1</i>	0	8	1	0	0	0	0	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Diplorickettsia 2</i>	1	6	1	0	0	0	0	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Rickettsiella</i>	0	4	0	0	2	0	1	1	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Diplorickettsiaceae bacterium 14</i>	0	0	1	0	1	0	8	3	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Diplorickettsiaceae bacterium 15</i>	0	0	1	3	0	0	0	0	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Diplorickettsiaceae bacterium 2</i>	1	0	1	2	1	0	5	4	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Diplorickettsiaceae bacterium 3</i>	1	0	0	0	0	0	6	0	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Diplorickettsiaceae bacterium 4</i>	1	1	0	1	0	0	0	3	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Diplorickettsiaceae bacterium 5</i>	0	6	0	0	0	0	0	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Diplorickettsiaceae bacterium 6</i>	1	1	0	1	0	0	0	3	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Citrobacter</i>	18	0	1	0	14	0	0	5	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Enterobacter</i>	21	4	11	0	0	5	0	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Escherichia-Shigella</i>	7	2	2	0	0	1	0	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Serratia</i>	166	0	0	2	11	0	1	2	12

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Yersinia</i>	71	0	0	0	5	0	0	3	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 1</i>	7	55	37	1	5	4	5	41	41
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 10</i>	24	113	95	12	1	53	21	14	274
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 11</i>	0	38	1	0	0	14	3	2	77
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 12</i>	470	114	159	140	51	364	210	28	275
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 13</i>	30	24	85	16	14	65	60	17	144
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 14</i>	6	1	3	6	2	8	3	0	6
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 15</i>	209	287	189	53	83	127	203	0	109
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 16</i>	2	1	3	5	4	3	24	9	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 17</i>	164	458	213	29	11	216	120	1	229
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 18</i>	1	0	0	0	0	0	3	1	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 19</i>	6	28	9	3	0	9	5	3	161
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 2</i>	1529	272	354	418	49	332	580	4	157
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 20</i>	16	12	9	0	1	8	13	0	14
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 3</i>	28	72	60	3	1	17	68	2	148
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 4</i>	68	22	44	30	0	19	60	3	119
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 5</i>	106	42	223	34	33	107	97	40	348
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 6</i>	32	11	70	27	43	32	55	71	184
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 7</i>	35	16	16	0	0	33	10	0	52
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 8</i>	1	1	3	13	1	2	56	6	6
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acidibacter 9</i>	125	271	163	81	164	77	681	516	414
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Candidatus Berkiella 1</i>	0	4	0	0	1	0	0	41	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Candidatus Berkiella 2</i>	5	1	0	0	0	1	3	0	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Candidatus Berkiella 3</i>	1	1	0	4	0	1	0	0	6
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Candidatus Berkiella 4</i>	0	3	0	0	0	0	0	10	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Candidatus Berkiella 5</i>	0	1	1	1	0	1	2	7	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Candidatus Berkiella 6</i>	7	2	3	0	0	3	8	1	7
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Candidatus Berkiella 7</i>	0	4	1	0	0	0	0	0	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Candidatus Berkiella 8</i>	3	0	1	0	0	0	4	0	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Candidatus Berkiella 9</i>	3	3	0	0	0	1	6	4	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Candidatus Ovatusbacter 1</i>	6	0	2	1	0	1	16	28	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Candidatus Ovatusbacter 2</i>	1	17	1	4	3	1	10	7	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Candidatus Ovatusbacter 3</i>	0	1	0	1	1	1	3	4	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Candidatus Ovatusbacter 4</i>	2	3	0	0	0	0	3	3	1
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>uncultured bacterium</i>	0	4	1	0	0	0	3	1	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown JG36- TzT-191 bacterium1</i>	0	0	5	0	2	0	6	25	7
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown JG36- TzT-191 bacterium2</i>	8	21	7	0	1	1	9	13	13
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown JG36- TzT-191 bacterium3</i>	7	0	16	2	1	6	6	1	38
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown JG36- TzT-191 bacterium4</i>	33	59	32	10	7	6	34	3	72
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown JG36- TzT-191 bacterium5</i>	75	255	121	15	4	39	58	14	390
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown KF- JG30-C26 bacterium</i>	14	20	46	8	3	12	86	26	102
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Legionella</i>	0	1	1	0	4	0	1	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown PLTA13 bacterium</i>	8	0	0	0	0	1	0	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acinetobacter 1</i>	4	0	0	3	15	6	0	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Acinetobacter</i> 2	0	1	0	0	0	5	0	0	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Alkanindiges</i>	2	5	0	0	0	0	0	2	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	unknown <i>Moraxellaceae</i> bacterium 1	0	0	1	0	0	0	4	4	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pseudomonas</i> 1	0	0	0	0	0	9	0	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pseudomonas</i> 3	320	59	1	18	11	7	49	111	78
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pseudomonas</i> 4	10	1	3	0	0	4	0	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pseudomonas</i> 6	11	0	0	6	1	0	3	0	2
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	unknown R7C25 bacterium	1	0	0	6	0	1	4	3	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Nevskia</i>	51	43	6	96	272	2	206	361	7
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Polycyclovorans</i> 1	0	0	2	9	1	2	37	36	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Polycyclovorans</i> 2	0	0	3	7	1	0	2	12	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	unknown <i>Solimonadacea</i> e bacterium 1	0	0	0	1	13	0	1	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	unknown <i>Solimonadacea</i> e bacterium 2	125	23	0	11	247	0	97	689	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	unknown <i>Solimonadacea</i> e bacterium 3	1	0	0	24	97	0	35	28	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	unknown <i>Solimonadacea</i> e bacterium 4	7	6	5	2	0	8	4	3	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	unknown <i>Solimonadacea</i> e bacterium 5	2	0	0	5	20	0	3	2	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Steroidobacter</i> 1	0	0	0	0	0	1	1	1	10
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Steroidobacter</i> 2	1	0	3	2	2	0	0	3	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Steroidobacter</i> 4	2	2	2	2	0	1	7	5	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Steroidobacter</i> 5	1	0	3	0	0	0	2	0	11
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	unknown <i>Steroidobacteria</i> ceae bacterium 1	9	1	7	11	0	2	16	0	8
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	unknown <i>Steroidobacteria</i> ceae bacterium 2	2	0	3	0	0	13	1	0	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	unknown <i>Steroidobacteria</i> ceae bacterium 4	1	0	0	1	0	3	0	0	4
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	unknown WD260 bacterium 1	12	10	9	1	0	14	9	6	34
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	unknown WD260 bacterium 2	765	1384	1268	165	564	761	1158	1532	1798
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Dokdonella</i>	0	0	19	2	0	2	3	4	16
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Rhodanobacter</i> 1	34	3	81	17	13	39	47	26	211
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Rhodanobacter</i> 2	0	0	12	0	0	6	0	0	29
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	unknown <i>Rhodanobacter</i> aceae bacterium 2	1	0	0	1	0	0	0	4	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Rhodanobacteraceae bacterium 3</i>	309	878	95	141	841	18	754	932	85
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Arenimonas</i>	3	0	1	54	21	1	16	16	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Lysobacter</i>	4	1	11	2	0	2	1	0	7
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Stenotrophomonas 1</i>	1	0	2	2	0	2	0	3	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Stenotrophomonas 2</i>	2	3	0	0	0	0	2	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Xanthomonadaceae bacterium 1</i>	0	1	2	15	3	3	23	20	24
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Xanthomonadaceae bacterium 2</i>	2	0	5	2	0	3	6	0	6
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Xanthomonadaceae bacterium 3</i>	0	0	1	1	0	0	4	0	15
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Xanthomonadaceae bacterium 4</i>	0	0	1	0	0	0	7	1	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Xanthomonadaceae bacterium 5</i>	0	1	0	3	0	0	1	3	3
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Xanthomonadaceae bacterium 6</i>	1	0	0	2	0	0	3	1	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Xanthomonadaceae bacterium 7</i>	3	0	1	0	0	0	0	0	5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Gammaproteobacteria bacterium 1</i>	5	0	0	1	0	0	1	0	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Gammaproteobacteria bacterium 6</i>	1	0	1	2	0	0	4	8	0
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>unknown Gammaproteobacteria bacterium 7</i>	0	8	0	0	0	0	3	0	0
<i>Rokubacteria</i>	<i>NC10</i>	<i>unknown Rokubacteriales bacterium</i>	0	4	3	0	0	0	0	0	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Candidatus Udaeobacter 1</i>	110	91	123	1	18	7	14	6	48
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Candidatus Udaeobacter 2</i>	0	1	5	0	1	0	5	0	19
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Candidatus Udaeobacter 3</i>	1	0	7	0	0	0	2	0	1
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Candidatus Udaeobacter 4</i>	3	1	0	0	1	0	0	0	2
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Candidatus Udaeobacter 5</i>	0	1	6	0	1	0	0	0	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Candidatus Udaeobacter 6</i>	59	14	70	0	3	1	10	1	22
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacter 1</i>	18	35	3	0	13	0	18	66	33
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacter 10</i>	2	20	7	0	5	0	6	4	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacter 11</i>	9	7	1	0	0	0	2	1	6

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacter 12</i>	0	3	1	0	0	0	1	0	1
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacter 2</i>	5	3	3	0	10	0	9	15	5
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacter 3</i>	2	2	0	0	7	0	5	9	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacter 4</i>	0	0	1	0	5	0	6	5	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacter 5</i>	3	4	1	0	0	0	1	0	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacter 6</i>	4	0	0	1	2	0	2	1	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacter 7</i>	0	8	0	0	1	0	2	5	8
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Chthoniobacter 8</i>	0	0	1	1	1	0	1	1	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Terrimicrobiaceae bacterium</i>	1	6	0	0	0	0	8	19	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Candidatus Xiphinematobacter 1</i>	142	685	332	0	217	6	53	7	121
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Candidatus Xiphinematobacter 2</i>	16	53	36	0	28	1	8	4	37
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Candidatus Xiphinematobacter 3</i>	21	24	9	1	23	0	6	1	5
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Methylocidiphilaceae bacterium 1</i>	31	66	8	2	8	0	9	34	18
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Methylocidiphilaceae bacterium 2</i>	1	2	0	0	0	0	0	21	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Methylocidiphilaceae bacterium 3</i>	0	7	1	0	1	0	0	3	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Methylocidiphilaceae bacterium 4</i>	3	6	1	0	0	0	1	0	2
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Lacunisphaera 1</i>	10	1	4	0	2	0	13	10	7
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Lacunisphaera 2</i>	44	196	24	0	17	0	36	94	45
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Lacunisphaera 3</i>	13	11	9	0	6	0	2	8	17
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Opitutus 1</i>	24	3	8	0	4	0	7	27	10
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Opitutus 3</i>	5	1	0	0	0	0	4	1	10
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Opitutaceae bacterium 1</i>	15	85	9	0	3	0	4	9	23
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Opitutaceae bacterium 2</i>	0	55	0	0	0	0	1	0	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 bacterium 1</i>	0	0	0	0	0	2	1	0	6
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 bacterium 2</i>	0	0	5	0	0	1	0	0	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 bacterium 3</i>	0	0	2	0	0	4	1	0	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 bacterium 4</i>	6	0	1	0	0	0	4	0	1
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 bacterium 5</i>	1	0	3	0	0	3	5	0	8
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 bacterium 6</i>	5	0	15	0	0	4	0	0	7
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 bacterium 7</i>	0	0	13	0	0	11	3	2	25
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 bacterium 8</i>	79	10	71	21	4	30	123	16	72

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 bacterium 8</i>	79	10	71	21	4	30	123	16	72
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>ADurb.Bin063-1 bacterium 9</i>	176	21	120	27	0	120	102	5	135
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Pedosphaera 1</i>	3	11	0	0	0	0	1	0	6
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Pedosphaera 2</i>	5	19	7	0	2	5	13	8	9
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Pedosphaera 3</i>	12	60	23	10	13	7	97	212	26
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Pedosphaera 4</i>	146	119	154	38	64	31	183	96	103
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 10</i>	1	50	0	0	1	0	3	108	7
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 11</i>	18	26	7	0	3	0	23	87	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 12</i>	4	55	5	1	3	0	7	2	40
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 13</i>	2	0	23	0	2	12	39	3	21
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 14</i>	0	0	1	4	19	4	12	5	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 15</i>	1	1	11	4	3	7	12	5	13
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 16</i>	0	0	1	2	4	8	6	11	17
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 17</i>	16	7	1	3	0	3	11	0	1
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 18</i>	0	0	4	3	1	6	9	1	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 19</i>	0	0	6	5	2	2	2	0	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 2</i>	1	0	0	1	2	0	3	0	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 20</i>	7	17	1	0	0	1	6	0	5
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 22</i>	0	0	7	0	3	0	2	1	8
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 23</i>	0	0	8	0	1	0	0	0	1
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 24</i>	5	2	1	2	0	0	1	0	9
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 25</i>	5	4	10	0	0	0	2	0	10
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 29</i>	0	0	2	0	0	2	5	1	5

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 3</i>	515	568	223	85	154	127	863	646	374
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 30</i>	2	11	23	0	2	2	9	13	29
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 31</i>	0	0	9	0	0	5	1	0	10
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 32</i>	0	0	0	4	9	0	0	5	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 33</i>	0	0	3	0	0	5	1	0	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 35</i>	1	0	3	0	0	0	9	0	3
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 37</i>	2	14	2	0	0	0	3	1	6
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 38</i>	5	5	0	1	1	0	2	9	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 4</i>	77	348	92	13	21	37	209	200	230
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 40</i>	2	3	0	0	0	0	1	0	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 41</i>	5	0	7	0	1	0	0	0	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 42</i>	9	0	0	0	0	0	0	0	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 43</i>	1	4	2	4	4	2	36	24	11
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 44</i>	0	6	1	0	0	0	0	0	1
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 45</i>	11	9	5	3	4	3	9	5	12
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 5</i>	31	235	27	1	28	6	40	101	100
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 50</i>	1	0	0	1	20	1	0	1	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 55</i>	0	2	0	0	1	0	1	9	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 57</i>	22	156	25	1	2	8	15	7	56

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Phylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 59</i>	10	0	4	2	0	0	7	0	1
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 6</i>	127	90	79	27	13	21	129	3	68
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 60</i>	0	0	0	0	0	6	1	0	6
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 61</i>	0	10	0	0	0	0	1	11	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 63</i>	4	0	0	1	1	0	0	2	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 7</i>	4	142	12	33	79	6	37	48	23
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 8</i>	27	202	29	0	13	0	14	127	52
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Pedosphaeraceae bacterium 9</i>	22	0	7	36	82	10	50	29	17
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown S-BQ2-57 soil group bacterium 1</i>	6	0	0	0	0	0	0	0	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown S-BQ2-57 soil group bacterium 2</i>	2	0	0	0	0	0	0	2	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown S-BQ2-57 soil group bacterium 3</i>	29	14	6	1	0	1	2	0	10
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Prostheco bacter</i>	6	1	0	0	0	0	0	6	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Verrucomicrobi um 1</i>	5	1	0	0	1	0	0	6	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Verrucomicrobi um 2</i>	32	2	0	1	19	0	0	6	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>Verrucomicrobi um 3</i>	2	6	1	0	1	0	2	1	4
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Verrucomicrobiaceae bacterium 1</i>	2	0	0	0	3	0	1	2	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Verrucomicrobiaceae bacterium 3</i>	0	2	0	0	2	0	4	17	0
<i>Verrucomicrobia</i>	<i>Verrucomicrobiae</i>	<i>unknown Verrucomicrobiaceae bacterium 4</i>	2	7	0	0	6	0	1	8	2
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 1</i>	2	3	3	0	0	0	0	0	2
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 2</i>	3	2	2	0	0	0	0	0	7
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 3</i>	0	2	0	0	0	0	1	4	0
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 4</i>	1	0	2	0	0	0	2	0	2
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 5</i>	0	5	0	0	2	0	0	1	0
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 6</i>	3	1	4	0	0	0	1	0	0

Annex 17 (Continuation)

Taxonomic classification			5 months (March 2018)			12 months (October 2018)			18 months (April 2019)		
<i>Pylum</i>	<i>Class</i>	<i>Genus</i>	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt	Burnt	Half- burnt	Non- burnt
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 7</i>	1	3	1	0	3	0	2	0	0
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 8</i>	2	4	3	0	0	0	2	0	2
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 9</i>	3	2	2	0	1	0	2	0	7
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 10</i>	1	0	0	0	0	0	2	14	0
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 11</i>	6	4	0	0	4	0	2	0	4
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 12</i>	1	8	8	0	0	0	1	2	4
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 13</i>	10	4	3	1	4	0	2	0	1
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 14</i>	15	2	3	0	2	0	4	0	0
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 15</i>	2	3	14	0	0	0	9	2	2
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 16</i>	10	0	13	0	0	1	1	0	9
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 17</i>	0	12	6	0	6	0	0	11	1
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 18</i>	13	6	1	0	3	0	3	13	1
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 19</i>	11	15	12	0	2	1	2	3	5
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 20</i>	30	6	11	0	0	0	16	1	1
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 21</i>	4	2	1	1	0	0	39	18	0
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 22</i>	6	8	18	0	5	0	24	8	6
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 23</i>	47	34	29	2	1	3	22	0	8
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 24</i>	41	32	28	1	10	1	21	6	15
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 25</i>	52	16	43	0	13	1	71	12	21
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 26</i>	24	106	37	3	46	1	33	24	5
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 27</i>	74	198	101	1	36	4	52	8	50
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 28</i>	179	40	1	3	36	0	276	9	0
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 29</i>	0	1	6	0	0	0	9	0	0
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 30</i>	1	23	3	1	1	0	4	0	1
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 31</i>	5	9	18	0	5	0	2	4	2
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 32</i>	2	8	18	0	15	0	10	16	4
<i>WPS-2</i>	<i>unknown WPS-2</i>	<i>unknown WPS-2 bacterium 33</i>	9	39	13	1	32	0	61	70	15