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CONFERENCE PROCEEDINGS

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МОСКВА – 2018

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peatlands of the forest tundra zone. It also deals with distribution of microscopic fungi (namber and species diversity) within seasonally-thawing layers of peat soil in dependence of vegetation.

The study was carried out under the support of the project "Identification of general patterns of the peat soils formation and functioning in the Arctic and Subarctic sectors of the Northeast European Russia" (AAAA-A17–117122290011–5) and of the project No. 18–9–4–40 "Microbial communities in the cryogenic soils as the basis for stable functioning of the terrestrial ecosystems in the Arctic and Subarctic under the climate changes and anthropogenic influence".

PENICILLIA DIVERSITY FROM FOOD IDENTIFIED POLYPHASICALLY, INCLUDING MYCOTOXIN PRODUCTION

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Penicillium is of high importance in food contamination particularly from mycotoxin production. The fungus is diverse and ubiquitous although it can be controlled from "field to fork". Mycotoxins are fungal secondary metabolites that cause disease or death in people or domesticated animals when ingested, inhaled, and/or absorbed. Major mycotoxins associated with penicillia are: ochratoxin A (OTA) (*P. verrucosum* and *P. nordicum*), patulin (*P. expansum*), citrinin (*P. expansum*), cyclopazonic acid (*P. camemberti*), penicillic acid (*P. radicicola*) and secalonic acid D, F (*P. griseofulvum*). Penicillia identification is often subjective based on conventional morphological methods and more objective methods involving a polyphasic approach are recommended, which includes phenotypic, biochemical and genotypic approaches. Identification of *Penicillium* strains isolated from Tunisian apples, Chilean chillis (the traditional *Merkén*), and Italian cheeses, with their capacity to produce patulin or OTA where appropriate is presented herein.

For morphological characterisation, isolates were inoculated in triplicate on different media and temperature conditions: Czapek yeast autolysate (CYA) agar at 17°C, 25°C, 30°C and 37°C; malt extract agar (MEA), oatmeal agar (OAT), yeast extract sucrose agar (YES), glycerol nitrate agar (G25N) and creatine sucrose agar (CSN) at 25°C. After seven days, digital images of colonies were obtained and macro- and micro-morphological characters were examined under light optical microscopy and when appropriate scanning electron microscopy. Multilocus sequence analysis was performed through comparison of partial β -tubulin, calmodulin and ITS sequences available in GenBank. Specific primers for genes involved in the mycotoxin pathways were used for PCR amplification. Patulin and OTA were quantified using HPLC-DAD and HPLC-FLD (fluorescence detection) respectively

A novel species was isolated from Tunisian apples with the proposed name, *Penicillium tunisiense* from section *Ramosa*. It is not a patulin producer, since the compound found at the same retention time as patulin has a different UV spectrum and the *idh* gene test was negative, in contrast to the other dominant *P. expansum* isolates that were patulin producers. The new species could not rot apples when tested, implying it may have potential as a biocontrol agent in apple orchards. Ochratoxigenic strains of *P. verrucosum* were rarely isolated from chillis and never from cheese or apples. However, *P. crustosum* was abundantly isolated from chilli and cheese samples in which OTA was detected in the food samples. The isolates were characterised with genes involved in the OTA biosynthesis pathway which demonstrated that key genes were present. The chromatographic analysis indicated that isolates were able to produce OTA. This fungus is not conventionally considered an OTA producer and more work is being undertaken.

Overall, our findings demonstrated that mycotoxigenic *Penicillium* species are important contaminants of food about which more information is required. Special attention needs giving to *Penicillium* species that are not currently considered as important mycotoxin producers, which might produce them in different environmental or food manufacturing process conditions, such as high NaCl concentrations.

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ABUNDANCE AND DIVERSITY OF PROKARIOTIC COMMUNITIES IN SOILS OF OASISES IN EAST ANTARCTICA

Lyudmila Lysak¹, Vera Soina¹, Alina Kudinova¹, Elena Lapygina¹, Mayya Petrova² ¹Faculty of Soil Science, Lomonosov Moscow State University, 119991, Leninskie gory, 1–12, Moscow, Russia, +7 (495) 9392217, lvlysak@mail.ru ² Institute of Molecular Genetics RAS

Detailed soil investigations in Antarctica are concentrated mainly on soil genesis, development of relatively precise soil maps and molecular-genetic analysis of microbial components in such soils. Molecular-genetic methods showed the diversity of bacteria in Antarctic soils, but these results don't reveal biological activity, physiological status and stability of microbes in external environment. A combination of culture-depended and independent techniques was used to characterize bacteria community in earlier not investigated soils in East Antarctic Coast. The samples of soils and barren rock with endolithic soil-like bodies were taken from the inter-hill wet valleys area (oasisis) in East Antarctica). The bottoms of inter-hill valleys show maximum biota concentration and highest bioand soil diversity. Moss, lichen and algae ground covers are formed here, as well as algal-bacterial mats and microorganisms develop various soil profiles in sandy granitoid sediments. The main feature of these soils is that they are formed under the protection of a gravel pavement, or detritus. ХХХVII Конференция европейской организации коллекций культур: Материалы Т67 конференции. 13–15 сентября 2018 г., Москва / Европейская организация коллекций культур; ФИЦ «Фундаментальные основы биотехнологии» РАН; Институт биохимии и физиологии микроорганизмов им. Г. К. Скрябина РАН; Институт экологии и генетики микроорганизмов Уральского отделения РАН; ФИЦ «Институт цитологии и генетики» РАН; Межрегиональное микробиологическое общество: – Москва: МАКС Пресс, 2018. – 138 с.

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