



XVI

CONGRESS OF  
EUROPEAN MYCOLOGISTS

[www.xvicem.org](http://www.xvicem.org)

Halkidiki, Porto Carras • 19-23/9/2011

BOOK OF  
ABSTRACTS



Thessaloniki 2011

lead to the human mycotic diseases. A number of issues concerning the prophylaxis, diagnosis and therapy of the mycosis have not been well investigated. For the solution of these problems it is necessary to identify and investigate the fungal species composition, their ecology as well as to estimate the extent of their pathogenicity. The objective of the current study was to explore the above mentioned problems.

In Armenia and for the first time the species composition of the air-polluting micromycetes in houses, museums and hospitals was described. Dangerous myco-destructors which colonize walls, wallpapers and ceilings were identified. A large percentage of these fungi cause mycotic diseases of the ear-nose-throat (ENT). During the study 91 species of micromycetes which belong to 30 genera, 8 families, 6 orders, 3 classes (Zygomycetes, Coelomycetes, Hyphomycetes) were detected. Representatives of the *Mycelia sterilia* group were also isolated.

During this research, 406 patients were examined. In 70% of the cases mycotic infection of the ENT organs were detected. From the mycotic infected ENT organs, representative species of the following genera *Aspergillus*, *Penicillium*, *Alternaria*, *Monilia*, *Mucor*, *Rhinocladium*, *Rhizopus*, *Paecilomyces*, *Scopulariopsis*, *Verticillium* were isolated. These pathogens were widespread in the investigated buildings. Out of 39 isolated species, 35 were detected for the first time in Armenia. Most of these fungi lead to the otomycosis infections. The conditions which favour the infections and the clinical pattern of the infected patients were described. For the investigated micromycetes a conspectus was produced which includes all the details of taxonomic composition and the ways the pathogens can spread.

## **Thematic area: Insect – fungus associations**

### **FUNGAL DIVERSITY AMONG DIFFERENT ANNUAL GENERATIONS OF *PRAYS OLEAE***

**I. Oliveira<sup>1</sup>, J.A. Pereira<sup>1</sup>, A. Bento<sup>1</sup>, P. Baptista<sup>1</sup>, T. Lino-Neto<sup>2</sup>**

<sup>1</sup> *CIMO / School of Agriculture, Polytechnic Institute of Bragança, Campus de Santa Apolónia, Apartado 1172, 5301-854 Bragança, Portugal*

<sup>2</sup> *BioFIG / Centre for Biodiversity Functional and Integrative Genomics, University of Minho, Campus de Gualtar, 4710-057 Braga, Portugal*

E-mail: [tlneto@bio.uminho.pt](mailto:tlneto@bio.uminho.pt)

**Keywords:** insect-fungus association, olive tree, *Prays oleae*

Olives and olive oil production are important agricultural activities in Portugal. In the region of Trás-os-Montes, olive orchards are strongly affected by *Prays oleae* Bern., which is responsible for high losses in olive production, as much as 40% of the expected yield. This lepidopteran

presents three generations per year (phyllophagous, antophagous and carpophagous) that damage the olive tree in different organs (leaves, flowers and fruits, respectively). In an attempt to identify fungi that might cause the death of olive moths, larvae and pupae of the three annual generations were collected and surveyed for natural fungal infection. After their isolation, the fungal agents were molecularly identified by sequencing the amplified internal transcribed spacer (ITS) region of rDNA.

In the present work, the diversity of fungal species associated to *P. oleae*, in several olive orchards located in Trás-os-Montes region, is discussed. The diversity and abundance of fungal species differed among all three generations. Higher diversity was found in the carpophagous generation, followed by the antophagous and phyllophagous generations. The use of already adapted fungal species to control one of the major pests of olive groves will increase the success of a future biocontrol strategy. In this context, the identification of fungi associated to *P. oleae* from olive orchards provided a pool of potential biocontrol agents. In this work, *Beauveria bassiana* proved to be the most promising fungus to be used as a biocontrol agent against the olive moth, being strongly associated to the phyllophagous generation. Other fungal species presenting entomopathogenic, antagonistic and phytopathogenic characteristics were also found.

**Acknowledgments:** This work has been supported by FCT (PTDC/AGR-AAM/102600/2008).

#### FUNGAL BIOTA ASSOCIATED WITH PINE SHOOT BEETLE *TOMICUS PINIPERDA* IN FINLAND

**X. Silva**<sup>1</sup>, **E. Terhonen**<sup>1</sup>, **R. Kasanen**<sup>1</sup>, **K. Heliövaara**<sup>1</sup>, **R. Jalkanen**<sup>2</sup>  
and **F. Asiegbu**<sup>1</sup>

<sup>1</sup>*University of Helsinki, Department of Forest Sciences, P.O. Box 27,  
FI-00014 Helsinki, Finland,*

<sup>2</sup>*Finnish Forest Research Institute, Rovaniemi Research Unit,  
Eteläranta 55, FI- 96300 Rovaniemi, Finland  
E-mail: ximena.silvapacios@helsinki.fi*

**Keywords:** insect-fungus associations, *Tomicus piniperda*, insect, fungus, Finland, DNA analysis, *Ophiostoma*

Fungi associated with the Scots pine bark beetle *Tomicus piniperda* were studied. *T. piniperda* were collected from *Pinus sylvestris* in Northern (Rovaniemi) and Southern (Hyytiälä) Finland in June 2010.

Both endo- and epi- entomophagus fungi were isolated. The fungi were identified using a combination of morphological features and molecular data. The results reveal a great diversity of fungal species associated with *T. piniperda*, with a total of 3073 isolates representing 23 species isolated. The