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**

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**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.

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**Fungal Biota Associated with Pine Shoot Beetle**

*Tomicus piniperda* **in Finland**

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**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- entomophagous 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