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Although several major tree disease outbreaks in forests and plantations have been caused by pathogens that are also known as seed-borne, tree seeds are generally considered a low-risk pathway for introducing plant-pathogenic fungi, and their movement remains largely unregulated. However, our recent analysis of the international tree seed trade revealed that approximately 2.5 million kilograms of tree seeds are exchanged between countries each year. Due to climate change-driven seed shortages, we anticipate that the volume of international seed trade will increase in the future. This is particularly concerning because our recent molecular studies, which examined multiple tree species originating from several continents, demonstrated that tree seeds harbour diverse fungal communities, including known pathogens. Furthermore, these seed-associated fungal communities were primarily structured by the host species rather than environmental factors, indicating strong host specificity, likely due to confirmed frequent vertical transmission. These findings suggest a significant risk of pathogen introduction through seed trade, with a higher likelihood of establishment in new areas if suitable host species are present. Nonetheless, further research is needed to understand the impact of seed-borne fungi in new environments and to develop effective risk management strategies.

POSTER PRESENTATIONS

Emerging fungal pathogens associated with holm oak decline in Southern Italy. C. DEL GROSSO^{1,2}, D. PALMIERI¹, L. MARCHESE¹, L. MELISSANO³, G. LIMA¹. ¹Department of Agricultural, Environmental and Food Sciences, University of Molise, 86100 Campobasso, Italy. ²Institute for Sustainable Plant Protection, National Research Council (CNR), 70126 Bari, Italy. ³Department of Agriculture, Environment and Rural Development, Sustainable Management and Protection of Natural and Forest Resources, Apulia Region, 70100 Bari, Italy. E-MAIL: lima@unimol.it, carmine.delgrosso@cnr.it

Holm oak (*Quercus ilex* L.) forests, iconic elements of the Mediterranean landscape, are increasingly threatened by complex decline phenomena. Since 2016, extensive dieback symptoms, such as cankers, branch necrosis, and crown thinning, have been observed in holm oak stands across the Salento Peninsula (Southern Italy), raising concerns about forest resilience under cli-

mate change. This study aimed to identify fungal isolates associated with holm oak decline and assess their pathogenic potential. Several fungal species of the Botryosphaeriaceae family, as in particular *Diplodia corticola* (Dc), *Diplodia quercivora* (Dq), and *Neofusicoccum vitifusiforme* (Nv), were identified. Pathogenicity tests on artificially stressed and inoculated holm oak seedlings revealed that Dc and Dq induced severe subcortical and leaf margin necrosis, while Nv induced similar but milder symptoms, suggesting its behaviour as a weak pathogen. These findings confirm the important role of Botryosphaeriaceae in holm oak decline but report for the first time Dq and Nv as *Q. ilex* pathogens in Italy. These pathogens may act within a broader decline syndrome in which abiotic stress factors, particularly alternating periods of droughts, heavy rainfall and heat waves, severely compromise tree vitality, favouring opportunistic infections. Furthermore, recent reports identifying bacterial agents associated with Acute Oak Decline (AOD) in the same geographical area, highlight the need for integrated and multidisciplinary approaches to monitor and manage this complex forestry issue and to develop the most appropriate strategies to counteract holm oak decline in Mediterranean forests.

The findings presented are based on a study published in *Journal of Fungi*, DOI: <https://doi.org/10.3390/jof10010035>.

Plasticity responses of *Hymenoschyphus fraxineus* populations to thermal stress in the Italian peninsula. L. STAZIONE^{1*}, C. AGLIETTI^{1*}, A.L. PEPORI², F. PECORI², G. GRAHAM¹, L. GHELARDINI¹, A. SANTINI². ¹Department of Agricultural, Food, Environmental and Forest Sciences and Technologies (DAGRI), University of Florence, Piazzale delle Cascine 18, 50144 Florence, Italy. ²National Research Council (CNR), Institute for Sustainable Plant Protection, Via Madonna del Piano, 10, 50019 Sesto Fiorentino, Italy. E-MAIL: leoneldaniel.stazione@unifi.it. *Equal contribution

Global change is a complex trend affecting the spread and establishment of non-native species. Among these, the invasive fungal pathogen *Hymenoschyphus fraxineus* was reported as a challenge threatening natural ash (*Fraxinus* sp.) populations of the whole Europe. In Italy, *H. fraxineus* was recently reported on *Fraxinus excelsior* at the southward of the country, being able of colonizing mediterranean habitats previously considered far from the growth optimum of the species. There is a gap of knowledge about *H. fraxineus* adaptability and distribution in Italy, also due to the highly fragmented geo-

graphic presence of the host, especially in the south of the country. The aim of this work is to characterize populational adaptive traits of *H. fraxineus* along the Italian peninsula. Samples were collected from symptomatic *F. excelsior* along the distribution of ash populations and fungal strains were identified by sequencing of nuclear and mitochondrial loci. The phenotypic responses were studied to assess optimal range and thermal stress tolerance by testing the mycelial growth of each strain against heat and cold thermal treatments, as well as their virulence by inoculation into the host tissues. Preliminary results clarify the possibility of further spread of the pathogen in the Mediterranean area, contributing to the understanding of the distribution and potential adaptive responses of invasive fungal pathogens in the context of fluctuating temperatures. Results will be useful to build an effective prevention and forest management strategy, helping the conservation of ash biodiversity richness at the southern edge of the species' natural distribution.

This research was financially supported by European Union - Next- GenerationEU - National Recovery and Resilience Plan (NRRP) – MISSION 4 COMPONENT 2, INVESTIMENT N. 1.1, CALL PRIN 2022 PNRR D.D. 1409 14-09-2022 – SAVEASH CUP N.B53D23032110001.

Preliminary findings of ophiostomatoid fungi from bark beetle galleries of the Bakhmaro Resort Forest, Georgia. T. ABRAMISHVILI¹, D. GAGANIDZE¹, M. GIORBELIDZE¹, A. DADEGASVILI¹, N. KHARABADZE², M. BURJANADZE², J. FOIT³, K. TOMANKOVA⁴. ¹Department of Plant Pest Diagnostic, State Laboratory of Agriculture, Tbilisi, Georgia. ²Vasil Gulisashvili Institute of Forestry, Agricultural University of Georgia, Tbilisi, Georgia. ³Department of Forest protection and management of environmental, Mendel University, Brno, Czech Republic. ⁴Central Institute for Supervising and Testing in Agriculture, Olomouc, Czech Republic. E-MAIL: tea.abramishvili@sla.gov.ge

Bark beetles are dangerous pests of forest crops and vectors of pathogens causing phytopathogenic fungal diseases. They introduce the fungal spores with their body into the passages made in the plant, where they cover the vascular fiber cones and hinder the physiological processes. Finally, the plant withers. The aim of the study is to detect and identify bark beetles as vectors of phytopathogenic fungi and the fungi spread by them in the coniferous forests of the resort zone Bakhmaro of Guria region of Western Georgia. The bark beetles and fungi were identified by morphological and molecular

methods (sequencing the ITS 1 and ITS2 2 regions of the ribosomal RNA operon 5.8S gene). Seven bark beetle species were identified: *Ips typographus*, *Cryphalus* sp., *Cryphalus asperatus*, *Phytoptorus polygraphus*, *Phytokteines spinidens*, *Pityophthorus* sp., *Cryphalus piceae*. From these species and their galleries, 114 fungal isolates were isolated: *Leptographium* sp. Was 55.2%, *Ophiostoma piceae* and *Ophiostoma ainoae* were each 3.5%. *Graphilbum* sp. was 15%. *Trichoderma* sp. 18.4% and *Lecanicillium* sp. 4.3%. This research first recorded two species of *Ophiostoma*—*O. piceae* and *O. ainoae*, as well as representatives of *Leptographium* and *Graphilbum* genera on spruce, in galleries of bark beetles. These findings expand the known diversity of ophiostomatoid fungi in the Caucasus region and underscore the need for continued monitoring of vector-pathogen relationships in Georgian coniferous forests, especially under climate-induced stress conditions.

Emerging association between *Neofusicoccum parvum* and the invasive *Ailanthus altissima*: a first report from Italy. I. GIUBILEI, M.I. DRAIS, D. COS, A. MAZZAGLIA. Department of Agriculture and Forest Sciences, University of Tuscia, Viterbo, Italy. E-MAIL: irene.giubilei@unitus.it

Ailanthus altissima (Tree of Heaven) is among the most aggressive invasive plant species worldwide, capable of outcompeting native flora and altering ecosystem dynamics. In 2024, a widespread dieback phenomenon affecting *A. altissima* was observed in Rome province, Italy. Symptomatic trees exhibited canopy decline, wood discoloration, and necrotic lesions. Fungal isolates obtained from infected tissues were identified morphologically and molecularly as *Neofusicoccum parvum*, an aggressive pathogen within the Botryosphaeriaceae family. The identity of the fungus was confirmed through multilocus sequencing (ITS, *tefl-α*, *tub2*, and *LSU*), and its pathogenicity was validated via inoculation trials, which reproduced disease symptoms and fulfilled Koch's postulates. This represents the first report of *N. parvum* infecting *A. altissima* in Italy. The occurrence of this pathogen on an invasive host species raises intriguing questions about potential biocontrol implications. As *N. parvum* is known for its virulence on a broad range of woody plants, its natural emergence on *A. altissima* may offer novel avenues for controlling this difficult-to-eradicate species. These findings provide new insights into the pathogen's ecology and underscore the importance of monitoring emerging host-pathogen interactions, particularly in