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ABSTRACT BOOK

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Family taxonomic rank, as well as extensive radiations of species from groups previously known from a small number, or even single collections. Many of these showed preferences to habitats with little representation in global collections. Collectively, our study demonstrates how thorough ecological sampling, coupled with informatic analyses of environmental DNA can begin to fill gaps in this enigmatic tree of life.

520A Fungal diversity associated with grapevine trunk diseases in Northern Italy and development of a qPCR for the detection of Botryosphaeriaceae Greta Dardani^{1,2}, Tawanda E. Maguvu^{3,4}, Rosa J. Frias^{3,4}, Davide Spadaro^{1,2}, Florent P. Trouillas^{3,4}, Vladimiro Guarnaccia^{1,2} ¹Dept of Agricultural, Forest and Food Sciences, University of Torino, ²Agroinnova, University of Torino, ³Dept of Plant Pathology, University of California, ⁴Kearney Agricultural Research and Extension Center

Grapevine Trunk Diseases (GTDs), caused by different fungal pathogens, are major threats to wine grapes in Mediterranean countries, causing severe economic losses. The colonization of woody tissues by those pathogens can occur at the nursery, where plant material collected from mother plants may already be contaminated. Despite significant knowledge about GTDs etiology and epidemiology, no curative methods are yet available, and prevention remain the most effective strategy. Due to limited information on GTD related pathogens in Northern Italy, a survey was conducted during 2021-2022 to investigate fungal species diversity and distribution associated with symptomatic plants. Four species associated with Botryosphaeria dieback, including *Botryosphaeria dothidea*, *Diplodia mutila*, *Diplodia seriata* and *Neofusicoccum parvum*, were recovered at high frequency. Additional pathogens were also isolated, including *Eutypa lata*, *Fomitiporia mediterranea*, *Phaeoconiella chlamydospora*, *Paraconiothyrium brasiliense*, *Seimatosporium vitis-viniferae* and *Truncatella angustata*. The high frequency of Botryosphaeriaceae isolated from diseased grapevines suggests these pathogens are rising in Italy, as observed in other Mediterranean countries in recent years. A reliable diagnostic tool targeting Botryosphaeriaceae could be used to test propagation material, such as canes from mother vines, at the nursery, and to facilitate the production of healthy cuttings, thus limiting the spread of contaminated plant material. This tool could also be used to facilitate early diagnosis in the field and to help grape farmers to promptly adopt best management strategies. For these reasons, we developed a quantitative method for assessment and quantification of *N. parvum* and *B. dothidea*. A qPCR assay with SYBR Green method was developed to detect and quantify the infection levels of both pathogens directly from grapevine wood.

521A Fungal diversity in deep-sea sunken plant substrates Yuriko Nagano, Yoshiyuki Ishitani, Noriyuki Isobe, Ryota Nakajima, Shunichi Ishii, Hiroyuki Kashima, Hidetaka Nomaki JAMSTEC

Fungi are the main decomposers of plants on land, and it is also presumed that they play an important role in the decomposition of sunken plants in deep-sea environments. However, the diversity, distribution, and ecology of deep-sea fungi associated with sunken plant substrates are still largely unknown and only six species of obligate deep-sea fungi that form fruiting bodies on sunken woods have been reported to date.

In this study, 21 samples (19 deep-sea sunken plants, 1 deep-sea sunken seaweed, and 1 shallow water sunken plant) were collected from 5 different sites (shallow water depth: 5m, deep water depths: 720–5,707m) in the Western Pacific Ocean off Islands of Japan, to investigate the diversity and distribution of fungi related to deep-sea sunken plant substrates. Fungal amplicon analysis was performed on the samples by targeting the ITS rRNA gene region.

As a results, fungal fruiting bodies were observed on one of the sunken wood samples which was collected at a water depth of 5,707m, and morphological and phylogenetic analysis suggested this fungus as novel sp. closely related to *Oceanitis scuticella*, one of the obligate deep-sea fungi. No fungal ascomata was observed in other samples, but amplicon analysis detected sequences highly homologous to *O. scuticella* in 8 samples collected from different depths and locations. These results indicated that *O. scuticella* and its relatives commonly exists in sunken plant substrates in deep-sea environments. Furthermore, sequences with highly homologous to *Ceriosporopsis halima*, a cosmopolitan shallow marine fungus, were predominantly detected in the sample collected from the shallow water. Interestingly, sequences which showed homologous to *C. halima* but presumed to be a different species (approximately 86% homology) were detected in 4 samples from deep-sea environments. This suggests that a novel species closely related to *C. halima* inhabit in deep-sea environments.

Our results indicated that there are many undiscovered deep-sea fungi and some obligate deep-sea fungi, such as *O. scuticella*, are distributed in a wide range of water depths, from bathyal to abyssal zones. Further comprehensive investigations on their diversity, distribution, physiology and genomics will provide key insights into the adaptation, evolution and ecology of deep-sea fungi.