

Topic: Genetic and phenotypic heterogeneity in fungal populations

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Title: Phenotypic and genotypic diversity in *Ciborinia camelliae* Kohn isolates from Italy

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Abstract:

Ciborinia camelliae, causal agent of Camellia flower blight, belongs to Ascomycota, family Sclerotiniaceae.

The pathogen shows host and organ specificity infecting only flowers of camellias, causing a serious damage not only to the ornamental component of the plant, but interfering with the fruit development reducing thus the seed yield and oil production. Interestingly, ascospores of *Ciborinia* show an anti-feeding effect on collembola, suggesting its importance for the production of novel bioactive compounds.

From Japan the pathogen spread worldwide quickly and despite it has been reported in all camellia-cultivated areas few studies have been carried out from a mycological and population variability point of view.

Thirty strains from five Italian regions were characterized on four different culture media at six temperatures, describing their development daily up to 14 days. Based on these data 10 different morphotypes of *C. camelliae* were characterized. Multigene sequencing and universally primed PCR technique were used to assess genetic variability among *C. camelliae* isolates. The genotypic approach confirmed the phenotypic variability among the Italian strains compared to the results of other research groups. Further studies are therefore needed in this sector considering also the geographical distribution of the pathogen. Finally, exploiting fungal variability found in our samples may lead to the identification of strains able to produce high levels of bioactive molecules against insect pests or microorganisms.