

Exploring *Ciborinia camelliae* diversity

Marco Saracchi, Andrea Kunova, Cristina Pizzatti, Paolo Cortesi, Matias Pasquali

DeFENS - Department of Food, Environmental and Nutritional Sciences, University of Milan, Milan Italy

Corresponding author: matias.pasquali@gmail.com

Ciborinia camelliae Kohn is the causal agent of camellia flower blight on plants of the genus *Camellia*. The fungus belongs to the Ascomycota family of Sclerotiniaceae. It has been reported in Japan, North America, Europe, Asia and Oceania. It is an interesting fungus from the phytopathological perspective as it is able to specifically colonize camellia producing molecules with potential insecticidal properties. Fungal diversity of a collection of *Ciborinia camelliae* (n= 68), including Australasian and European strains was assessed. Multilocus sequence typing using rDNA internal transcribed spacer (ITS1,5.8S, ITS2), beta-tubulin (TUB), elongation factor (EF1), and Glyceraldehyde 3-phosphate dehydrogenase (GPDH) sequences was carried out to correctly define phylogenetic position of the isolates. Morpho-phenotypic analysis on four culture media at six different temperatures and UP-PCR polymorphism (primer combination n=6) allowed to assess the level of diversity within the species. MLST showed high uniformity among Italian and European isolates, but significant differences with respect to isolates from China and New Zealand. UP-PCR allowed to discriminate isolates from the same collection site without strong correlation with morphotypes. Further studies aimed at characterising worldwide population are warranted.