

Introducing Two Species of *Parastagonospora* (Phaeosphaeriaceae) on Grasses from Italy and Russia, Based on Morphology and Phylogeny

Authors : Ishani D. Goonasekara, Erio Camporesi, Timur Bulgakov, Rungtiwa Phookamsak, Kevin D. Hyde

Abstract : Phaeosphaeriaceae comprises a large number of species occurring mainly on grasses and cereal crops as endophytes, saprobes and especially pathogens. *Parastagonospora* is an important genus in Phaeosphaeriaceae that includes pathogens causing leaf and glume blotch on cereal crops. Currently, there are fifteen *Parastagonospora* species described, including both pathogens and saprobes. In this study, one sexual morph species and an asexual morph species, occurring as saprobes on members of Poaceae are introduced based on morphology and a combined molecular analysis of the LSU, SSU, ITS, and RPB2 gene sequence data. The sexual morph species *Parastagonospora elymi* was isolated from a Russian sample of *Elymus repens*, a grass commonly known as couch grass, and important for grazing animals, as a weed and used in traditional Austrian medicine. *P. elymi* is similar to the sexual morph of *P. avenae* in having cylindrical asci, bearing 8, overlapping biseriate, fusiform ascospores but can be distinguished by its subglobose to conical shaped, wider ascospores. In addition, no sheath was observed surrounding the ascospores. The asexual morph species was isolated from a specimen from Italy, on *Dactylis glomerata*, a commonly found grass distributed in temperate regions. It is introduced as *Parastagonospora macrouniseptata*, a coelomycete, and bears a close resemblance to *P. allouniseptata* and *P. uniseptata* in having globose to subglobose, pycnidial conidiomata and hyaline, cylindrical, 1-septate conidia. However, the new species could be distinguished in having much larger conidiomata. In the phylogenetic analysis which consisted of a maximum likelihood and Bayesian analysis *P. elymi* showed low bootstrap support, but well segregated from other strains within the *Parastagonospora* clade. *P. neoallouniseptata* formed a sister clade with *P. allouniseptata* with high statistical support.

Keywords : dothideomycetes, multi-gene analysis, Poaceae, saprobes, taxonomy

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