



Editorial – special issue

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Discovering and dealing with the unknown aspects of *Colletotrichum*

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Colletotrichum species have diverse life styles as pathogens, endophytes and saprobes, and have attracted great attention from mycologists and plant pathologists, since the introduction by Corda in 1831. This genus was also a main source of confusion among taxonomists due to the belief that species were host-specific. After several morphological revisions, a special issue on *Colletotrichum* published in Fungal Diversity in 2009 provided a background to series of studies that used molecular phylogeny, together with morphology, to resolve species. Recent polyphasic approaches have helped to define species in the genus, especially in resolving the species complexes. In 2012, a special issue of Studies in Mycology resolved species in three major species complexes and established a list of accepted species for this genus. Many other studies have also been conducted in resolving species complexes and identifying species on various hosts.

Although there have been great improvements in the taxonomy of *Colletotrichum*, at present there is no consensus as to which loci should be used to infer phylogeny. As morphological characters and ITS sequence data alone do not provide significant resolution for distinguishing closely related species, it has become important to use a secondary barcodes to identify *Colletotrichum* species.

The present issue of Mycosphere comprises of two mycosphere essays and seven papers on *Colletotrichum*, that represent current interest and future perspectives. In the first essay Jayawardena et al. (Paper 1) emphasises the importance of accurately naming *Colletotrichum* species. Sharma and Shenoy (Paper 2) discuss the methods prevalent in *Colletotrichum*

systematics and also provide suggestions towards developing a stable and reliable classification system. This paper also emphasises the need for a secondary barcodes to resolve *Colletotrichum* species. Huang et al. (Paper 3) assess the genetic diversity of the grape ripe rot pathogen *C. gloeosporioides* using SRAP markers. Hou et al. (Paper 4) describe two new holomorphic species of *Colletotrichum* from China and Japan. Whole genome re-sequencing of *C. gloeosporioides* was carried out by Huang et al. (Paper 5), which provides the first comprehensive transcriptomic resource available for this species. Jayawardena et al. (Paper 6) studied species associated with strawberry anthracnose in China, providing an update of the causal agents, and revealing a new species. The second essay by Jayawardena et al. (Paper 7) emphasises the importance of *Colletotrichum* species in biological control, as well as its uses in industrial applications. Lei et al. (Paper 8) studied the species causing grape ripe rot in southern China and provide reports of two new host records. In the final paper Jayawardena et al. (Paper 9) provide an updated list of species in *Colletotrichum* together with their habit, host and geographic distribution, phylogenetic position, their sexual morphs and industrial uses if applicable. It also suggests the genes and combination of genes that can be used for identification of the various species complexes.