EDITORIAL

Emerging and established diseases caused by fungi pose a serious threat to biodiversity as well as global food and fibre supply. Although there are several major groups of pathogens, the present volume focuses exclusively on plant pathogenic fungi. Presently more than 800 million people do not have adequate food, and at least 10 % of global food production is lost due to plant disease (Christou & Twyman 2004). Likewise, fungi also play a major role in tree disease, leading to significant loss in timber and pulp production (Wingfield *et al.* 2001).

As many different genera of phytopathogenic fungi play a role in plant disease, its impossible to treat all in a single issue of *Studies in Mycology*, and hence only a few can be dealt with here. One of these genera is *Bipolaris* (= *Cochliobolus*; *Pleosporaceae*), which has species that are commonly associated with leaf spots, leaf blights, root and foot rots, and other disease symptoms of high value field crops in the *Poaceae*, including rice, maize, wheat and sorghum. Their global distribution may result from the transfer of agricultural commodities including plants and seeds across geographical borders. Lack of ex-type or authenticated sequences in public databases is a drawback in the accurate molecular identification and detection of *Bipolaris* species, since the names are the key to accessing accumulated knowledge (see Manamgoda *et al.* 2014)

Species of *Colletotrichum* (= *Glomerella*; *Glomerellaceae*) are commonly associated with anthracnose diseases of crops in tropical and subtropical regions. This species-rich genus has a wide host range, and taxa on important crops such as clover, alfalfa, cowpea and lentil, are difficult if not impossible to identify based solely on morphological characters (see Damm *et al.* 2014). *Pestalotiopsis* species (= *Pestalosphaeria*; *Amphisphaeriaceae*) are commonly isolated as endophytes, but also include phytopathogens that cause a variety of post-harvest diseases, fruit rots and leaf spots, as well as other emerging diseases (see Maharachchikumbura *et al.* 2014). Similar to *Pestalotiopsis*, the genus *Alternaria* (= *Lewia; Pleosporaceae*) is also omnipresent, causing disease on a range of agriculturally important crops. The revision of the species of *Alternaria* associated with diseases of potato, tomato, sweet potato and onion, is therefore of huge economic importance (see Woudenberg *et al.* 2014).

Rice is currently the world's most widely consumed staple food. Rice blast (*Pyricularia oryzae*) results in losses of 10–30 % of this crop each year (Talbot 2003). Several *Pyricularia* pathogens (magnaporthe-like sexual morphs; *Pyriculariaceae*), and many newly introduced pyricularia-like genera also occur on other cereals, further affecting global yield of field crops. Species of *Nakataea* (= *Magnaporthe*) and *Gaeumannomyces* (harpophora-like asexual morphs), however, cluster in the *Magnaporthaceae* (see Klaubauf *et al.* 2014).

The genus *Ceratocystis sensu lato* (*Ceratocystidaceae*) includes serious plant pathogens, significant insect symbionts and agents of timber degradation that result in substantial economic losses. In recent years it has become very obvious that this genus incorporates a wide diversity of very different fungi. Results obtained by De Beer *et al.* (2014) made it possible to distinguish seven major groups for which generic names have been chosen and descriptions are either provided or emended. This major revision of the generic boundaries in *Ceratocystis s. lat.* will provide a stable platform to facilitate future research on this important group of fungi, including distantly related species aggregated under this name.

Given the breadth of scope of the current volume of *Studies in Mycology*, covering pathogens in a range of genera, including *Alternaria, Bipolaris, Ceratocystis, Colletotrichum, Pestalotiopsis* and *Pyricularia*, many which have members that are known to include endophytic phases in their life cycles, it is clear that they represent a major challenge to international trade in agricultural and forestry produce. Although it remains difficult, if not impossible, to combat or contain that which you cannot see or recognise, one of our aims was to define DNA barcodes that would reliably distinguish the taxa treated. Armed with this knowledge, it is our hope that agricultural and forest pathologists would be better equipped to recognise these pathogens, enabling them to come up with better disease control strategies, as well as more efficient mechanisms for pathogen detection.

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