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## Editorial

# *Botryosphaeriaceae*: Systematics, pathology, and genetics

The *Botryosphaeriaceae* are well-known as pathogens of woody plant hosts, although some genera also occur on non-woody plants of agricultural importance. These fungi cause a wide range of disease symptoms including stem and branch cankers as well as leaf, fruit, seed and root diseases (Slippers *et al.* – this issue). Several studies have shown that disease expression is usually associated with or triggered by stress to infected plants in which these fungi can survive in an asymptomatic condition for many years. The relationship of the *Botryosphaeriaceae* with stress is increasingly important against the background of global climate change where stressful conditions are imposing increasingly negative impacts on agriculture and forestry (Zlatković *et al.* 2016). Prior to the 1990's it was difficult to identify members of *Botryosphaeriaceae*, because many species share very similar morphologies and many also fail to sporulate in culture.

Fundamental breakthroughs that have allowed researchers to unravel the relationships of species in the *Botryosphaeriaceae* include the development of pine needle agar as medium to induce sporulation (Smith *et al.* 1996), typification and genetic characterisation of the type species, *Botryosphaeria dothidea*, which allowed researchers to distinguish other taxa in the complex (Slippers *et al.* 2004), and the recognition of different phylogenetic clades as genera in what was previously treated simply as '*Botryosphaeria*' (Crous *et al.* 2006). The latter study also provided the first example where fungal genera were described based on their phylogenetic relationships, and provided substantial impetus for the Amsterdam Declaration calling for 'one fungus one name' (Hawksworth *et al.* 2011); ultimately leading to the abandonment of the dual nomenclature for fungi and with significant implications for plant pathology (Wingfield *et al.* 2012).

This issue of *Fungal Biology* includes nine papers that address various aspects of the *Botryosphaeriaceae* including their identification, taxonomy, pathology and genetics. Based on a multigene analysis of 499 isolates, Yang *et al.* (this issue) recognised two new families; *Endomelanconiopsisaceae* (*Endomelanconiopsis*) and *Pseudofusicoccumaceae* (*Pseudofusicoccum*) and one new genus, *Oblongocollomyces*, while *Spencermartinsia* was reduced to synonymy under *Dothiorella*. In a review of the *Botryosphaeriales*, Slippers *et al.* (this issue) recognised nine families in the order, and 23 genera in the family *Botryosphaeriales,* with very few species of *Botryosphaeriaceae* appearing to be host specific. In addition to recommending a combination of different markers to define species boundaries in different genera, the potential impact of the 11 newly released genomes for the order is discussed.

Importantly, this issue includes studies providing evidence of hybrids in the *Botryosphaeriaceae*, with four hybrids of *Lasiodiplodia* being described by Cruywagen *et al.* (this issue), and one hybrid species of *Lasiodiplodia* being recognised by Rodrigues-Galvez *et al.* (this issue). This discovery is of fundamental importance to future studies seeking to name species in the *Botryosphaeriaceae,* and where very clear evidence needs to be provided that newly described taxa are not hybrids. Lopes *et al.* (this issue) explore the potential of mating type (MAT) gene sequences as phylogenetic markers for species delimitation in the genus *Neofusicoccum*. Results of that study show that MAT genes can discriminate between the species analysed, and that the resulting phylogenies are consistent with the results obtained applying more conventional multilocus phylogenetic studies.

An investigation of gummosis disease symptoms on *Anacardium* in Brazil, Netto *et al.* (this issue) led to the identification of ten species of *Botryosphaeriaceae*, including *Lasiodiplodia gravistriata* sp. nov. Mehl *et al.* (this issue) found that an ability to infect multiple hosts and to move among unrelated hosts facilitates the establishment and spread of species and genotypes of *Botryosphaeriaceae* to new areas. Osorio *et al.* (this issue) considered the occurrence of endophytic *Botryosphaeriaceae* along the entire distribution of mangroves in South Africa, reporting 14 species in the *Botryosphaeriaceae* residing in *Botryosphaeria*, *Diplodia*, *Lasiodiplodia*, and *Neofusicoccum* and including five new species. *Botryosphaeriaceae* spp. associated with dieback and canker disease of bay laurel (*Umbellularia californica*) in a northern California forests is investigated by Lawrence *et al.* (this issue). Results of that study revealed three species of which two, *B. dothidea* and *Neofusicoccum nonquaesitum* were able to cause disease, while a third species, *Dothiorella californica* sp. nov., did not induce any symptoms on inoculated healthy plants.

The papers in this volume cover a wide range of issues relating to the *Botryosphaeriaceae* and they include some important new discoveries. They highlight the fact that these fungi are common endophytes mainly in woody plants and that they have the ability to cause serious diseases particularly when plants are predisposed due to environmental stress. Clearly, there are many aspects of these fungi that remain poorly understood, such as for example, the discovery of hybrid species that illustrates how little we know about these fungi. There is a great need for studies on the *Botryosphaeriaceae* particularly those considering their biology. The availability of whole genome sequences and interrogation of these powerful data sets will contribute substantially to filling these gaps as recently illustrated by Marsberg *et al.* (2017), Massonnet *et al.* (2017), and others. Due to their endophytic nature, these fungi are clearly moving globally under the 'radar' of quarantine regulations (Wingfield *et al.* 2015; Crous et al. 2016; Burgess & Wingfield 2017) and they are likely to increase in importance as plant pathogens in the future. At the taxonomic level, we now have a solid phylogenetic backbone for the *Botryosphaeriaceae*. This will make it possible to rapidly identify genera and species, providing a foundation for the important biological studies and those of relevance to food and fibre biosecurity to be undertaken in a meaningful way.

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