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Changing the game: resolving systematic issues in key *Fusarium* species complexes

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The genus *Fusarium* represents a ubiquitous group of fungi found in most natural substrates as either pathogens or non-pathogens associated with other fungi, plants and animals including humans (Leslie & Summerell 2006, Aoki et al. 2014). These fungi are also well-known for their ability to produce a cocktail of secondary metabolites that include important mycotoxins that pose a significant health risk to animals, humans and plants (Marasas et al. 1985, Logrieco et al. 2002, O'Donnell et al. 2018). Therefore, it is not unusual for this genus to be rated among the top 10 most economically and scientifically important plant pathogenic genera (Dean et al. 2012). However, as a large number of *Fusarium* species complexes include numerous cryptic species, several taxonomic/classification systems, most not subject to the International Code of Nomenclature for algae, fungi, and plants (ICN; Thurland et al. 2018), have been applied, sometimes resulting in erroneous assumptions. Furthermore, the lack of living ex-type cultures for several important *Fusarium* species has been a serious stumbling block in providing Latin binomials for several economically important cryptic *Fusarium* species.

Recent developments in the taxonomy of *Fusarium* and allied genera resulted in improved phylogenetic backbones for many species complexes (Guarnaccia et al. 2018, Sandoval-Denis et al. 2018, Maryani et al. 2019a, Lombard et al. 2019b, Sandoval-Denis & Crous 2019). However, much effort is still needed to fully discern the complexity of such a diverse group of taxa. This dedicated volume accommodates five papers mainly focusing on providing taxonomic stability to two important *Fusarium* species complexes (*F. oxysporum* (FOSC) and *F. incarnatum-equiseti* (FIESC)), and the related genus *Neocosmospora*. The intention of this volume is to highlight the importance of nomenclatural type studies to provide a stable platform for phylogenetic research to allow for the naming of cryptic species.

Fusarium oxysporum is probably the most commonly encountered species of *Fusarium,* and ranked fifth in the top 10 list of plant pathogenic fungi (Dean et al. 2012). This soil-borne asexual fungus includes both pathogenic (plants and animals, including humans) and non-pathogenic strains that display a complex phylogenetic structure of cryptic species. In the paper by Lombard et al. (2019a), *F. oxysporum* s.str. is epitypified to allow for the formal naming of 15 of these cryptic taxa. In addition, the various subspecific classification systems used for the FOSC are discussed, highlighting their limitations.

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Panama disease, a devastating Fusarium wilt of both wild and cultivated banana, is associated with species in the FOSC (Maryani et al. 2019a), which have been well studied in recent years (Fourie et al. 2011, Ordonez et al. 2015). However, limited information is available on non-FOSC *Fusarium* species also isolated in association with pathogenic *Fusarium* species causing Panama disease of banana. An extensive survey of local banana varieties in Indonesia resulted in a collection of 20 non-FOSC that were shown to belong to the *F. fujikuroi* (FFSC), FIESC and *F. sambucinum* (FSSC) species complexes, including five novel species for which Koch's postulates were tested (Maryani et al. 2019b).

Members of the FIESC include saprobes, fungicolous species, secondary invaders and pathogens of animals, humans and plants (O'Donnell et al. 2009, 2012, Sandoval-Denis et al. 2018). Using multi-locus phylogenies and Genealogical Concordance Phylogenetic Species Recognition (GCPSR), over 30 phylogenetic species have been recognised in this complex (O'Donnell et al. 2009, 2012, Villani et al. 2016, Maryani et al. 2019b, Santos et al. 2019, Torbati et al. 2019) for which less than 10 phylogenetic species have been provided with Latin binomials. This problem relates to the lack of nomenclatural types for several *Fusarium* species in this complex. In a survey of more than 22 plant species collected in eight provinces of China a total of 77 isolates were found to include 14 species in the FIESC, which included nine novel species provided with Latin binomials (Wang et al. 2019). Following this, Xia et al. (2019) provided more taxonomic stability to the FIESC through the epitypification of *F. compactum*, *F. incarnatum* and *F. scirpi*, and neotypification of *F. camptoceras*. This allowed for naming of 20 newly resolved and previously known phylogenetic species in the FIESC that lacked formal descriptions.

The genus *Neocosmospora*, previously known as the *F. solani* species complex, is ubiquitous, including saprobes, insect symbiont species as well as plant endophytes and important pathogens (animals, humans and plants) (Guarnaccia et al. 2018, Sandoval-Denis et al. 2018, Sandoval-Denis & Crous 2019). This genus encompasses a poorly characterised species-rich diversity, only now becoming evident through modern phylogenetic studies. However, several species in this genus lack nomenclatural types, placing a serious constraint on providing Latin binomials to new as well as already recognised phylogenetic species. In the monograph of Sandoval-Denis et al. (2019), a large number of type specimens and representative cultures were examined by means of morphology and phylogenetic inference. Through epi-, neo- and lectotypification, 68 species are now accepted in *Neocosmospora*, which also includes 13 new combinations and 29 new species. A further 11 recognised phylogenetic species remain undescribed and 17 doubtful or excluded taxa are also briefly discussed.

Given the ubiquitous nature of *Fusarium*, and its importance as plant, human and animal pathogen, the incredibly high number of undescribed species that still exist in nature pose a serious threat for future food and fibre security. Furthermore, the high number of 'known' *Fusarium* species that are not tied to genetically well-characterised ex-type cultures is also a serious cause for concern. Papers in this volume provide an onset in addressing this issue, and clearly highlight the importance of nomenclatural type studies in resolving taxonomic difficulties surrounding important species complexes in the genera *Fusarium* and *Neocosmospora*. Making these types and associated DNA barcodes easily accessible through accessible public collections and databases is therefore of the utmost importance for future studies.

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