

ARE CRYPTIC SPECIES REAL?

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Since Darwin and Wallace introduced the concept on the evolution of species, scientists have been furiously debating what species are, and how to define them. This basic yet intriguing question has bothered us ever since, as communicating to fellow biologists about fungal species is the very cornerstone of mycology.

For the fungal species presently known, communication has largely been accomplished via Latin binomials linked to morphology in the absence of DNA barcodes (Hebert et al. 2013). In recent years mycologists have embraced the ribosomal ITS as official barcode region for Fungi (Schoch et al. 2012), and this locus is also mainly used in environmental pyrosequencing studies. Furthermore, DNA data can now also be used to describe sterile species in the absence or lack of distinct morphological structures. Recent developments such as the registration of names in MycoBank (Crous et al. 2004), and linking the phenotype to the genotype, have significantly changed the face of fungal systematics.

By employing the Consolidated Species Concept (Quaedvlieg et al. 2014), incorporating genealogical concordance, ecology and morphology, robust species recognition is now possible. Several

international initiatives have since built on these developments, such as the DNA barcoding of holdings of Biological Resource Centres, followed by the Genera of Fungi Project (Crous et al. 2014), aiming to recollect, and epitypify all type species of all genera. What these data have revealed, is that most genera are poly- and paraphyletic, and that morphological species normally encompass several genetic entities, which may be cryptic species. Examples being discussed address genera such as *Alternaria* (Woudenberg et al. 2013, 2014), *Cladosporium* (Bensch et al. 2012), *Colletotrichum* (Damm et al. 2012a, b), *Exserohilum*, *Ilyonectria* (Lombard et al. 2014), *Macrophomina* (Sarr et al. 2014), *Phyllosticta* (Wikee et al. 2013), *Ramularia* (Videira et al. 2015) and *Sporothrix* (Zhang et al. 2015). Once we provide a stable genetic backbone capturing our existing knowledge of the past 250 years, we will be able to accommodate novelties obtained via environmental sequencing platforms. Being able to communicate these species to other biologists in a clear manner that is DNA-based, will enable scientists to elucidate the importance, role and ecological interactions that these fungi have on our planet.

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