

The Necessity of Working with “Orphaned” Asexual Genera

Wijayawardene NN*

Center for Yunnan Plateau Biological Resources Protection and Utilization, Qujing Normal University, China

***Correspondence:** Nalin N. Wijayawardene, Center for Yunnan Plateau Biological Resources Protection and Utilization, Qujing Normal University, China

Received on 14 October 2019; Accepted on 27 October 2019; Published on 07 November 2019

Copyright © 2019 Wijayawardene NN. This is an open access article and is distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Editorial

The use of DNA sequences in fungal taxonomy commenced three decades ago [1] and has improved our understanding of fungal diversity immensely. Nowadays, fungal taxonomy is relying on an integrative approach combining morphological and molecular phylogenetic data [2–8]. Still, hundreds of asexual genera are currently treated as “orphaned” genera, meaning they do not have a formal placement in family or other higher ranks [9, 10]. Most of the genera that lack DNA sequences are listed as Ascomycota genera *incertae sedis*. Nevertheless, a large number of hyphomycetous genera and several coelomycetous genera are linked with Basidiomycota [9]. In other words, it is questionable to conclude that all genera lacking DNA sequences belong in Ascomycota genera *incertae sedis*.

Taxonomists mainly use DNA sequences to introduce new species and resolve species complexes, to establish generic boundaries and resolve polyphyletic genera, to provide familial placement, and to link asexual and sexual genera following the principle of one fungus–one name. When fungal strains are selected for phylogenetic analyses, taxonomists try to include ex-type strains. It is essential to include ex-type strains of the type species for the representation of genera. This is common practice among taxonomists who work on both asexual and sexual fungi. However, still, there are many genera that lack DNA sequences for their type species or existing strains are not ex-type strains (including ex-epitype, ex-neotype).

It is possible to place sexual fungi in current classification systems without DNA sequences using most prominent morphological features such as number of ascus layers, apicular chambers, ascospore characteristics, etc. However, in the case of asexual fungi, it is essential to have DNA sequences to place them in family level or higher rank. The reason for this is that asexual genera a) have little discriminative morphological features and b) they show considerable morphological plasticity. Some morphologically similar taxa could be phylogenetically distinct genera, e.g., *Hormotomyces* and *Stilbospora* *fide* [11, 12]; camarosporium-like taxa *fide* [13, 14]; *Pithomyces* and *Pseudopithomyces* *fide* [15].

Moving forward, it is important to revisit these “orphaned” asexual genera and study them with combined morphological and molecular analyses. Moreover, nomenclatural issues need to be addressed, because recent published data are scattered (e.g., a checklist for coelomycetes have not been published since Sutton) [16], and the one fungus–one name concept needs to be implemented [17]. It is important to make fresh collections of “orphaned” genera based on their originally reported hosts and compare morphology with the original protologue. Finally, the importance of studying fungi in tropical regions has been recognized as vital in the future of fungal taxonomy [18]. Hence, this type of studies will be helpful to continue one fungus–one name concept, which is one of the key stone areas in mycology in this era and also to clarify the global fungal species number.

References

1. White TJ, Bruns T, Lee S, et al. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis M, Gelfand D, Sninsky J, White T, eds. PCR Protocols: a guide to methods and applications. 1st ed. San Diego: Academic Press; 1990. p. 315-22.
2. Pringle A, Baker DM, Platt JL, et al. Cryptic speciation in the cosmopolitan and clonal human pathogenic fungus *Aspergillus fumigatus*. *Evolution*. 2005;59(9):1886-99.
3. Grünig CR, Duo A, Sieber TN, et al. Assignment of species rank to six reproductively isolated cryptic species of the *Phialocephala fortinii* s.l.-*Acephala applanata* species complex. *Mycologia*. 2008;100(1):47-67.
4. Stefani FO, Jones RH, May TW. Concordance of seven gene genealogies compared to phenotypic data reveals multiple cryptic species in Australian dermocyboid *Cortinarius* (Agaricales). *Mol Phylogenet Evol*. 2014;71:249-260.
5. Singh G, Dal Grande F, Divakar PK, et al. Coalescent-based species delimitation approach uncovers high cryptic diversity in the cosmopolitan lichen-forming fungal genus *Protoparmelia* (Lecanorales, Ascomycota). *PLoS One*. 2015;10(5):e0124625.
6. Li YM, Shivas RG, Cai L. Cryptic diversity in *Tranzscheliella* spp. (Ustilaginales) is driven by host switches. *Sci Rep*. 2017;7(1):43549.
7. Haelewaters D, Kesel AD, Pfister DH. Integrative taxonomy reveals hidden species within a common fungal parasite of ladybirds. *Sci Rep*. 2018;8(15966):1-16.
8. Accioly T, Sousa JO, Moreau PA, et al. Hidden fungal diversity from the Neotropics: *Geastrum hirsutum*, *G. schweinitzii* (Basidiomycota, Geastrales) and their allies. *PLoS One*. 2019;14(2): e0211388.
9. Wijayawardene NN, Hyde KD, Tibpromma S, et al. Towards incorporating asexual fungi in a natural classification: checklist and notes 2012–2016. *Mycosphere*. 2017;8(9):1457-1554.
10. Wijayawardene NN, Hyde KD, Lumbsch HT, et al. Outline of Ascomycota: 2017. *Fungal Diversity*. 2018;88(1),167-263.
11. Crous PW, Groenewald JZ, Lombard L, et al. *Homortomyces* gen. nov., a new dothidealean pycnidial fungus from the cradle of humankind. *IMA fungus*. 2012;3(2):109-15.
12. Wijayawardene NN, Hyde KD, Camporesi E, et al. *Homortomyces tamaricis* sp. nov. and convergent evolution of *Homortomyces* and *Stilbospora*. *Phytotaxa*. 2014;176(1):156-163.
13. Wijayawardene NN, Bhat DJ, Hyde KD, et al. *Camarosporium* sensu stricto in Pleosporinae, Pleosporales with two new species. *Phytotaxa*. 2014;183(1):16-26.
14. Wijayawardene NN, Hyde KD, Bhat DJ, et al. *Camarosporium*-like species are polyphyletic in Pleosporales; introducing *Paracamarosporium* and *Pseudocamarosporium* gen. nov. in Montagnulaceae. *Cryptogam Mycol*. 2014;35(2):177-98.
15. Ariyawansa HA, Hyde KD, Jayasiri SC, et al. Fungal diversity notes 111–252—taxonomic and phylogenetic contributions to fungal taxa. *Fungal Divers*. 2015;75(1):27-274.

16. Sutton BC. Nomenclature of generic names proposed for Coelomycetes. *Mycological Papers*. 1977;141:1-253.
17. International Code of Nomenclature for algae, fungi and plants (Melbourne Code) adopted by the Eighteenth International Botanical Congress Melbourne, Australia, July 2011.
18. Hawksworth DL, Lücking, R. Fungal diversity revisited: 2.2 to 3.8 million species. *Microbiol Spectr*. 2017;05(4):1-2.