

Outlineoffungi.org - Note 728 *Arthrodermataceae*

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Arthrodermataceae Locq. ex Currah

The dermatophytes, classified in a single family *Arthrodermataceae* (*Onygenales*), have been studied since the mid-19th century, when skin lesions were recognized for the first time to have a fungal etiology. Since then, phenotypic species recognition has been applied successfully for more than 150 years. However, conventional taxonomy appeared to match poorly with modern, experimental data ([Gräser et al. 2000](#)). Therefore, a new, molecular classification has been proposed (de Hoog et al. 2017). The phylogeny of *Arthrodermataceae* appeared to be remarkably stable, not only using ITS rDNA but also with other genes ([Rezaei-Matehkolaei et al. 2014](#); [Mirhendi et al. 2015](#); [Zhan et al. 2018](#)): the geophilic *Arthroderma* species are found at the base, and the anthropophilic species in *Trichophyton*, infecting the evolutionary most recent host, *Homo sapiens*, at the top.

Zhang et al. (2022) collected a massive amount of multilocus data, applying sequences of ITS, LSU, *tub2*, *tef3*, 60S L1 rDNA, mostly downloaded from GenBank. Multi-locus phylogenetic reconstruction, a distance-based analysis using SplitsTree, and ITS haplotype network were used to capture the diversity in *Arthrodermataceae*. Their results further confirm the basic structure of *Arthrodermataceae* with the distinction of nine genera (*Arthroderma*, *Ctenomyces*, *Epidermophyton*, *Guarromyces*, *Lophophyton*, *Microsporum*, *Nannizzia*, *Paraphyton*, *Trichophyton*). Most genera were highly supported in this novel multilocus analysis, but, as previously noted, *Arthroderma* species are highly diverse. In contrast, species of *Trichophyton* are highly similar, several being grouped together in species complexes. The taxonomic approach of Zhang et al. (2022) is dual: one phylogenetic criterion is bootstrap support, whereas illustrative haplotype networks use distance as an alternative parameter. These methods are effective at different levels of diversity. In their paper, the phylogenetic approach can be applied at family level, while haplotype networks maximally reach the genus level. Nevertheless, this combination of approaches generates more solid taxonomic conclusions than pure phylogeny. All data confirm the high diversity of the ancestral genus *Arthroderma*. Zhang et al. (2022) consider the genus as being polyphyletic, and distinguish three remotely related groups. In *Nannizzia*, a single species is considered too remote to belong to the same genus. Even *Trichophyton*, though showing differences at a much lower level of diversity, is suggested to be split up in three groups. The authors are to be congratulated for not having formalized these subdivisions, but their suggestions are likely to stimulate taxonomic rearrangements in the future.

Before the suggestions are followed, some inconsistencies in Zhang et al.'s proposal should be noted. The grouping of *Trichophyton* is based on bootstrap support of individualized clusters, while overall sequence diversity within the genus is low. In *Nannizzia*, the proposed separation of the single known strain of *N. polymorpha* is based purely on distance. The latter proposal might be impacted by sampling effects, as only a single strain of the maverick, *N. polymorpha* is known. It differs in 66 SNPs from its nearest neighbor, *N. corniculatum*. Knowing that the internal ITS variability of a better represented species as *N. fulva* is 33 bp, and assuming that *N. polymorpha* should have a similar degree of variance when properly sampled, a distance of 66 bp hardly justifies the erection of a separate genus. The position of the rare species is instable: earlier publications ([Dukik et al. 2020](#)) came to another conclusion with nearly the same data. When more strains become available allowing a better picture of intraspecific variability, the deviant character of *N. polymorpha* may disappear. In general, it is not recommended to introduce taxonomic changes on the basis of a single strain in a single research paper – which the authors luckily indeed did not do.

The situation with *Arthroderma* is ambiguous. It is known since decades that this genus is highly diverse. Zhang et al. (2022) found the genus to be polyphyletic. Although not explicitly mentioned, this was also noted by earlier authors (e.g. Ahmadi et al. 2016; Hainsworth et al. 2021). Zhang et al. (2022) distinguished at least three separate groups, with the suggestion that these could be genera. Is this a basis for novel taxonomy? The genus suffers even more from sampling effects than *Nannizzia*. Most species in *Arthroderma* are known from just a single strain or a pair of mating isolates. Several species seem to be associated with particular mammal hosts or vectors. Many habitats and regions such as the tropics have poorly been investigated. Quite in contrast to the overclassified genus *Trichophyton* (Gräser et al. 2008), and other onygenalean genera with continuous name changes (Kandemir et al. 2022), a large part of the extant diversity of *Arthroderma* is yet to be described. Reclassification on the basis of the currently available, relatively limited dataset would be premature.

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