

## Outlineoffungi.org - Note 1358 *Parahypoxylon*

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***Parahypoxylon*** M. Cedeño-Sanchez, E. Charria-Girón & M. Stadler

This genus was segregated from *Hypoxylon* by Cedeño-Sanchez et al. (2023), based on a combination of molecular phylogenetic and chemotaxonomic data to accommodate *H. papillatum*, a species that had already shown an aberrant position in the phylogeny by Wendt et al. (2018), where it appeared basal in the *Hypoxylaceae* clades in a phylogeny inferred from ITS, LSU, *rpb2* and *tub2* data. Its teleomorphic (stromata with KOH-extractable pigments; dark brown ellipsoid ascospores; discoid amyloid apical apparatus) and anamorphic (nodulisporium-like conidiophores) characters are the same as in most species of *Hypoxylon* and other genera in the family. Phylogenetically closest relative is *Durotheca*, which lacks apparent stromatal pigments that are extractable with KOH. The characteristic secondary metabolites of *Parahypoxylon* are yet unidentified azaphilones of the cohaerin type that are similar to those of the genus *Jackrogersella*. The genus contains two species, *P. papillatum* (which is almost exclusively found in temperate North America, and the African monotypic species, *P. ruwenzoriense*. Both of them form stromata on dead angiosperm wood, but are probably saprotrophic with an endophytic stage in their life cycle, as is usually the case with the members of this family. A peculiar feature of the ex-epitype strain was recently found in a study comparing the genomes of over 50 members of the *Hypoxylaceae*. Cedeño-Sanchez et al. (2024) found that the genome contains an extraordinary number of paralogs one of which turned out to be due to the presence of a pseudogene. Consequently, if the taxonomy of this and other fungi were allowed to be based on molecular data alone, the mycologists who believe in DNA-only taxonomy have created two different orders out of the data that are present in the same genome. The aforementioned study, as well as concurrent work by others (cf Bradshaw et al. 2023) showed that it is nonsense to base species segregation based on differences in the ITS or LSU regions because of the frequently occurring polymorphisms of the rDNA cistron. Sequencing of the same strain is therefore often not reproducible.

### References

- Bradshaw MJ, Aime MC, Rokas A, Maust A, Moparthi S et al. 2023. Extensive intragenomic variation in the internal transcribed spacer region of fungi. *Iscience* 26(8).
- Cedeño-Sanchez M, Charria-Girón E, Lambert C, Luangsa-ard JJ et al. 2023. Segregation of the genus *Parahypoxylon* (*Hypoxylaceae*, *Xylariales*) from *Hypoxylon* by a polyphasic taxonomic approach. *Mycology* 95, 131.
- Cedeño-Sanchez M, Cheng T, Lambert C, Kolarík M et al. 2024. Unraveling intragenomic polymorphisms in the high-quality genome of *Hypoxylaceae*: a comprehensive study of the rDNA cistron. *Mycological Progress* 23, 5.

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