

## Outlineoffungi.org - Note 220, [Hypomontagnella](#)

[Hypomontagnella](#) Sir, L. Wendt & C. Lamb.

The genus [Hypomontagnella](#) (*Hypoxylaceae*) had recently been segregated from [Hypoxylon](#) based on a multi-locus phylogeny ([Lambert et al. 2019](#)), and three strains of [Hypomontagnella](#) were recently included in the first phylogenomic study that was based on 3<sup>rd</sup> generation DNA sequencing techniques. On the one hand, analysis of these data revealed a substantial degree of intragenomic polymorphisms in the rDNA cistron (Stadler et al. 2020), revealing multiple paralogs of the ITS located in one and the same genome that only showed 90% homology to each other for *Hypomontagnella monticulosum*. On the other hand, analysis of the complete genomes resulted in the recognition of a new species derived from a marine sponge based on a phylogenomic analysis in comparison to its next related, terrestrial plant-associated counterpart ([Wibberg et al. 2021](#)). In-depth genomic comparison (revealing differences in over 700 strain-specific proteins) and morphological differences of the cultures were observed. Thus, *Hypomontagnella spongiphila* is the first fungal species that was recognized based on state of the art genomics technology, such as PACBIO and Oxford nanopore (M. Stadler).

### Reference

- Lambert C, Wendt L, Hladki A, Stadler M, Sir EB. 2019 – *Hypomontagnella* (*Hypoxylaceae*): a new genus segregated from *Hypoxylon* by a polyphasic taxonomic approach. *Mycological Progress* 18, 187–201. [Doi 10.1007/s11557-018-1452-z](https://doi.org/10.1007/s11557-018-1452-z)
- Wibberg D, Stadler M, Lambert C, Bunk B et al. 2021 – High quality genome sequences of thirteen *Hypoxylaceae* (*Ascomycota*) strengthen the phylogenetic family backbone and enable the discovery of new taxa. *Fungal Diversity* 106, 7–28. [Doi 10.1007/s13225-020-00447-5](https://doi.org/10.1007/s13225-020-00447-5)