

Outlineoffungi.org - Note 575 *Melanodevriesia*

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Melanodevriesia H.L. Si, W.Q. Cao & T. Bose

Chang et al. (2022) introduced *Melanodevriesia* within Xenodevriesiaceae with the type species *M. melanelixia* based on maximum likelihood analysis of the ITS-LSU nucleotide alignment. The monotypic genus was associated with medullary tissue of *Melanelixia subargentifera* (Parmeliaceae) as an endolichenic fungi in terrestrial habitats in Nei Mongol, China. It was described based on its two thallus morphologies, branched, septate, hyaline to brown, guttulate pseudohyphae in a yeast-like state and branched, septate, cylindrical, hyaline to pale brown hyphae and spherical to ovoid, monilioid chlamydospores in the mycelial state. *Melanodevriesia* is an endolichenic, oleaginous black yeast genus that may allow lichens to flourish in harsh environments (Crous et al. 2009; Gostinčar et al. 2012; Chang et al. 2022). Phylogenetically, *Melanodevriesia melanelixiae* was allied with *Xenodevriesia strelitziiicola*, isolated from a Strelitzia sp. (Strelitzianaceae) in South Africa and formed a sister group within the family Xenodevriesiaceae (Crous et al. 2009, 2019). The clustering demonstrated that the LSU gene was the only significant gene to delimit this family (Chang et al. 2022). However, *Melanodevriesia* can be distinguished by its yeast-like and mycelial morphologies and chlamydospores produced only in *Melanodevriesia* (Crous et al. 2019; Chang et al. 2022).

References

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