

Outlineoffungi.org - Note 1139 *Leptomelanconium*

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Leptomelanconium Petr.

Kowalski et al. (2018) provided ITS and LSU sequences for specimens authentic for the type species of *Leptomelanconium*, *L. allescheri* (= *L. asperulum*), a needle pathogen of *Pinus* spp. Previously, the only DNA sequence data available for the genus was *L. australiense* (= *Teratosphaeria australiensis*, *Teratosphaeriaceae*, *Mycosphaeriales*). The new sequence data placed the type species of *Leptomelanconium* in the unnamed monophyletic clade containing *Piceomphale bulgarioides*, sister and basal to *Sclerotiniaceae* plus *Rutstroemiaceae* in *Helotiales* (Kowalski et al. 2018, Johnston et al. 2019). This position has morphological support from the structure of the amyloid ring at the ascus apex, typical of the *Sclerotinia* type. With all *Leptomelanconium* spp. known only from their asexual states, the phylogenetic position of the other species requires confirmation with DNA sequences.

References

- Kowalski T, Boroń P, Bartnik C, Rossa R. 2018 – Morphological and molecular characterization of *Leptomelanconium allescheri* associated with necrotic lesions on *Pinus mugo* needles in the Polish Tatra Mountains. *Forest Pathology* 48(3), e12420. <https://doi.org/10.1111/efp.12420>
- Johnston PR, Quijada L, Smith CA, Baral HO et al. 2019 – A multigene phylogeny toward a new phylogenetic classification of *Leotiomyces*. *IMA Fungus* 10, 1. <https://doi.org/10.1186/s43008-019-0002-x>

Entry by

H.-O. Baral, Independent Researcher, Blaihofstr. 42, D-72074 Tübingen, Germany

P.R. Johnston, Manaaki Whenua – Landcare Research, Private Bag 92170, Auckland 1142, New Zealand

(Edited by **Vinodhini Thiyagaraja**, **Maryam Tavakol Noorabadi** & **Subodini N. Wijesinghe**)

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