Melnikomyces vietnamensis
**Melnikomyces** Crous & U. Braun, *gen. nov.*

*Etymology.* Named in honour of Dr Vadim Mel’nik, in recognition of his contribution to the systematics of ascomycetous fungi.

*Mycelium* consisting of brown, septate, branched, smooth, thick-walled hyphae. *Conidiophores* dimorphic. Type A conidiophores reduced to conidiogenous cells, terminal and intercalary; loci inconspicuous, truncate, 1.5–2 µm diam. *Conidia* globose to subglobose, occurring in short, branched chains, brown, smooth, guttulate, chlamydospore-like in appearance, disarticulating into solitary conidial propagules. Type B conidiophores subcylindrical, brown, smooth, erect, straight or once geniculate, reduced to conidiogenous cells, or long flexuous, multisepitate. *Conidigenous cells* subcylindrical to subclavate, mostly terminal but also intercalary, brown, smooth, developing a rachis with numerous denticle-like loci, 0.5 µm long. *Conidia* solitary, brown, verruculose, fusoid-ellipsoidal, medianly 1-septate, ends subobtuse, young conidia with visible basal marginal frill, 0.5 µm long, 7–9–10–(11) × (2.5–3)–(3.5) µm.

*Culture characteristics.* Colonies spreading, erumpent, with sparse to moderate aerial mycelium; surface folded with numerous mucus. On OA surface olivaceous-grey with wide brown border; reverseumber. On OA surface wing with copious amounts of mucus.

**Melnikomyces vietnamensis** Crous & U. Braun, *sp. nov.*

*Etymology.* Named after the country from where it was collected, Vietnam.

*Mycelium* consisting of brown, septate, branched, smooth, thick-walled hyphae. *Conidiophores* dimorphic. Type A conidiophores reduced to conidiogenous cells, terminal and intercalary; loci inconspicuous, truncate, 1.5–2 µm diam. *Conidia* globose to subglobose, occurring in short, branched chains, brown, smooth, guttulate, chlamydospore-like in appearance, 5–10 µm diam, disarticulating into solitary conidial propagules. Type B conidiophores subcylindrical, brown, smooth, erect, straight or once geniculate, reduced to conidiogenous cells, or long flexuous, multisepitate, 10–60 × 2.5–4 µm. *Conidiogenous cells* 5–15 × 2.5–4 µm, subcylindrical to subclavate, mostly terminal but also intercalary, brown, smooth, developing a rachis with numerous denticle-like loci, 1 µm long. *Conidia* solitary, brown, verruculose, fusoid-ellipsoidal, medianly 1-septate, ends subobtuse, young conidia with visible basal marginal frill, 0.5 µm long, (7–)9–10–(11) × (2.5–)3–(3.5) µm.

*Notes.*—The *Scolecobasidium* complex represents several genera. Seifert et al. (2011) commented on a humicola-like synasexual morph linked to some species, which would suggest that our taxon, with its dimorphic conidiophores, could be accommodated here. Unfortunately, *Scolecobasidium terreum* (type of *Scolecobasidium*) clusters distant to our fungus. Samerpitak et al. (2014) recently reviewed this complex, and introduced the genus *Verruconis* for thermophilic species (brain infections), while *Ochroconis* was seen as mesophilic, linked to infections in cold-blooded animals. Phylogenetically, *M. vietnamensis* is allied to *Scolecobasidium cateniphorum* (Chaeto-thyrales, incertae sedis). *Verruconis verruculosa* and *Scolecobasidiella avellanea* (type of *Scolecobasidiella*).

Two species are presently known in *Scolecobasidiella*, namely *S. avellanea* and *S. tropicalis*. However, the phylogenetic relationship of *Scolecobasidiella* to *Melnikomyces* is still somewhat distant. Morphologically, *Melnikomyces* fits the general characteristics of the genus, except that has a synasexual morph forming globose conidia, which has not been observed in any of the other two species.

**ITS.** Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Daetlyaria purpureella* (GenBank:EF059036; Identities = 538/624 (86 %), Gaps = 34/624 (5 %)), *Ochroconis humicola* (GenBank:AY265334; Identities = 525/629 (83 %), Gaps = 41/629 (6 %)) and *Scolecobasidium terreum* (GenBank:FJ832480; Identities = 294/330 (89 %), Gaps = 13/330 (3 %)).

**LSU.** Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Scolecobasidiella avellanea* (GenBank:EF204505; Identities = 796/830 (96 %), Gaps = 1/830 (0 %)), *Verruconis verruculosa* (GenBank:KF282668; Identities = 819/869 (94 %), Gaps = 5/869 (0 %)) and *Scolecobasidium cateniphorum* (GenBank:EU107309; Identities = 786/834 (94 %), Gaps = 8/834 (0 %)).