Fungal Planet 605 – 20 June 2017

**Myotisia** Kubátová, M. Kolařík & Hubka, gen. nov.

*Etymology.* Refers to the bat (*Myotis myotis*) on whose excrement the fungus was found.

*Classification.* — *Onygenaceae, Onygenales, Eurotiomyces.*

**Ascomata** gymnothecial, solitary or in clusters, whitish, spherical. **Peridium** consisting of a network of branched hyaline septate hyphae; surface peridial hyphae undulated or dichotomously branched, asperulate, 2.9–4.5 µm thick. **Asci** 8-spored, globose, 6–7 µm diam; **ascospores** 1-celled, globose, hyaline, whitish in mass, smooth-walled. **Conidial morph** malbranchea-like.

**Notes.** — CCF 5407 has an identical ITS sequence to that of CCF 5406. Based on ITS sequences, *M. cremea* is 99% (486/492) similar to strain UAMH 3124 (GenBank KF477240) isolated from a reptile during the study of Sigler et al. (2013); the similarity of the other sequences deposited in GenBank did not exceed 87%. The LSU rDNA sequence exhibited the highest similarity (95%) to various species of *Arthroderma, Microsporum* and *Onygena*. Sigler et al. (2013) investigated taxonomic position of the strain UAMH 3124 and classified it as an undetermined fungus at generic as well as species level, which belonged to the phylogenetic lineage of *Arachnotheca glomerata*. We used the LSU sequence dataset of onygenalean fungi published by Hirooka et al. (2016) to assess the phylogenetic position of *M. cremea* (data not shown). The fungus was resolved as a member of the family *Onygenaceae* and clustered with members of the ‘*Onygenaceae 3*’ clade together with *Arachnotheca glomerata* UAMH 3551 (NR_111884) with 94% sequence similarity (553/591). Morphologically, *Myotisia* can be easily distinguished from *Arachnotheca* by smooth-walled ascospores.

**Myotisia cremea** Kubátová, M. Kolařík & Hubka, sp. nov.

*Etymology.* Refers to the cream colour of ascomata and mycelium.

**Ascomata** gymnothecial, solitary or in clusters, whitish, spherical, 320–480 µm diam. **Peridium** consisting of a network of branched hyaline septate hyphae; surface peridial hyphae undulated or dichotomously branched, asperulate, 2.9–4.5 µm thick. **Asci** 8-spored, globose, 6–7 µm diam; **ascospores** 1-celled, globose, hyaline, whitish in mass, smooth-walled. **Conidial morph** malbranchea-like, *arthroconidia* verruculose, terminal arthroconidia obvoid to ellipsoidal, intercalary arthroconidia alternate, barrel-shaped to ellipsoidal, 3.5–6.5 x 2.5–3 µm.


**Notes.** — CCF 5407 has an identical ITS sequence to that of CCF 5406. Based on ITS sequences, *M. cremea* is 99% (486/492) similar to strain UAMH 3124 (GenBank KF477240) isolated from a reptile during the study of Sigler et al. (2013); the similarity of the other sequences deposited in GenBank did not exceed 87%. The LSU rDNA sequence exhibited the highest similarity (95%) to various species of *Arthroderma, Microsporum* and *Onygena*. Sigler et al. (2013) investigated taxonomic position of the strain UAMH 3124 and classified it as an undetermined fungus at generic as well as species level, which belonged to the phylogenetic lineage of *Arachnotheca glomerata*. We used the LSU sequence dataset of onygenalean fungi published by Hirooka et al. (2016) to assess the phylogenetic position of *M. cremea* (data not shown). The fungus was resolved as a member of the family *Onygenaceae* and clustered with members of the ‘*Onygenaceae 3*’ clade together with *Arachnotheca glomerata* UAMH 3551 (NR_111884) with 94% sequence similarity (553/591). Morphologically, *Myotisia* can be easily distinguished from *Arachnotheca* by smooth-walled ascospores.


**Colour illustrations.** Underground tunnel of Malá Amerika mine (Czech Republic) with cluster of *Myotis myotis* individuals; colonies on cornmeal agar after 2 mo at 25 °C; malbranchea-like asexual morph; *arthroconidia*; gymnothecial ascoma, peridial hyphae; ascospores. Scale bars = 20 µm, scale bar of ascospores = 2 µm.