

Aspergillus contaminans



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Aspergillus contaminans Hubka, Jurjević, S.W. Peterson & Lysková, *sp. nov.*

Etymology. *contaminans* (*con.ta'mi.nans*. L. adj.); contaminating, polluting, referring to the origin of the ex-type strain, which represented a clinical sample contaminant.

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

On MEA: *Stipes* pale brown with age becoming brown, smooth, occasionally finely roughened, (100–)250–600(–800) × 4–7(–8) µm; *conidial heads* radiate to columnar, pale brown to brown; biseriate; *vesicle* nearly globose or pyriform, (12–)15–24(–28) µm diam; *metulae* cylindrical, covering 1/2 to 2/3 (rarely all) of the vesicle, (3–)4–7(–8) × (2.5–)3–4(–5) µm; *phialides* ampulliform, (6–)7–9 × (2–)2.5–3(–3.5) µm; *conidia* globose to subglobose, occasionally ellipsoidal, rough-walled to spinose, green-brown in mass, 3–4(–4.5) µm diam including ornamentation (3.7 ± 0.2), spore body 2.3–3.5 µm diam (2.9 ± 0.2); *Hülle cells* subglobose, ovoid, elongated or irregularly shaped, frequently curved, 15–40(–52) × 8–18(–20) µm, L/W 1.1–3.8 (2.2 ± 0.7).

Culture characteristics — (in the dark, 25 °C after 7 d): Colonies on MEA 32–33 mm diam, sporulating area pale brown to olive-brown, good sporulation, mycelium white to pale yellow, floccose, centrally abundant aggregations of pale yellow Hülle cells, lightly overgrown with hyphae, exudate clear, no soluble pigments, reverse buff. Colonies on CYA 35–36 mm diam, sporulating area greyish brown, poor sporulation, inconspicuous, covered with white to very pale yellow mycelium, lightly floccose to nearly velutinous, radially and concentrically moderately deeply sulcate, pale yellow Hülle cell aggregations at the centre of the colony, exudate clear to pale yellow only at the centre of the colony, no soluble pigments, reverse buff yellow. Colonies on OA 31–32 mm diam, pale brown to brown, sporulation moderately good, mycelium white to pale, floccose, abundant aggregations of pale yellow Hülle cells covered with hyphae, exudate clear to pale brown, no soluble pigments, reverse pale brown. Colonies on PDA 30–31 mm diam, sporulation area pale buff to pale brown, very good sporulation at the centre of the colony, mycelium white to pale yellow, floccose, occasionally radially lightly sulcate, Hülle cells abundant, covered with a mat of hyphae, exudate clear to pale brown, no soluble pigments, reverse buff to pale yellow. Colonies on CY20S 30–31 mm diam, sporulating area brown, poor to good sporulation, mycelium white, floccose, no exudate, no soluble pigments, reverse pale to pale buff. Colonies on CREA growing more slowly compared with other media, 19–20 mm diam, poor sporulation, mycelium white, Hülle cells sparse, no production of acid compounds. No growth on MEA and CYA at 37 °C.

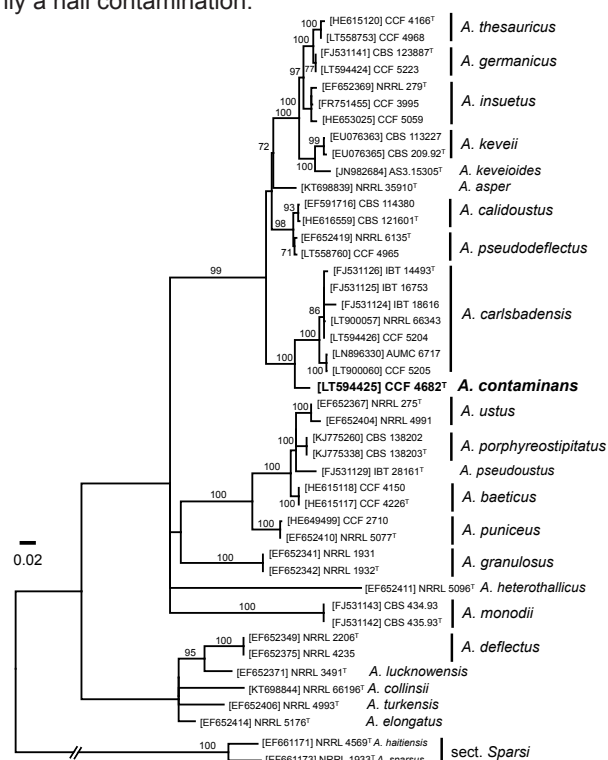
Typus. CZECH REPUBLIC, Prague, fingernail of 18-yr-old woman (contamination), 2012, isol. *P. Lysková* (holotype PRM 944503, isotype PRM 935097, culture ex-type CCF 4682 = CBS 142451 = NRRL 66666; ITS, LSU, β-tubulin, calmodulin and *rpb2* sequences GenBank LT594451, LT855552, LT594443, LT594425 and LT594434, MycoBank MB821684).

Colour illustrations. Laboratory of Medical Mycology, Prague, Czech Republic where *A. contaminans* was isolated; 7-d-old colonies of *A. contaminans* on MEA; conidia; conidiophores; Hülle cells. Scale bars = 10 µm.

Notes — BLAST analysis with the ITS, β-tubulin, calmodulin and *rpb2* sequences of *A. contaminans* with the reference sequences published by Samson et al. (2014) showed highest hits with *A. carlsbadensis*: ITS 99 %; β-tubulin 97 %; calmodulin 94 %; *rpb2* 97 %.

Aspergillus contaminans belongs to *Aspergillus* sect. *Usti* and is morphologically similar to *A. carlsbadensis*. The two species can be distinguished by growth at 30 °C where *A. contaminans*, after 7 d, attains 2–4 mm on MEA and 4–5 mm on CYA, while *A. carlsbadensis* attains 28–32 mm on MEA and 19–24 mm on CYA.

Aspergillus contaminans was isolated from a fingernail of a Czech patient with mycologically proven onychomycosis caused by the zoophilic dermatophyte *Trichophyton benhamiae*. It was apparently not a cause of onychomycosis but represented only a nail contamination.



A 50 % majority rule consensus maximum likelihood tree calculated from calmodulin sequences showing the relationships of taxa within *Aspergillus* sect. *Usti*. The partitioning scheme and substitution models for analysis were selected using Partition-Finder v. 1.1.1 (Lanfear et al. 2012). The HKY+I model was used for introns, TrN model for the 1st, F81 for the 2nd and HKY+I for the 3rd codon positions. The tree was constructed with IQ-TREE v. 1.4.0 (Nguyen et al. 2015). The dataset contained 45 taxa and a total of 805 characters of which 419 were variable and 360 parsimony-informative. Bootstrap support values at branches were obtained by generating 1000 bootstrap replicates. Only bootstrap support values ≥ 70 % are shown; ex-type strains are indicated by a superscript †. The tree is rooted with *A. sparsus* NRRL 1933† and *A. haitiensis* NRRL 4569†.