



Fungal Planet 1150 – 19 December 2020

Cyberlindnera dauci A.M. Glushakova, M.A. Tomashevskaya & Kachalkin, *sp. nov.*

Etymology. Name refers to *Daucus carota* from which the species was isolated.

Classification — *Wickerhamomycetaceae*, *Saccharomycetales*, *Saccharomycetes*.

On glucose peptone yeast extract agar (GPYA) and 5 % malt extract agar (MEA), after 7 d at 25 °C, streak is white-cream, butyrous, with a smooth surface and entire margin. Cells are subglobose, ovoid to elongate (2–5.5 × 2.5–6.5 µm) and occur singly or in pairs, dividing by multilateral budding. After growth on potato dextrose agar (PDA) cells have visible lipid-like body. *Ascospores*, *pseudohyphae* and *true hyphae* have not been observed during 4 wk at 10 and 25 °C in culture (pure cultures and in mating test) grown on GPYA, MEA, PDA, cornmeal agar (CMA), McClary acetate agar and yeast nitrogen base with 0.5 % glucose (YNB) agar. Fermentation of glucose, sucrose and raffinose are positive. Glucose, inulin, sucrose, raffinose, trehalose (delayed weak), cellobiose, salicin, L-rhamnose, D-xylose, ethanol, glycerol, D-mannitol (weak), D-glucitol, DL-lactic acid (weak), succinic acid, citric acid and arbutin are assimilated; no growth occurs on melibiose, galactose, lactose, maltose, melezitose, methyl alpha-D-glucoside, soluble starch, L-sorbose, L-arabinose, D-arabinose, D-ribose, methanol, erythritol, ribitol, galactitol, *myo*-inositol, D-glucosamine, N-acetyl-D-glucosamine, hexadecane, 2-keto-D-gluconate, 5-keto-D-gluconate and D-glucuronate. Assimilation of nitrogen compounds: positive for ammonium sulfate, cadaverine, creatinine, creatine, L-lysine, D-glucosamine, and negative for potassium nitrate. Growth on vitamin-free medium and on 50 % w/w glucose / yeast extract (0.5 %) agar is positive. Growth on MEA with 10 % NaCl is delayed weak. Growth with 0.01 % and 0.1 % cycloheximide is negative. Starch-like compounds are not produced. Diazonium blue B colour and urease reactions are negative. Maximum growth temperature is 27.5 °C.

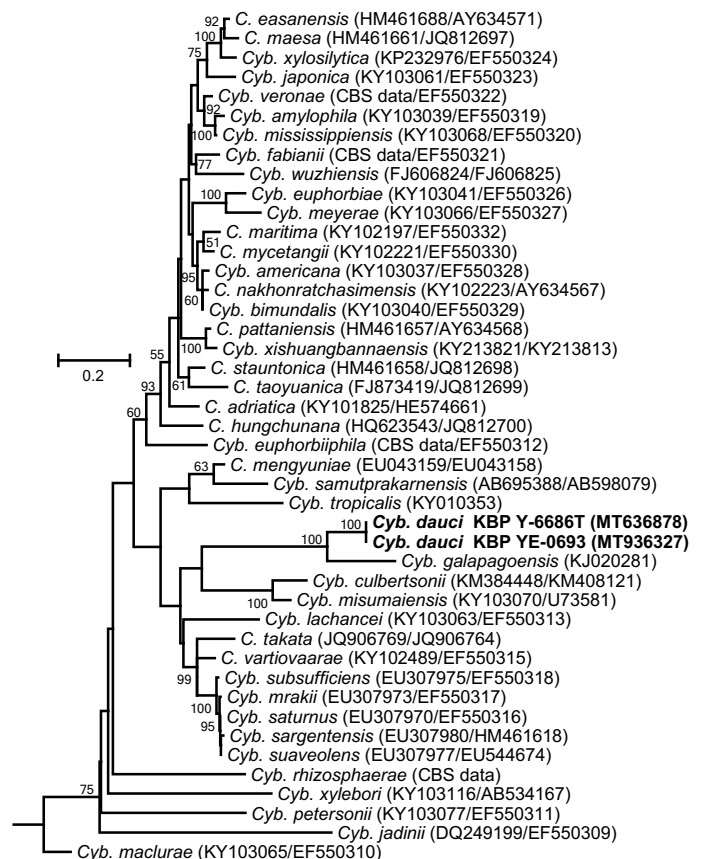
Typus. RUSSIA, Moscow region, from carrot sample bought on local market, Feb. 2020, A.M. Glushakova, fvmr-2 (holotype KBP Y-6686, preserved in a metabolically inactive state, ex-type cultures VKM Y-3058 = DSM 111207 = CBS 16524, SSU, ITS-D1/D2 domains of LSU nrDNA, *tef1* and *rpb1* sequences GenBank MT636884, MT636878, LR814018 and LR814019, MycoBank MB836776).

Additional material examined. RUSSIA, Moscow region, from carrot sample bought on local market, Feb. 2020, A.M. Glushakova, KBP YE-0693, ITS-D1/D2 domains of LSU nrDNA sequences GenBank MT936327 and MT939260.

Notes — Analysis of the ITS-D1/D2 regions of the surveyed asexual yeasts suggested that they were conspecific and represented a hitherto undescribed species of *Cyberlindnera*. Based on the NCBI GenBank nucleotide database, the best hit

Colour illustrations. Russia, Moscow region, carrots on local market (photo provided by Yu.A. Kachalkina). *Cyberlindnera dauci* KBP Y-6686: growth of yeast colonies on MEA, yeast cells on PDA and MEA (after 7 d at 25 °C). Scale bar = 5 µm.

using the ITS sequence is *Cyberlindnera galapagoensis* CBS 13997T (GenBank NR_159816; 86.56 % similar, 48 subst. and 29 gaps), using LSU it is *Cyb. galapagoensis* CBS 13997T (GenBank KJ020281; 96.98 % similar, 17 subst.), using SSU it is *Candida mengyuniae* CBS 10845T (GenBank EU043157; 96.28 % similar, 48 subst. and 14 gaps), using *tef1* it is *Cyb. mrakii* CBS 1707T (GenBank EU307984; 92.92 % similar, 26 subst. and 4 gaps) and using *rpb1* it is *Cyb. fabianii* YJS4271 (GenBank LK052886; 82.51 % similar, 109 subst. and 1 gap). In compliance with a recent phylogenetic analysis of the *Cyberlindnera* clade (Zheng et al. 2017), the placement of the new species is demonstrated using the combined ITS and LSU rDNA phylogeny. *Cyberlindnera dauci* can be physiologically differentiated from the phylogenetically most close species *Cyb. galapagoensis* based on its ability to assimilate trehalose, cellobiose, L-rhamnose and DL-lactic acid.



Maximum likelihood (ML) tree for the *Cyberlindnera* clade obtained from the combined analysis of ITS and LSU sequence data. The alignment included 1194 bp and was performed with MAFFT v. 7 (Katoh et al. 2019). The General Time Reversible model (GTR) with Gamma distribution and invariant sites (G+I) was used as the best nucleotide substitution model. The phylogenetic analysis was conducted in MEGA v. 6 (Tamura et al. 2013). *Pichia membranifaciens* NRRL Y-2026 (DQ104710/U75725) was used as outgroup (hidden).

Anna M. Glushakova, Lomonosov Moscow State University, 119234, Moscow, Leninskie Gory Str. 1/12, Russia, and Mechnikov Research Institute for Vaccines and Sera, 105064, Moscow, Maly Kazenniy by-street, 5A, Russia; e-mail: glushakova.anya@yandex.ru
 Maria A. Tomashevskaya, All-Russian Collection of Microorganisms, G.K. Skryabin Institute of Biochemistry and Physiology of Microorganisms RAS, 142290, Pushchino, pr. Nauki 5, Russia; e-mail: tomkotik@rambler.ru

Aleksey V. Kachalkin, Lomonosov Moscow State University, 119234, Moscow, Leninskie Gory Str. 1/12, Russia, and All-Russian Collection of Microorganisms, G.K. Skryabin Institute of Biochemistry and Physiology of Microorganisms RAS, 142290, Pushchino, pr. Nauki 5, Russia; e-mail: kachalkin_a@mail.ru