

Candida pellucida



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Candida pellucida A.M. Glushakova, M.A. Tomashevskaya & Kachalkin, *sp. nov.*

Etymology. The name refers to *Exomias pellucidus* from which the ex-type strain was isolated.

Classification — *Debaryomycetaceae*, *Saccharomycetales*, *Saccharomycetes*.

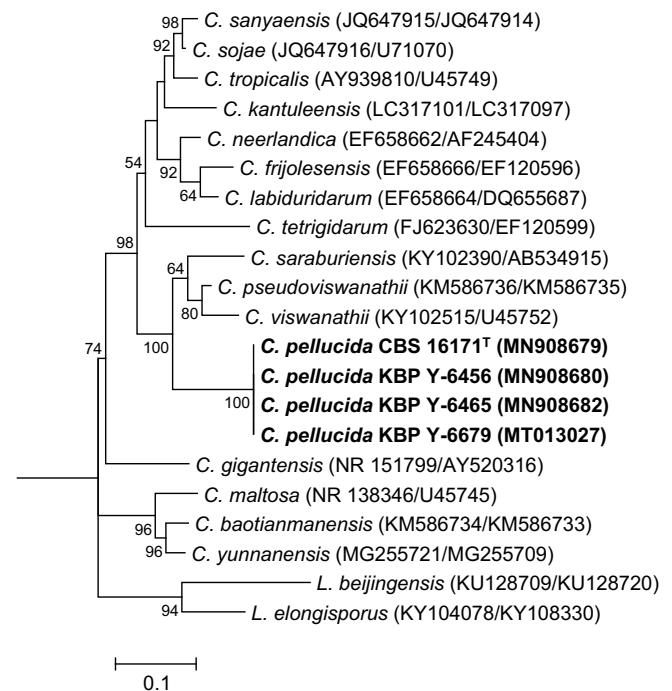
On glucose peptone yeast extract agar (GPYA) and 5 % malt extract agar (MEA), after 7 d at 25 °C, streak is white-cream, semi-glistening, with a smooth surface and entire margin. Cells are ovoid to elongate (2–6 × 5–8 µm) and occur singly or in pairs, dividing by polar and multilateral budding. Rare pseudohyphae are produced on potato dextrose agar (PDA) and cornmeal agar (CMA). *Ascospores* 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, CMA and yeast nitrogen base with 0.5 % glucose (YNB) agar. Fermentation of glucose, galactose (delayed weak), trehalose and maltose (delayed) are positive, but negative for sucrose, lactose and raffinose. Glucose, sucrose, galactose, maltose, cellobiose, trehalose, melezitose, methyl alpha-D-glucoside, D-xylose, L-arabinose, D-glucosamine, ethanol, glycerol (weak), ribitol, D-mannitol, D-glucitol, salicin (weak), DL-lactic acid (weak), succinic acid (weak), citric acid, 2-keto-D-gluconate, arbutin are assimilated; no growth occurs on lactose, melibiose, raffinose, soluble starch, inulin, D-arabinose, D-ribose, L-sorbose, L-rhamnose, galactitol, erythritol, *myo*-inositol, 5-keto-D-gluconate, D-glucuronate and methanol. Nitrogen compounds: ammonium sulfate, potassium nitrate (weak), creatinine, creatine, L-lysine, D-glucosamine (weak) are assimilated. Growth on vitamin-free medium, on MEA with 10 % NaCl and on 50 % w/w glucose / yeast extract (0.5 %) agar is positive. Growth with 0.01 % and 0.1 % cycloheximide is weak. Starch-like compounds are not produced. Gelatin liquefaction and casein hydrolysis tests are positive. Diazonium blue B colour and urease reactions are negative. Maximum growth temperature is 42–44 °C.

Typus. RUSSIA, Moscow, Park Tsaritsyno, from *Exomias pellucidus* (*Curculionidae*), Oct. 2018, A.M. Glushakova, Ins19-23 (holotype KBP Y-6457 preserved in a metabolically inactive state, ex-type culture VKM Y-3050 = DSM 110120 = CBS 16171; SSU, ITS-D1/D2 domains of LSU nrDNA, *TEF1* and *RPB1* sequences GenBank MN908677, MN908679, LR745525 and LR745526, MycoBank MB834513).

Additional materials examined. RUSSIA, Moscow, Park Tsaritsyno, from *E. pellucidus*, Oct. 2018, A.M. Glushakova, KBP Y-6456, KBP Y-6465 and KBP Y-6466; ITS-D1/D2 domains of LSU nrDNA sequences GenBank MN908680, MN908681 and MN908682; Moscow, as endophyte from almond seeds bought on local market, Oct. 2019, A.M. Glushakova, KBP Y-6679; ITS-D1/D2 domains of LSU nrDNA sequence GenBank MT013027.

Colour illustrations. Russia, Moscow, Park Tsaritsyno, meadows with herbaceous flowering plants (the habitat of *Exomias pellucidus*). *Candida pellucida* KBP Y-6457: growth of yeast colonies on MEA, yeast cells on MEA (after 7 d at 25 °C). Scale bar = 10 µm.

Notes — Analysis of the ITS-D1/D2 regions of the surveyed yeasts suggested that they were conspecific and represented a hitherto undescribed species of the *Candida/Lodderomyces* clade. Based on the NCBI GenBank nucleotide database, the best hits using the **ITS** sequence are *Candida viswanathii* CBS 7889 (GenBank KY102513; 90.24 % similar, 18 subst. and 23 gaps) and *Candida viswanathii* ATCC 22981T (GenBank NR_138345; 88.07 % similar, 24 subst. and 36 gaps), using **LSU** it is *Candida viswanathii* CBS 4024T (GenBank KY106885; 98.20 % similar, 9 subst.), using **SSU** it is *Candida labiduridarum* NRRL Y-27940T (GenBank NG_063271; 99.88 % similar, 2 subst.), using **TEF1** it is *Candida dubliniensis* CD36T (GenBank XM_002417390; 95.67 % similar, 19 subst.) and using **RPB1** it is *Candida viswanathii* CBS 4024T (GenBank AY497714; 88.83 % similar, 66 subst.). In compliance with a recent phylogenetic analysis of the genus (Zhai et al. 2019), the placement of the new species is demonstrated using the combined ITS and LSU rDNA phylogeny. *Candida pellucida* can be differentiated from the phylogenetically most close species *C. viswanathii* based on its ability to grow on vitamin-free medium, good growth at the temperature 42 °C, and negative growth on soluble starch.



Maximum likelihood (ML) tree obtained from the combined analysis of ITS and LSU sequence data. Bootstrap support values above 50 % are shown at the nodes. The alignment included 965 bp and was performed with MAFFT v. 7 (Kato et al. 2019). The General Time Reversible model (GTR) with Gamma distribution and invariant sites (G+) was used as the best nucleotide substitution model. The phylogenetic analysis was conducted in MEGA v. 6 (Tamura et al. 2013). *Saccharomyces cerevisiae* (AB018043/JQ689017) was used as outgroup (hidden).

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