

Candida xylosifermentans sp. nov., a D-xylose-fermenting yeast species isolated in Thailand

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Abstract

Three strains, representing a novel anamorphic and D-xylose-fermenting yeast species, were isolated from moss (ST-302^T), seawater (ST-1169) and peat (DMKU-XE12) collected from the southern part of Thailand. The three strains had identical sequences of the D1/D2 regions of the large subunit (LSU) rRNA gene and the internal transcribed spacer (ITS) regions. *Candida floscolorum* CBS 10566^T and *Candida sharkiensis* CBS 11368^T were the most closely related species with 7.9% nucleotide substitutions in the D1/D2 regions of the LSU rRNA gene, and 10.3 and 12.6% nucleotide substitutions in the ITS regions, respectively. Phylogenetic analysis based on the concatenated sequences of the ITS and the D1/D2 regions confirmed that the three strains represented a distinct anamorphic species in the *Clavispora* clade. Therefore, the three strains were described as a novel species, for which we propose the name *Candida xylosifermentans* sp. nov.

According to Daniel *et al.* [1] the *Clavispora* clade consists of 40 *Candida* species, including *Clavispora aechmeae*, *Clavispora akabanensis*, *Clavispora asparagi*, *Clavispora blattae*, *Clavispora dosseyi*, *Clavispora haemulonii*, *Clavispora heveicola*, *Clavispora oregonensis*, *Clavispora ruelliae* and *Clavispora sharkiensis*. In 2016, *Candida vulturna* in this clade was proposed based on strains isolated from flowers and clinical samples [2]. Moreover, the other *Candida* species of this group were isolated from various habitats including plants, soil, insects, fish, fresh water, miso fermentation and clinical samples [1, 3, 4]. Some *Candida* species in this clade were found to assimilate D-xylose, but information on the ability of these species to ferment D-xylose, which is the second-most abundantly found sugar in plant cell-wall carbohydrates [3], is limited. The ability of yeasts to ferment D-xylose is of interest as it can be applied to bioethanol production from lignocellulosic biomass [5, 6]. D-Xylose-fermenting yeasts have been found in xylose-rich habitats, such as in wood-ingesting insects, which host species such as *Candida insectorum*, *Candida jeffriesii*, *Scheffersomyces segobiensis*, *Scheffersomyces parashehatae*, *Scheffersomyces stipitis* and *Spathaspora passalidarum* [3, 7–12], in insect frass from

which *Cyberlindnera xylosilytica* and *Issatchenkia hanoiensis* were isolated [13, 14] and in rotting wood, in which species such as *Candida ligosa*, *Candida tropicalis*, *Scheffersomyces stipitis* and *Scheffersomyces queirozia* [3, 15–18] have been found. D-Xylose-fermenting yeasts have also been isolated from sources less rich in xylose such as various fruits (*Candida famata* and *Candida guilliermondii*) [19, 20], mushrooms (*Scheffersomyces shehatae*) [21] and sugarcane juice (*Meyerozyma guilliermondii*) [22].

In the present study, three D-xylose-fermenting yeast strains, ST-302^T, ST-1169 and DMKU-XE12, which were respectively isolated from moss, seawater and peat, were found to represent a novel *Candida* species in the *Clavispora* clade based on the sequence analysis of the D1/D2 regions of the large subunit (LSU) rRNA gene and the internal transcribed spacer (ITS) regions. *Candida xylosifermentans* sp. nov. is proposed to accommodate these three strains.

YEAST ISOLATION

Strain ST-302^T was isolated from moss collected on 12 May 2001 from Leam Ta Chi, Yaring district, Pattani province,

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Keywords: *Candida xylosifermentans* sp. nov.; new yeast species; xylose fermenting yeast; Thailand.

Abbreviations: ITS, internal transcribed spacer; LSU, large subunit; PDA, potato dextrose agar; YCBY, yeast carbon base agar supplemented with 0.01% yeast extract; YM, yeast extract–malt extract; YNB, yeast nitrogen base; YP, yeast–peptone.

The GenBank/EMBL/DBJ accession numbers for the sequences of the D1/D2 regions of the LSU rRNA gene of strains ST-302^T, ST-1169 and DMKU-XE12 are AB525240, AB525241 and LC317098, and of the ITS regions are LC440109, LC440110 and LC317102, respectively. The MycoBank number for *Candida xylosifermentans* sp. nov. is MB829899.