**Naumovozyma baii** sp. nov., an ascomycetous yeast species isolated from rotten wood in a tropical forest

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Two strains isolated from rotten wood were included in the *Saccharomyces* group based on morphological characteristics. However, rRNA gene sequence analyses (including the 18S rRNA gene, 26S rRNA gene D1/D2 domain and internal transcribed spacer region) indicated that these two strains represent a novel species of *Naumovozyma*, for which the name *Naumovozyma baii* sp. nov. is proposed (type strain: BW 22T = CGMCC 2.04520T = CBS 12642T). The MycoBank number of the new species is MB800484.

Based on a multigene phylogenetic analysis of the Saccharomycetaceae (Kurtzman & Robnett, 2003), the genus *Naumovia* Kurtzman (2003) was described to accommodate two yeast species previously classified in *Saccharomyces sensu lato*. The generic name *Naumovozyma* was proposed to replace *Naumovia* because the latter is a younger homonym of *Naumovia* Dobrozh (1928) (Dothideomycetes), and is therefore illegitimate (Kurtzman, 2008). *Naumovozyma* is closely related to the genera *Saccharomyces* and *Kazachstania* and, at the time of writing, comprised only two species: *Naumovozyma castellii* and *Naumovozyma dairenensis* (Vaughan-Martini et al., 2011).

During our survey on the ecological distribution of *Saccharomyces* species in nature performed in recent years, two strains representing a novel species of *Naumovozyma* were identified by sequence analyses of the 18S rRNA gene, 26S rRNA gene D1/D2 domain and internal transcribed spacer (ITS) region, for which the name *Naumovozyma baii* sp. nov. was proposed.

Strains BW 21 and BW 22T were isolated from two rotten wood samples collected in the Bawangling National Nature Reserve (coordinates: 18°50′–19°05′ N 109°05′–109°25′ E), Hainan Province, southern China, in July 2007 by using the enrichment method. The enrichment medium contained (w/v) 1 % yeast extract, 1 % peptone, 1 % glucose, 8 % (v/v) ethanol and 200 μg chloramphenicol ml⁻¹. The morphological, physiological and biochemical characteristics were examined by standard methods described by Kurtzman et al. (2011). Nuclear DNA was extracted using the method of Wang & Bai (2008). The ITS region and 26S rRNA gene D1/D2 domain sequences were determined using the methods described by Bai et al. (2002). PCR for amplification of the 18S rRNA gene and cycle sequencing using PCR products were performed as described by Wang et al. (2003). The BLAST search program (Altschul et al., 1990) was used to compare the sequences generated in this study and those of other yeasts in GenBank. Sequence alignments were done using the CLUSTAL_W program (Thompson et al., 1997). Phylogenetic trees were constructed based on distances transformed by the method of Kimura (1980) using the neighbour-joining method (Saitou & Nei, 1987). Bootstrap analyses (Felsenstein, 1985) were performed from 1000 random resamplings.

Strains BW 21 and BW 22T had identical sequences in the ITS region, D1/D2 domain of the 26S rRNA and 18S rRNA genes, which indicated that they were conspecific. A BLAST search of sequences of the above three regions in the NCBI database (http://blast.ncbi.nlm.nih.gov/Blast.cgi) showed that the closest matches to the sequence of strains BW 21 and BW 22T were members of the species *N. castellii* and *N. dairenensis*. The phylogenetic tree constructed by the combination of 18S, 5.8S and D1/D2 sequences also supported the close relationship between the two isolates and the type strains of *N. castellii* and *N. dairenensis* (Fig. 1). The two isolates also clustered together with *N. castellii* and *N. dairenensis* in the D1/D2 tree (see Fig. S1 available in IJSEM Online), which included strains of all known species of *Naumovozyma*, *Kazachstania* and *Saccharomyces*. Although the two isolates differed from *N. castellii* and *N. dairenensis* by 2–5 nt in the 18S rRNA region, they differed from them by 15–19 (3 %) mismatches (13–15 substitutions.....
and 2–4 indels) in the D1/D2 domain. There were 176–210 nt mismatches shown between the isolates and the type strains of the two known species in the ITS region sequence alignment. Therefore, the two isolates represent a novel *Naumovozyma* species, for which the name *Naumovozyma baii* sp. nov. is proposed.

The two strains of *N. baii* were isolated from rotten wood collected in tropical forests with a mean annual temperature of 23.6 °C and mean annual rainfall of 1500–2000 mm, which indicated that this novel species has a different ecological distribution to the other members of the genus *Naumovozyma*. *N. castelli* is widely distributed and has been found in Africa, Finland, The Netherlands and the USA; strains have been isolated from various substrates, such as soil, fermenting cucumbers, buttermilk, ensiled maize and baboon caecum contents ( Vaughan-Martini et al., 2011). *N. dairenensis* has been found associated with dried fruit, probably in Japan, and ensiled crops in The Netherlands (Middelhoven et al., 1990; Vaughan-Martini et al., 2011).

**Description of Naumovozyma baii** Q.-M. Wang, W.-Q. Liu, P.-J. Han & J.-Z. Qiu sp. nov.

*Naumovozyma baii* (bai.i. N.L. gen. masc. n. baii of bai, named in honour of Feng-Yan Bai, professor at the Institute of Microbiology, Chinese Academy of Sciences, for his contributions to the taxonomy of yeasts in China).

In YM broth, after 3 days at 25 °C, cells are ellipsoid (Fig. 2a), 3.0–4.5 × 5.0–7.5 μm, and occur singly or in pairs. Budding

![Phylogenetic tree](image)
occurs singly. After 1 month at 25 °C, sediment is present. After 1 month at 25 °C, the streak culture is butyrous and cream-coloured. The surface is smooth and the margin is entire. Pseudohyphae are not observed in cultures grown on cornmeal agar. Sporulation is observed on McClary acetate agar after 7 days at 25 °C; vegetative cells transform directly into persistent asci each containing one to four globose ascospores (Fig. 2b). Glucose and galactose are fermented; sucrose, maltose, lactose and raffinose are not fermented. Glucose, galactose and trehalose are assimilated; L-sorbose, sucrose, maltose, cellobiose, lactose, melibiose, melezitose, raffinose, inulin, soluble starch, D-xylene, L-arabinose, D- arabinose, D-ribose, L-rhamnose, D-glucosamine, methanol, ethanol, glycerol, erythritol, ribitol, galactitol, D-mannitol, methyl x-D-glucoside, salicin, DL-lactic acid, succinic acid, citric acid, inositol and hexadecane are not assimilated. Ammonium sulfate is assimilated; potassium nitrate, sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine hydrochloride are not assimilated. Growth in vitamin-free medium is negative. Starch-like compounds are not produced.

The type strain, BW 22T (=CGMCC 2.04520T=CBS 12642T), was isolated from rotten wood, Bawangling, Hainan province, in July 2007. Strain BW 21 (=CGMCC 2.04519=CBS 12641) is a reference strain of this species. The MycoBank number of Naumovozyma baii sp. nov. is MB800484.

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**References**


