Lipomyces orientalis sp. nov., a yeast species isolated from soil in Vietnam

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Five strains of the novel ascogenous yeast species Lipomyces orientalis sp. nov. were isolated from soil samples collected in Vietnam. The yeast forms ascii containing one to four ascospores. The ascospores of L. orientalis have warty surfaces and differ from the characteristic striated ascospores of Lipomyces tetrasporus. Phylogenetic analyses of D1/D2 26S rDNA and ITS sequences indicate that L. orientalis and L. tetrasporus are closely related, but they differ from each other by 6 nucleotides in the D1/D2 region and 16 nucleotides in the ITS region. The type culture is strain Lip 95T (=CBS 10300T=NRRL Y-27927).

Yeasts of the genus Lipomyces are true soil inhabitants and have a worldwide distribution. The genus Lipomyces and associated genera (Dipodascopsis, Zygozyma, Myxozyma) represent a unique branch in the evolution of the ascomycetes (van der Walt, 1992). Currently 11 species of Lipomyces are recognized, Lipomyces doorenjorgii, L. japonicus, L. kockii, L. kononenkoae, L. lipifer, L. mesembrius, L. spencermartinsiae, L. starkeyi, L. tetrasporus, L. yamadae and L. yarrowii (van der Walt et al., 1997; Smith, 1998; van der Walt et al., 1999). Despite the worldwide distribution of the genus, some geographical and geochemical preferences have been recorded for some species. For example, L. lipifer is restricted to temperate zones (Canada, Russia) whereas L. kononenkoae and L. spencermartinsiae can be commonly found in ferric soils of the tropics (Mali, Nigeria, Trinidad) (Babjeva & Gorin, 1987). In a survey of the diversity of soil yeasts in Vietnam, strains representing a novel species of the genus Lipomyces were isolated.

A total of 52 soil samples from different locations in Vietnam were collected and analysed (see Supplementary Fig. S1 for locations of sampling sites). For isolation of lipomycetaceous yeasts, soil particles were sprinkled over agar plates containing nitrogen-depleted medium (1 % glucose, 2 % agar). A protocol describing the preparation of the malt broth is available as supplementary material in IJSEM Online.

The GenBank/EMBL/DBJ accession number for the 26S rDNA D1/D2 and ITS sequences of strain Lip 95T are DQ275615 and DQ275616.

A protocol for the preparation of malt broth, a map showing the locations of the sampling sites, an electron micrograph of ascospores of strain Lip 95T and a neighbour-joining tree based on D1/D2 sequences are available as supplementary material in USEM Online.
The five novel strains differed from the standard description of L. tetrasporus in three assimilation tests (assimilation of propane-1,2-diol, butane-2,3-diol and nitrite). These five lipomycetaceous strains were isolated from three soil samples collected at Thanh Hoa (strain MD66-1), Quang Ninh (strains MD88-4 and MD89-4) and Nha Trang (strains Lip 51 and Lip 95T) (Table 1). The distances between these locations are roughly 260, 940 and 1000 km.

Extraction and purification of the coenzyme Q system were performed according to Yamada & Kondo (1973). Reversed-phase HPTLC was used for identification of coenzyme Q. Reversed-phase HPTLC plates (silica gel 60 for nano TLC; Merck) were prepared by dipping in n-hexane containing 5% liquid paraffin. The plates were air-dried. Coenzyme Q samples and standards were spotted on the plates, which were then developed with methanol/isopropanol (1:1) saturated with liquid paraffin. Visualization was done by dipping the plates in 0.2% KMnO4 for 5 min. This procedure ensures good separation of CoQ-6, CoQ-7, CoQ-8, CoQ-9 and CoQ-10. To separate CoQ-10 and CoQ-10(H2), a developing system containing acetone/acetonitrile (1:1) saturated with liquid paraffin was used. The major ubiquinone of the novel strains was Q-9.

For DNA extraction, strain Lip 95T was grown on YMA (0.3% yeast extract, 0.3% malt extract, 0.5% peptone, 1% glucose, 2% agar) for 3 days at 25°C. One loopful of cells was transferred to a microfuge tube containing 1 ml 2 x SSC and heated at 99°C for 10 min. Cells were collected and washed once with 1 ml sterile deionized water by centrifugation. To the cell pellet, about 75 ml glass beads (0.2–0.5 mm in diameter), 75 ml phenol/chloroform and 100 ml water were added. The tube was shaken at 1400 r.p.m. for 10 min and then centrifuged at 10 000 g for 10 min. The upper layer was transferred to a new microfuge tube and used directly as template for PCR. Due to the well-known inhibition effect of slimy substances of Lipomyces on the PCR (Nishimura et al., 2002), care is needed regarding the age of culture and the cultivation medium.

The ITS-D1/D2 region was amplified using primers ITS1 and NL4 on a GeneAmp PCR System 9700 (PE Applied Biosystems). The PCR conditions were as follows: an initial denaturation step of 94°C for 3 min followed by 30 cycles of 94°C for 30 s, 52°C for 40 s and 72°C for 60 s, with a final extension step at 72°C for 7 min. The PCR product was purified by using a QIAEX II agarose gel extraction kit (Qiagen). The DNA was sequenced by the dideoxy chain-termination method using primers ITS1, ITS4, NL1 and NL4 described by Kurtzman & Robnett (1998) and Esteve-Zarzoso et al. (1999). A model 377 automated DNA sequencer (Applied Biosystems) was used. For phylogenetic analyses, the resulting sequences were compared with known sequences in GenBank using the web-based nucleotide-nucleotide BLAST search engine hosted by the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov) (Altschul et al., 1997). The most similar sequences were edited using the program BioEdit (Hall, 1999) and aligned using CLUSTALX version 1.81 (Thompson et al., 1997). The fixed-gap and floating-gap penalty values used were respectively 10 and 0.2. Phylogenetic trees were constructed from distance data transformed according to Kimura (1980), using the neighbour-joining method (Saitou & Nei, 1987) in

Fig. 1. (a) Asci and ascospores of Lipomyces orientalis sp. nov. Lip 95T grown on diluted malt/glucose agar for 4 weeks at 25°C. (b–c) Scanning electron micrographs of Lipomyces orientalis Lip 95T (b) and Lipomyces tetrasporus Lip 5 (c) grown on diluted malt/glucose agar for 4 weeks. Bars, 5 μm (a) and 1 μm (b, c).
Table 1. Isolation sources of strains of Lipomyces orientalis sp. nov.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Other collection numbers</th>
<th>Source of isolation</th>
</tr>
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<tbody>
<tr>
<td>Lip 51</td>
<td>CBS 10301, NRRL Y-27928</td>
<td>Mixed forest soil, hillside (bottom part), 50 m from water edge, Bai San island, Nha Trang</td>
</tr>
<tr>
<td>Lip 95$^T$</td>
<td>CBS 10300$^T$, NRRL Y-27927$^T$</td>
<td>Mixed forest soil, hillside (bottom part), 50 m from water edge, Bai San island, Nha Trang</td>
</tr>
<tr>
<td>MD66-1</td>
<td>CBS 10302, NRRL Y-27929</td>
<td>Grassland soil, hillside (bottom part), Cam Thuy, Thanh Hoa</td>
</tr>
<tr>
<td>MD88-4</td>
<td>CBS 10303, NRRL Y-27930</td>
<td>Mixed forest soil, hillside (bottom part), 100 m from water edge, Cat Ba island, Quang Ninh</td>
</tr>
<tr>
<td>MD 89-4</td>
<td>CBS 10304, NRRL Y-27931</td>
<td>Mixed forest soil, hillside (bottom part), 100 m from water edge, Cat Ba island, Quang Ninh</td>
</tr>
</tbody>
</table>

CLUSTAL X. Bootstrap analyses were performed from 1000 random resamplings (Felsenstein, 1985). The phylogenetic tree was displayed using TreeExplorer version 1.21 (which can be downloaded from http://evolgen.biol.metro-u.ac.jp/pub/MolEvol/TE212.zip). Sequences from Stephanoascus smithiae strains NRRL Y-17849 (GenBank accession no. U76531) and CBS 5657 (AJ606463) were used as the outgroups for the D1/D2 and ITS trees, respectively.

ITS and 26S rDNA D1/D2 sequences were obtained for strain Lip 95$^T$. In the phylogenetic tree constructed based on D1/D2 sequences, Lip 95$^T$ clustered with L. kononenkoae, L. spencermartinsiae, L. starkeyi and L. tetrasporus but formed an out-branch (see Supplementary Fig. S3 in IJSEM Online). In the D1/D2 region, Lip 95$^T$ was closest to L. tetrasporus but differed from the latter at six positions (five substitutions and one insertion). In the ITS tree, Lip 95$^T$ clustered with L. tetrasporus (Fig. 2). They differed from each other at 16 positions in the ITS region. Based on the distinctive phenotypic characteristics and phylogenetic position amongst established taxa, a novel species of Lipomyces, Lipomyces orientalis sp. nov., is proposed to accommodate the new isolates.

Latin diagnosis of Lipomyces orientalis Thanh sp. nov.


Table 2. Neighbour-joining tree depicting the relationships between Lipomyces orientalis and neighbouring taxa. The tree was constructed from nucleotide divergence in the ITS region using the program CLUSTAL X. Bootstraping was done with 1000 replications; values above 50% are given. Stephanoascus smithiae CBS 5657$^T$ was used as the outgroup. GenBank accession numbers are given after strain names.
Description of Lipomyces orientalis Than sp. nov.

Lipomyces orientalis (o.ri.en.tal’is. L. masc. adj. orientalis from the East, referring to the fact that the species was first isolated from soil in Vietnam).

On YMA after 3 days at 25 °C, cells are ovoidal, 4–9 × 5–12 μm, and occur singly or in pairs (Fig. 3). The streak culture on malt agar is mucoid, partly hyaline, partly creamish-opaque, smooth and glistening, with an entire margin. In Dalmau plate cultures on cornmeal agar after 10 days at 25 °C, neither hyphae nor pseudohyphae are formed. In YM broth after 1 month at 25 °C, sediment is present. Ascii are attached as a rule, saccate to irregularly tubular or contorted, with slowly deliquescent walls. Mature ascospores are ellipsoid, amber-coloured, warty, 2.2–2.7 × 3.2–3.9 μm, one to four per ascus, and conglutinative when liberated (Fig. 1b). Does not ferment D-glucose. Assimilates D-glucose, D-galactose, L-sorbose, D-xylose, L-arabinose (weakly or not at all), D-arabinose (weakly), L-rhamnose (maybe weakly), sucrose, maltose, α,α-trehalose (weakly), methyl α-D-glucoside, cellobiose (maybe weakly), salicin (maybe weakly), arbutin (weakly), melibiose (maybe weakly), lactose (weakly or not at all), raffinose, melezitose, inulin, starch (weakly), erythritol, ribitol (delayed and weakly), xylitol, D-glucitol, D-mannitol, galactitol, D-glucono-1,5-lactone (weakly), 2-keto-D-gluconate, 5-keto-D-gluconate (weakly), D-gluconate (weakly), succinate (weakly), citrate (weakly) and ethanol (weakly). Does not assimilate D-glucosamine, D-ribose, glycerol, myo-inositol, D-galacturionate, D-lactate, methanol, propane-1,2-diol or butane-2,3-diol. Assimilates nitrite, L-lysine, glucosamine and imidazole. Does not assimilate nitrate. Produces starch-like substances. Urease reaction is negative. Does not grow in YNB medium (Difco) containing 10 % NaCl and 5 % glucose. Grows in vitamin-free medium. Does not grow at 35 °C, but grows at 30 °C. Growth in medium containing 0–1 % cycloheximide is positive. The major ubiquinone is Q-9.

The type strain, Lip 95T (=CBS 10300T = NRRL Y-27927T), as well as strains Lip 51 (=CBS 10301 = NRRL Y-27928), MD 66-1 (=CBS 10302 = NRRL Y-27929), MD 88-4 (=CBS 10303 = NRRL Y-27930) and MD 89-4 (=CBS 10304 = NRRL Y-27931), were isolated from uncultivated soil in Vietnam and have been deposited in the Yeast Collection of the Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands, and the Agricultural Research Service Yeast Collection, US Department of Agriculture, Peoria, IL, USA.

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References


