Occurrence of Candida orthopsilosis in Brazilian tomato fruits 
(Lycopersicum esculentum Mill.)

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Abstract

We aimed to isolate and identify yeasts found in the tomato fruit in order to obtain isolates with biotechnological potential, such as in control of fungal diseases that damage postharvest fruits. We identified Candida orthopsilosis strains LT18 and LT24. This is the first report of this yeast on Lycopersicum esculentum fruits in Brazil.

Key words: Lycopersicum esculentum Mill, Candida orthopsilosis, tomato fruits.

The tomato fruit (Lycopersicum esculentum), which is used as a vegetable, is one of the most consumed food ingredients in the world (Mata et al., 2003), and Brazil is one of the major producers of tomato. In 2009, the national production reached 4.3 million tons and the world production was more than 152 million tons (FAOSTAT, 2011).

Yeast are a large and diverse group of microorganisms consisting of more than 1000 species and can be found in soil, air, water, and food (Mislivec et al., 1992). Some species also co-exist with the natural microflora of fruits and vegetables and their colonization is influenced by environmental, harvest, or storage conditions (Skinner, 1980). Generally, many fruits and vegetables present nearly ideal conditions for the survival and growth of several types of microorganisms (Barth et al., 2009). Ferreira et al. (2010) studied the postharvest quality of the tomato fruit and revealed that the yeast and mold count decreases with the ripening of the fruit, but remains around the order of $10^7$ CFU/g, indicating that the tomatoes preserved at room temperature need to be cleaned efficiently before consumption.

A diverse community of epiphytic microorganisms also colonizes the tomato fruit surface, effectively providing a further competitive barrier against the spoilage organisms (Barth et al., 2009). Therefore, the yeast microflora in the tomato fruit may present a biotechnological potential, such as in the fungal diseases control on postharvest fruit. The main mechanisms for the control of postharvest diseases by using microbial antagonists exploit microbial competition for nutrients and space, induced resistance, production of antibiotics, and direct parasitism (Sharma et al., 2009).

Pichia guilliermondii presents potential biocontrol activity against Botrytis cinerea in apples (Trofa et al., 2008) and against Rhizopus nigricans in tomato fruits (Zhao et al., 2008). Pichia anomala, isolated from the surface of coffee berries, is able to inhibit the spore production of Aspergillus ochraceus and Penicillium roqueforti (Ramos et al., 2010). Candida lambica is able to reduce up to 95.87% of A. ochraceus biomass in submerged culture (Beux, 2004). Therefore, we aimed to isolate and identify yeasts from the tomato fruit, which display characteristics similar to the Pichia genus in order to obtain isolates with biotechnological potential.

Ten tomato fruit samples were collected from different markets in Curitiba, Paraná State, Brazil, on October

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2006. Tomato broth was prepared by disintegration and homogenization of tomatoes by using a sterile metal shredder. The broth was separated into sterile Erlenmeyer flasks and cultivated in a biochemical oxygen demand (BOD) incubator at $28^\circ C$ for 5 days. Subsequently, the microorganisms were isolated on potato dextrose agar (PDA) (Merck, Darmstadt, Germany) by serial dilution in 0.1% peptone water.

The yeast groups were identified by the ability to ferment sugars such as glucose, galactose, sucrose, maltose, fructose, mannose, and raffinose according to the method described by Rocha (2006). The results were compared with those of a prior study (Back, 2006; Barnett and Pankhurst, 1974). Later, the yeasts were identified by growing them on CHROMAgar Candida (BD), by using the API 20C AUX system (bioMérieux) and by sequencing the ITS of their rDNA.

About 1 cm$^2$ colonies of 5-day-old cultures were transferred to 2-mL Eppendorf tubes, each containing 300 $\mu$L cetyltrimethylammonium bromide (CTAB) buffer (2% CTAB [w/v], 1.4 M NaCl, 100 mM Tris-HCl, pH 8.0, 20 mM EDTA, 0.2% $\beta$-mercaptoethanol [v/v]) and approximately 80 mg of a silica mixture (silica gel H; Merck/Celite 545-Macherey Nagel & Co.; 2:1, w/w). The cells were disrupted manually using a sterile pestle for approximately 5 min. Subsequently, 200 $\mu$L CTAB buffer was added again, the mixture was vortexed, and then incubated for 10 min at 65 °C. After adding 500 $\mu$L chloroform, the solution was mixed and centrifuged for 5 min at 20,500 $\times$ g force value and the supernatant was transferred to a new tube containing 2 volumes of ice-cold 96% ethanol. The DNA was allowed to precipitate for 30 min at -20 °C and then centrifuged again for 5 min at 20,500 $\times$ g force value. Subsequently, the pellet was washed with cold 70% ethanol. After drying it at room temperature, the pellet was resuspended in 97.5 $\mu$L TE-buffer with 2.5 $\mu$L RNAse (20 U/mL) and incubated for 5 min at 37 °C; thereafter, it was stored at -20°C (Gerrits and Hoog, 1999).

The ITS of the ribosomal DNA (rDNA) was amplified using the primers V9G (5'-TTACGTCCCTGCCCCCTTGTGA-3') and LS266 (5'-GCATTCCCAAACAATCGACTC-3') (9) and sequenced using ITS5 (5'-GGAAGTAAAGTCGTAACAGG-3') and ITS4 (5'-TCTTCCGGCTATTGATATGC-3') (White et al., 1990). Amplicons were cleaned using the GFX PCR DNA purification kit (GE Healthcare) and sequenced using an ABI 3130 automatic sequencer (Applied Biosystems). Sequences were edited and aligned using the Staden sequence analysis package v. 1.6.0 (Staden, 1996). Sequence analysis was performed using the sequence alignment software BLASTn run against the NCBI database. Phylogenetic analysis was performed using the software Mega 4.0.2 (Tamura et al., 2007) by applying the neighbor-joining method (Saitou and Nei, 1987) and the Jukes-Cantor correct distance model (Jukes and Cantor, 1969). The nucleotide sequence obtained in this study was submitted to GenBank.

Seventeen species of filamentous fungi were isolated from the tomato broth, and the analysis of macromorphology and reproductive structures revealed that they belonged to 4 genera: *Penicillium*, *Aspergillus*, *Acremonium*, and *Trichoderma* (Data not shown). Some species (e.g., *Trichoderma harzianum*) of these genera have previously shown the ability to control postharvest diseases in fruits (Batta, 2007), whereas others such as *Penicillium expansum* were agents of postharvest diseases (Yu et al., 2012). However, we chose to focus this work on yeast, so that the future implementation and bioprocess viability could be easily achieved.

We isolated 2 strains of yeast labeled LT18 and LT24, whose colonies were bright white, flat, and smooth, with regular, rounded borders and no pseudohyphae. Fermentation of the carbon sources was assessed in a previous identification of the yeast isolates, revealing that the strains could potentially belong to *Pichia*.

The morphological and physiological characters of LT18 and LT24 were similar to *Pichia* sp.; hence, a further identification was carried out. The strains LT18 and LT24 presented pink pigmentation and smooth texture on the chromogenic medium CHROMAgar, and they were identified as *Candida parapsilosis* by using the API 20C AUX system.

Sequences of ITS1-5.8S-ITS2 revealed a fragment of 422 bp for LT18 and 423 bp for LT24. Sequences of both strains presented with 98% (LT18) and 99% (LT24) similarity with the *Candida* orthopsilosis sequence EU557371. The sequences of the isolates LT18 and LT24 were deposited in GenBank with the respective accession numbers JN797502 and JN797503.

Twenty sequences previously deposited at GenBank (Table 1), which showed similarity in the range of 95-99% to the sequences of the isolates obtained in this study, were employed for constructing a phylogenetic tree (Figure 1). Three groups that showed high bootstrap values were obtained. Group A, 88% consistent, was composed of isolates of *C. orthopsilosis*, including the ones obtained in our study, LT18 and LT24; group B, with a bootstrap value of 92%, is represented by members of *Candida metapsilosis*; and finally group C, with a bootstrap value of 100%, contained isolates from *C. parapsilosis*.

Identification via conventional biochemical systems corroborated with the data obtained by Tay et al. (2009), who also used the API 20C AUX system for preliminary identification of the isolates from the bloodstream of infected patients. All isolates were initially identified as *C. parapsilosis*, but were later differentiated into *C. parapsilosis*, *C. orthopsilosis*, *C. metapsilosis*, and *Lodderomyces elongisporus* through RAPD and ITS sequencing. Others studies (Silva et al., 2009; Toro et al., 2010) also differentiated a large set of *C. parapsilosis* iso-
lates, previously identified by biochemical tests, into C. parapsilosis sensu stricto, *C. orthopsilosis*, and *C. metapsilosis* species by molecular identification (SADH gene restriction profile).

Further, Pitt and Hocking (1997) have isolated *C. parapsilosis* from fruit juices, olives, meat, and seafood. This particular species is well known for causing nosocomial blood infections, especially among neonates and the immuno-compromised, and it is associated with candidemia due to contaminated intravascular devices and parenteral nutrition (Almirante et al., 2006; Girmenia et al., 1996; Pfaller and Diekema, 2002, 2007; Safdar et al., 2002; Trofa et al., 2008). This yeast was also isolated from robusta coffee samples from the Congo Republic, akin to others species from this genera including *Candida pelliculosa*, *Candida famata*, and *Candida tropicalis* (Pee and Castelein, 1971).

The taxon *C. parapsilosis* was traditionally divided into 3 groups, I, II, and III. Recently, Tavanti et al. (2005) investigated the genetic heterogeneity of the taxon and proposed replacing groups II and III with *C. orthopsilosis* and *C. metapsilosis*, respectively.

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**Figure 1** - Phylogenetic analysis of yeasts LT18 and LT24 belonging to the *C. orthopsilosis* specie. Neighbor-joining method. Numbers on the tree branches indicate the *bootstrap* value found from 10000 replicates. Mega Software 4.0.2 release. Strains available in GenBank accession Nos JN797502 and JN797503.
The phylogenetic tree clusterings of all 3 species for the ITS region are consistent with those reported by Gomez-Lopez et al. (2008), Tavanti et al. (2005) and Tay et al. (2009), in which the differences in the sequence alignment validated the species separation. This result showed that C. orthopsilosis and C. metapsilosis are more closely related to each other than to C. parapsilosis, as shown in Figure 1.

In conclusion, our study is likely the first report of C. orthopsilosis found in L. esculentum Mill. fruits in Brazil. We recommend further studies on these strains in order to screen for biotechnologically important characteristics and exploit their use in postharvest fungal diseases control.

References


### Table 1 - Sequences from Candida spp. deposited in GenBank used in the phylogenetic analysis.

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