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Saccharomycopsis praedatoria sp. nov., a predacious yeast isolated from soil and rotten wood in an Amazonian rainforest biome

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Abstract

Three yeast isolates were obtained from soil and rotting wood samples collected in an Amazonian rainforest biome in Brazil. Comparison of the intergenic spacer 5.8S region and the D1/D2 domains of the large subunit rRNA gene showed that the isolates represent a novel species of the genus *Saccharomycopsis*. A tree inferred from the D1/D2 sequences placed the novel species near a subclade containing *Saccharomycopsis lassenensis*, *Saccharomycopsis fermentans*, *Saccharomycopsis javanensis*, *Saccharomycopsis babjevae*, *Saccharomycopsis schoenii* and *Saccharomycopsis oosterbeekiorum*, but with low bootstrap support. In terms of sequence divergence, the novel species had the highest identity in the D1/D2 domains with *Saccharomycopsis capsularis*, from which it differed by 36 substitutions. In contrast, a phylogenomic analysis based on 1061 single-copy orthologs for a smaller set of *Saccharomycopsis* species whose whole genome sequences are available indicated that the novel species represented by strain UFMG-CM-Y6991 is phylogenetically closer to *Saccharomycopsis fodiens* and *Saccharomycopsis* sp. TF2021a (=*Saccharomycopsis phalluae*). The novel yeast is homothallic and produces asci with one spheroidal ascospore with an equatorial or subequatorial ledge. The name *Saccharomycopsis praedatoria* sp. nov. is proposed to accommodate the novel species. The holotype of *Saccharomycopsis praedatoria* is CBS 16589^T. The MycoBank number is MB849369. *S. praedatoria* was able to kill cells of *Saccharomyces cerevisiae* by means of penetration with infection pegs, a trait common to most species of *Saccharomycopsis*.

INTRODUCTION

The genus *Saccharomycopsis* contains species that are characterized by multipolar budding, production of septate hyphae, and ascospores with different morphologies, such as hat-shaped, spheroidal to elongated, and with or without equatorial ledges; the species may be homothallic or heterothallic [1–3]. *Saccharomycopsis* belongs to the class *Saccharomycetes*, order *Ascoideales* and family Saccharomycopsidaceae [4]. Twenty species of *Saccharomycopsis* have been described, and some present interesting biotechnological applications [2, 3, 5, 6]. The most interesting ability of the genus it is the capacity to penetrate and kill yeasts and other micro-organisms, as will be exemplified below [7–10]. Recently, Yuan *et al.* [3] described the novel species *Saccharomycopsis phalluae* and showed that it was able to cause a severe disease (yellow rot disease) in the mushroom *Phallus rubrovolvatus*.

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Abbreviations: ANI, average nucleotide identity; ITS, intergenic spacer; LSU, large subunit; YM, yeast extract–malt extract; YNB, yeast–nitrogen base.

The GenBank/EMBL/DDBJ accession numbers for ITS-5.8S region and the D1/D2 domains of the large subunit rRNA gene sequences of strain UFMG-CM-Y6632 are OQ641694 and OM321353, respectively. The Whole Genome Shotgun project of strain *Saccharomycopsis praedatoria* UFMG-CM-Y6991 has been deposited at DDBJ/ENA/GenBank under accession JASJSC000000000. The version described in this paper is version JASJSC010000000.

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Two supplementary tables and one supplementary figure is available with the online version of this article.

The occurrence of physical predation of several yeast species by species of the genus *Saccharomycopsis* was demonstrated by Lachance and Pang [7]. In that work, special emphasis was placed on *Candida* sp. strain UWOPS95-697.4, a predominantly unicellular yeast isolated from a beetle collected from a flower of the Australian tree, *Hibiscus heterophyllus*. This yeast was later described as *Saccharomycopsis fodiens* [9]. Strain 95–697.4 was able to predate all yeasts tested, both ascomycetous and basidiomycetous species, except for *Schizosaccharomyces pombe*. The yeast-like mould *Aureobasidium pullulans* was susceptible to predation by this yeast, and the mould *Penicillium chrysogenum* induced formation of infection pegs and penetration of conidia, but not hyphae. Lachance *et al.* [8] reported that the yeasts identified as predators belong to the *Saccharomycopsis* clade. These authors showed that the range of susceptible prey covers both ascomycetes and basidiomycetes, and includes *Saccharomycopsis pombe*, which was previously thought to be immune. Predacious species attack other predacious species, and in some cases, young cultures may penetrate older cultures of the same strain. Pimenta *et al.* [5] tested the potential of a strain of *Saccharomycopsis crataegensis* to control infections of oranges by *Penicillium digitatum*, a causative agent of postharvest decay of these fruits. The yeast alone reduced the severity of decay by 41%, and in association with sodium bicarbonate, a generally regarded as safe (GRAS) substance, led to a delay in the development of symptoms from 2 to 10 days. Junker *et al.* [10] showed that *Saccharomycopsis schoenii* efficiently kills sensitive and multi-drug resistant isolates of *Candida auris*, as well as clinical isolates of other opportunistic pathogenic yeast species.

During studies of yeast communities present in soil and rotting wood of an Amazonian rainforest biome, three isolates of a new species of the genus *Saccharomycopsis* were obtained. Sequence analyses of the intergenic spacer (ITS)-5.8S region and the D1/D2 domains of the large subunit (LSU) rRNA gene suggested that the novel species is phylogenetically related to a subclade containing *Saccharomycopsis lassenensis*, *Saccharomycopsis fermentans*, *Saccharomycopsis javanensis*, *Saccharomycopsis babjevae*, *Saccharomycopsis schoenii* and *Saccharomycopsis oosterbeekiorum*. The aim of this work is to describe the novel species and report on its ability to predate cells of *Saccharomyces cerevisiae*.

METHODS

Yeast isolation and identification

The isolates were obtained from samples collected from two sites in an Amazonian rainforest biome, specifically the municipality of Itacoatiara, located in the state of Amazonas, northern Brazil, during February 2019. Isolates UFMG-CM-Y6632 and UFMG-CM-Y6898 were taken from soil samples collected from the Piquiá Sol Nascente Community (03° 01.045′ S 58° 28.830′ W). One gram of each soil sample was cultured separately in 15 ml flasks with 10 ml YNB–glucose medium (yeast–nitrogen base 0.67%, glucose 0.8%, chloramphenicol 0.02%) and incubated at 25°C. When growth was observed, 1 ml of the culture was transferred to a tube containing 5 ml of the same medium and incubated as above. When growth was observed, yeast colonies were recovered by plating appropriate decimal dilutions on YM agar plates (yeast extract 0.3%, malt extract 0.3%, peptone 1%, glucose 2%, chloramphenicol 0.1%, agar 2%), which were incubated at 25°C for 7 days. Representative colonies of the different yeast morphotypes were purified by repeated streaking on YM agar plates. Isolate UFMG-CM-Y6991 was obtained from a rotting wood sample collected from Campus II of Universidade Federal do Amazonas (03° 05.654′ S 58° 27.464′ W). The samples were stored in sterile plastic bags and transported under refrigeration to the laboratory immediately for processing. For yeast isolation, 0.5 g of the rotting wood sample was incubated in 1:2 diluted sugarcane bagasse hydrolysate as described by Barros *et al.* [11]. The yeasts were morphologically and physiologically characterized using standard methods [12].

Species identification was performed by sequencing of the ITS-5.8S region and the D1/D2 domains of the LSU rRNA gene [13–16]. The amplified DNA was concentrated, cleaned, and sequenced in an ABI 3130 Genetic Analyzer automated sequencing system (Life Technologies, California, USA) using BigDye version 3.1 and POP7 polymer. The sequences were edited and aligned using the program MUSCLE provided in the MEGA6 package [17]. They were compared with those in the GenBank database using the Basic Local Alignment Search Tool (BLAST; www.ncbi.nlm.nih.gov/pubmed/2231712) [18]. A phylogram based on the D1/D2 domains of the LSU rRNA gene sequences was reconstructed by neighbour-joining analysis (in the MEGA6 software package) of 556 aligned positions using the number of substitutions as the distance metric. Bootstrap values were determined from 1000 pseudoreplications.

Genome sequencing, assembly and phylogenomic analysis

Genomic DNA (gDNA) of strain UFMG-CM-Y6991 was isolated using a modified phenol–chloroform method [19]. Libraries were prepared with NEBNext Ultra DNA Library Prep Kit for Illumina (NEB No. E7370L), which was performed according to the manufacturer's protocol, and submitted for 2×150 bp sequencing on an Illumina NovaSeq 6000 instrument. We first preprocessed the raw sequenced reads by trimming of adapters and low-quality bases with Trimmomatic version 0.33 [20]. We then used the processed sequence reads as input into *de novo* assembly tool SPAdes version 3.13.1 [21]. The resulting genome assembly was assessed for quality with QUAST version 5.2.0 [22]. Genes were predicted with a Maker2 [23] pipeline using Augustus and Snap predictors. Transfer RNA was detected using tRNAscan-SE [24].

A maximum-likelihood (ML) phylogenomic tree was reconstructed based on the 1061 single-copy orthologs identified by BUSCO version 5 [25], which were present in 90% of 12 other members of the newly introduced order Ascoidales (formerly CUG-Serine 2 clade) [19], as well members with whole genomes available, UFMG-CM-Y6991 and *Spathaspora boniae* Y-CM-306 (outgroup) (Table S1, available in the online version of this article). Each BUSCO sequence was aligned using MUSCLE version 5.1 [26], quality-trimmed with trimAL version 1.4.1 [27], and concatenated to generate a single matrix with 453 012 positions using the BUSCO_phylogenomics script (https://github.com/jamiemcg/BUSCO_phylogenomics, last accessed on 22 April 2023). We inferred an ML phylogeny using IQ-TREE version 2.1.3 [28], with 1000 ultrafast bootstrap replicates, a partitioning scheme and substitution models. Average nucleotide identity (ANI) values was calculated using orthoANI [29]. ANI and the tetranucleotide correlation coefficients were determined using the TETRA method described in Richter and Rosselló [30] and implemented in the Python module pyani (version 0.2.12 https://github.com/widdowquinn/pyani).

Assessment of predation

The predation tests were done as described by Lachance and Pang [7] and Junker *et al.* [10]. Approximately equal amounts of recently grown culture (24 h on YM agar) of the isolates and prey (*Saccharomyces cerevisiae* UFMG-CM-Y7149, isolated from tree bark collected in a Cerrado ecosystem in Brazil) were mixed together on glucose–YNB without amino acids agar plates (YNB without amino acids 0.67%, glucose 2.0%, agar 2.0%) and incubated at 25°C. Mixtures were examined daily by microscopy for signs of predation (infection pegs and/or cell penetration) for 2 days. Signs of predation were normally observed in the first 18 h of the experiment. The same experiment was done using glucose–YNB without amino acids broth.

RESULTS AND DISCUSSION

Species delineation and phylogenetic placement

Three isolates of the candidate of novel *Saccharomycopsis* species were obtained from the same Amazonian rainforest biome. Based on the analysis of the D1/D2 sequences, which are available for all known species, the new species occupies an early emerging position with respect to a subclade containing *S. lassenensis*, *S. fermentans*, *S. javanensis*, *S. babjevae*, *S. schoenii* and *S. oosterbeekiorum* (Fig. 1), but with low bootstrap support. The highest identity with the aligned sequences was with *Saccharomycopsis capsularis*, with 36 substitutions, which we take as strong evidence for treating the isolates as representative of a new species. A BLAST search also identified *S. capsularis* as having the highest identity in the ITS region, with 62 substitutions, which adds additional support to our conclusion. The three isolates of the new species presented identical ITS and D1/D2 sequences. The yeast produced asci and ascospores on 2% malt agar and V8 sporulation media after 4 days at 25°C. Asci were persistent, spheroidal, and borne laterally or terminally on hyphae (Fig. 2). They occurred singly and contained only one spherical or ovoid ascospore with an equatorial or subequatorial ledge. The name *Saccharomycopsis praedatoria* sp. nov. is proposed to accommodate these isolates.

The phylogenomic analysis confirms that the novel species belongs to the genus *Saccharomycopis* and that this genus is phylogenetically related to *Ascoidea* as shown by Shen *et al.* [19]. The Whole Genome Shotgun project of strain *S. praedatoria* UFMG-CM-Y6991 has been deposited at DDBJ/ENA/GenBank under accession JASJSC000000000. The version described in this paper is version JASJSC010000000. The analysis placed *S. praedatoria* UFMG-CM-Y6991 closer to *S. fodiens* and *Saccharomycopsis* sp. TF-2021a (=*S. phalluae*, Fig. 3). However, whole genome sequences were available for only eight of the 19 known species of *Saccharomycopsis* (Table S1), such that the precise placement inferred from phylogenomics may change as more sequences are obtained. The ANI, measured from the identity percentage calculated by BLAST+, for *S. praedatoria* UFMG-CM-Y6991 with species with known genomes was on the order of 70% (Table S2). The lowest ANI value was with *S. fodiens* (65.8%), and the highest was with *S. fibuligera* (71%), which would appear to contradict the patterns shown in Fig. 3. However, as explained in some detail by Lachance *et al.* [29], it is important to remember that genetic distances inferred from pairwise sequence divergence should not be interpreted as strict measures of phylogenetic relatedness, which must be inferred from the topology of phylogenetic trees. The authors observed that an ANI value of 95% constitutes a good threshold for species recognition, at least for a rich set of data relevant to the biological, phylogenetic, and genetic species concepts for haplontic, heterothallic *Metschnikowia* species.

The TETRA analysis, which generates correlation coefficients for the occurrence of four-nucleotide motifs across genomes, linked *S. praedatoris* to a subclade containing *S. crataegensis*, *S. fibulgera* and *Saccharomycopsidaceae* sp. CTeuk-1920 (a genome obtained from a soil metagenome work reported by Saraiva *et al.* [31]) with a value of 0.93 for the last species (Fig. 4). This result was unexpected in view of the branching orders obtained in either the phylogenomic analysis or the tree inferred from barcodes. The analysis also linked *S. fodiens* CBS 8332 and *Saccharomycopsis* sp. TF-2021a with a correlation of 0.82, and it paired *S. fermentans* CBS 7830 with *S. schoenii* CBS 7425 with a correlation of 0.95. Again, these results invite caution against the hasty interpretation of phylogenomic metrics and show the need to include all available species in order to calibrate new criteria before applying them to species circumscription. A TETRA analysis was used by Freitas *et al.* [32] to show that *Kluyveromyces starmeri* is a separate species in the genus *Kluyveromyces*. At the very least, the lack of concordance for relationships or distances inferred by four different methods demonstrates the lack of a

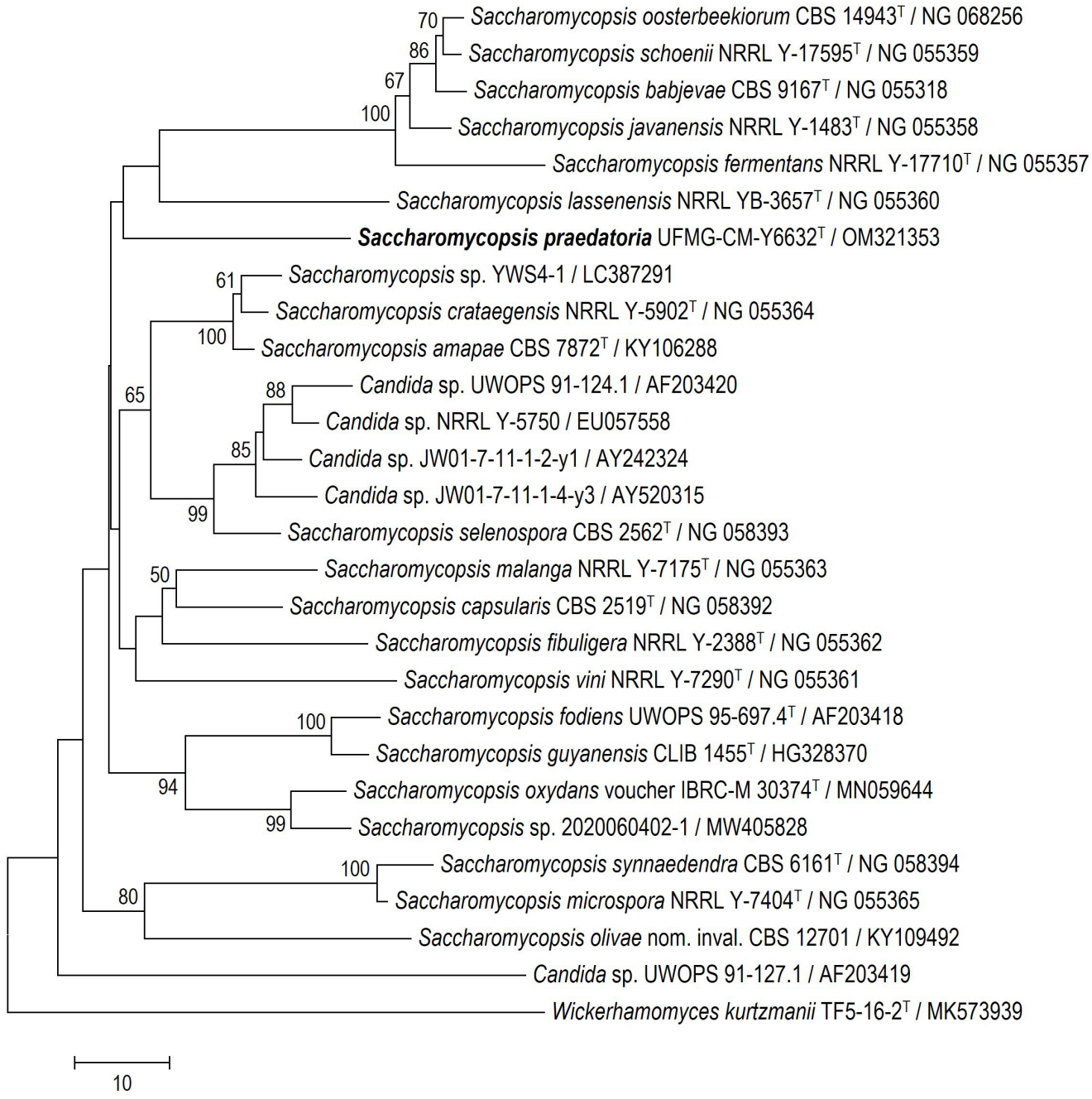

Fig. 1. Neighbour-joining phylogram showing the placement of *Saccharomycopsis praedatoria* sp. nov. within the genus. The tree was inferred from 556 aligned positions for the D1/D2 domains of the large subunit rRNA gene. The distance metric was the number of substitutions. Bootstraps (n=1000) are shown for values of 50% and above.

clear phylogenetic signal among *Saccharomycopsis* species. Notwithstanding this, the separation of *S. praedatoria* from other species in the genus is unanimously supported and in conformity with both the phylogenetic and the genetic distance species concepts.

We obtained 2450584 reads totaling 740076368 bases with an estimated 56× coverage. The assembled draft genome of *S. praedatoria* consisted of 13241612 bp distributed across 170 contigs over 500 bp long. The largest contig had a length of 585195 bp and the whole genome presented G+C content of 35 mol%. The contig mean length was 77891 bp and the N50 value was 196298 bp. Gene prediction identified 6293 protein-coding sequences. Sequence similarity searching showed matches with 4736 proteins (75%) against the Uniprot Swissprot and 557 proteins (~9%) against the Uniprot Trembl databases. We found 157 tRNA genes and eight pseudo tRNA genes.

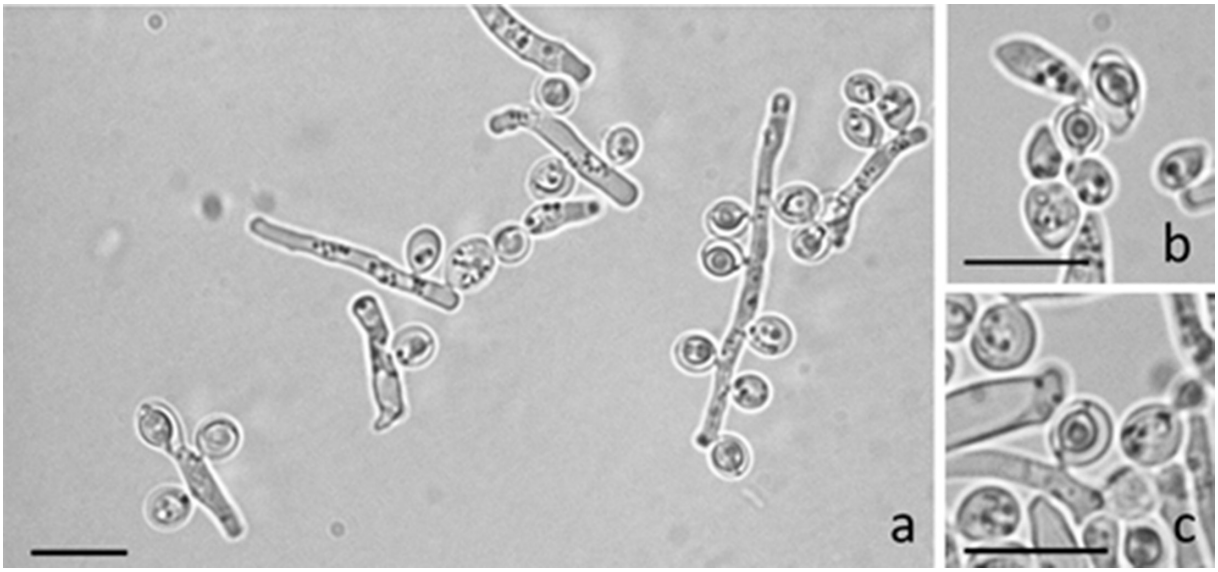

Fig. 2. Microscope images of *Saccharomycopsis praedatoria* strain UFMG-CM-Y6632 on 2% malt medium, after 4 days of incubation at 25°C. (a) The asci were spheroidal and usually arose laterally or terminally on the hyphae. (b, c) The ascospores were spheroidal or ovoid, with an equatorial edge. Only one spore per ascus was observed. Scale bar, 10 µm.

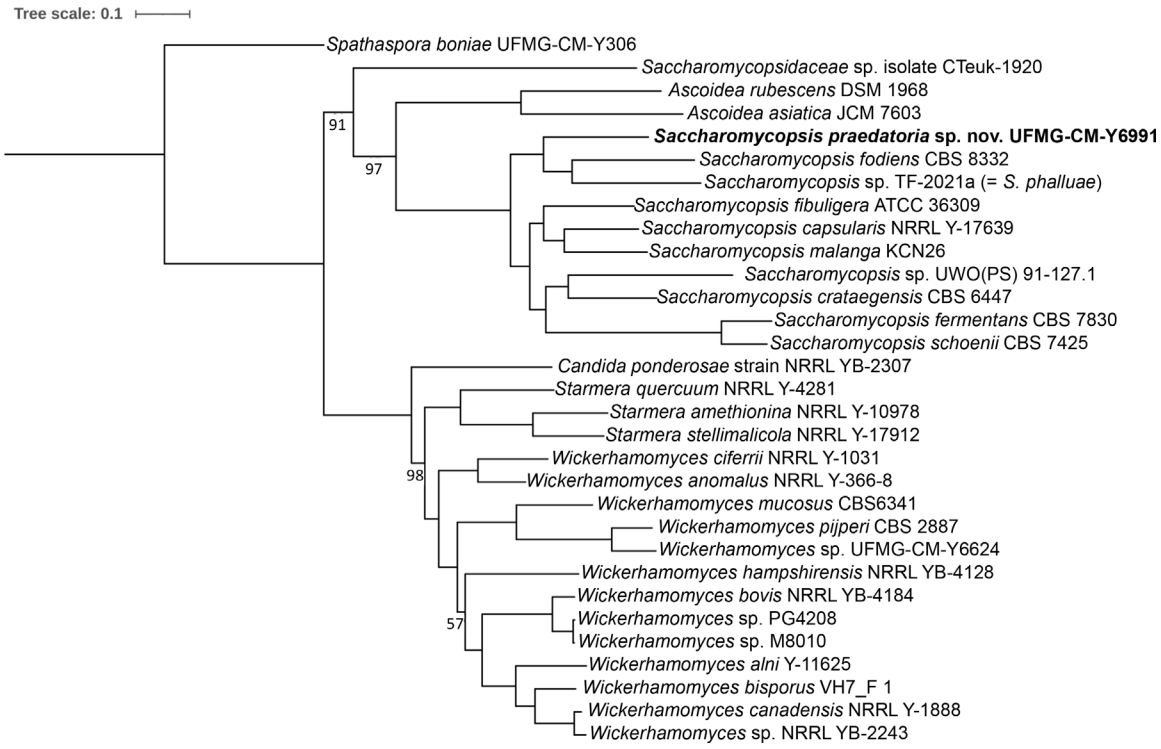

Fig. 3. Phylogenetic tree reconstructed from the alignment of 1061 orthologous proteins of *Saccharomycopsis praedatoria* sp. nov., found in 90% of the 12 other members of the newly revised order Ascoidales, as well as three *Starmera* and 14 *Wickerhamomyces* members with available whole genomes. *Spathaspora boniae* UFMG-CM-Y306 was used as the outgroup. The analysis was performed using IQ-TREE and iTOL. Bootstrap values (1000 pseudoreplicates) are displayed only for cases where the values were less than 100%. Branch length represents amino acid residue substitution per site.

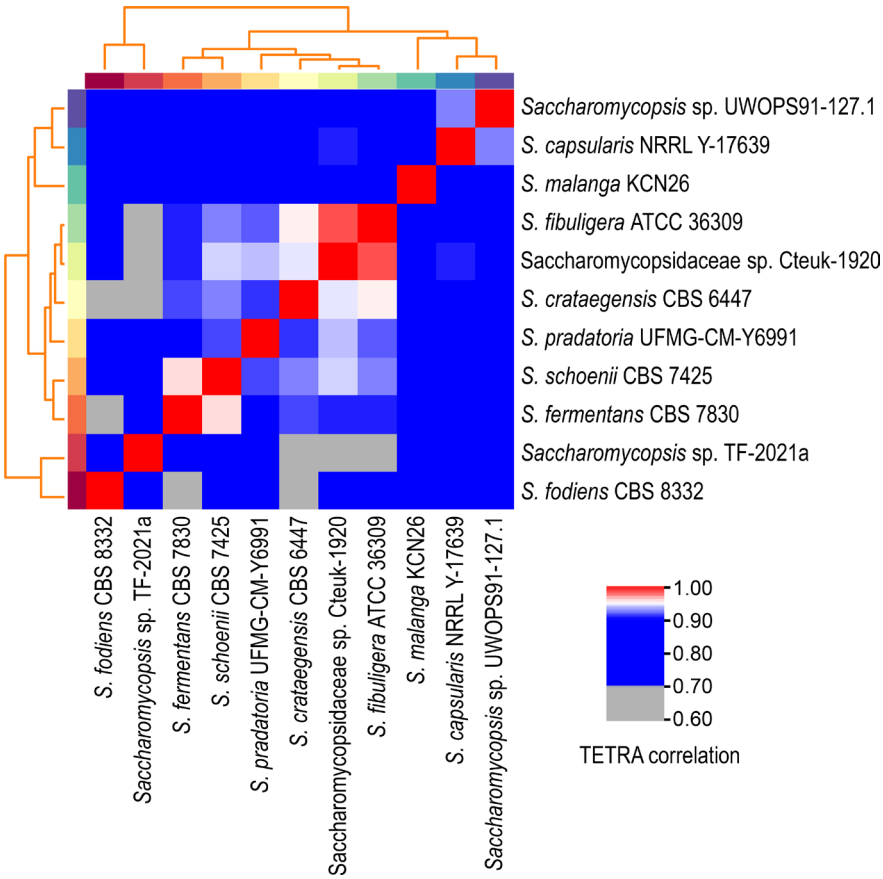

Fig. 4. Heatmap of tetranucleotide frequency correlation coefficients (TETRA) of seven *Saccharomycopsis* species with available genomes. Red cells correspond to 95% or more TETRA correlation, which is interpreted as a sign of conspecificity as described by Richter and Rosselló-Móra [30]. Blue cells (70–90%) correspond to correlations interpreted to mean distinct species. Intermediate colours indicate correlations ranging from 90 to 95%. The coloured rectangles above and to the left of the heatmap show that each genome used in this analysis corresponds to a distinct species. Dendrograms were reconstructed by single linkage clustering of TETRA correlations.

S. praedatoria has the second smallest genome among members of the genus that have been sequenced, with sizes varying between 22.2 Mb for *Saccharomycopsidaceae* sp. CTeuk-1920 and 12.1 Mb for *Saccharomycopsis* sp. UWO PS91-127.1 (Fig. S1).

Differentiation based on growth characteristics between *S. praedatoria* and its close relatives is shown in Table 1. The new species can be distinguished from *S. lassenensis* by growth on L-sorbose, sucrose, cellobiose and D-xylose, which is positive for *S. praedatoria*

Table 1. Differential physiological characteristics among *Saccharomycopsis praedatoria* and close relatives (+, positive; –, negative; +w, weak positive; +s, positive slow; v, variable)

Characteristic	*S. praedatoria*	*S. fodiens*	*S. lassenensis*	*S. fermentans*	*S. javanensis*	*S. babjevae*	*S. schoenii*	*S. oosterbeekiorum*
L-Sorbose	+	+	–	v	+	–	v	+
Sucrose	+	–	–	–	–	+	v	+
Maltose	+	–	–	–	–	–	–	–
Trehalose	–	+	–	+s	+	+	+s	+
Cellobiose	+s	+	–	–	–	–	–	–
D-Xylose	+	+	–	–	v	–	v	–
Erythritol	+	+	+	–	–	–	–	–
D-Mannitol	+	+	+w	–	–	–	–	–

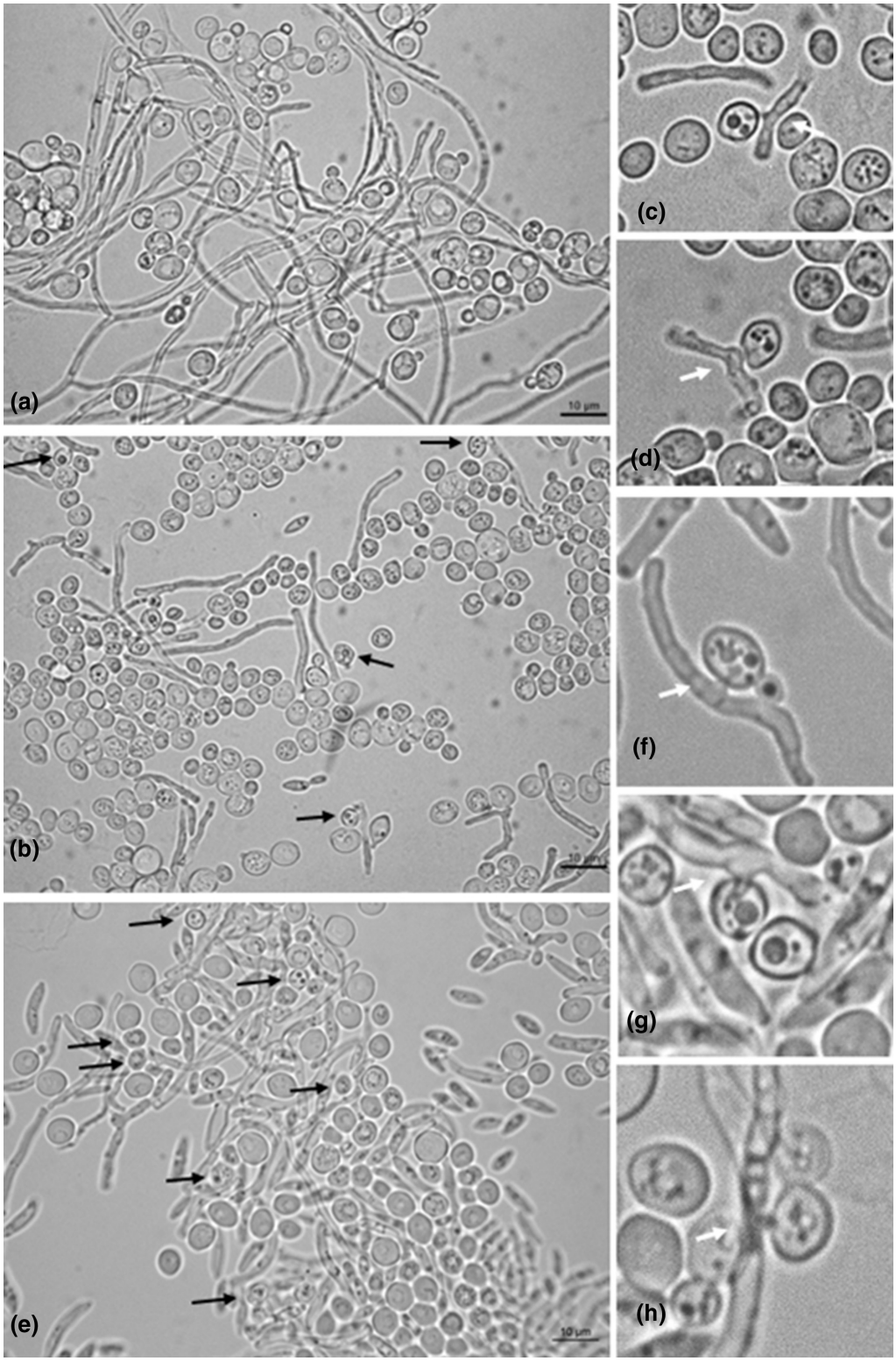

Fig. 5. Microscope images showing predation by *Saccharomycopsis praedatoria* against *Saccharomyces cerevisiae*. (a) In liquid medium, filamentous growth was observed, with no evidence of predation after 18 h of incubation. (b) On solid medium, after 18 h, several collapsed prey cells are observed attached to the predator thallus. (c, d) In detail, infection pegs inside prey cells after 18 h of incubation. (e, f, g, h) Predator–prey mixture after 44 h interaction showing abundant collapsed prey cells and active predation. Black arrows show collapsed prey cells. White arrows show infection pegs inside prey cells.

and negative for the latter species. *S. praedatoria* grew on maltose and sucrose whereas *S. fodiens* did not. The new species grew on erythritol and D-mannitol whereas *S. fermentans*, *S. javanensis*, *S. babjevae*, *S. schoenii* and *S. oosterbeekiorum* did not.

The new species was isolated from soil and rotting wood in the Amazonian rainforest biome. These substrates are not likely to represent the true niche of this species, where its occurrence is probably transient. Indeed, of 60 soil and 20 rotting wood samples collected in these sites, the new species was isolated only twice in soil and once in rotting wood. As some *Saccharomycopsis* species (*i.e.*, *S. fermentans*, *S. javanensis*, *S. schoenii* and *S. oosterbeekiorum*) were described based on isolates obtained from soil in different regions of the world [1, 33], an association with soil for *S. praedatoria* cannot be ruled out entirely at this time. The utilization of D-xylose by the yeast suggests that it may benefit from the degradation of lignocellulosic materials in soil. *Papiliotrema laurentii* and two candidates of new species related to *Candida inulinophila* and *Candida thaimueangensis* were also isolated from the sample that yielded UFMG-CM-Y6632. A possible new *Galactomyces* species, related to *Galactomyces geotrichum*, was isolated from the same sample that yielded UFMG-CM-Y6898. No other species were obtained from the sample that yielded UFMG-CM-Y6991.

Fig. 5 shows the interaction between the predatory strain UFMC-CM-Y6632 and its prey (*S. cerevisiae* UFMG-CM-Y7149). *Saccharomycopsis praedatoria* exhibits predominantly filamentous growth, and after 18 h of incubation of the predator-prey mixture on glucose–YNB without amino acids agar plates, several collapsed cells of *S. cerevisiae* could be observed. Infection pegs could also be seen inside the prey cells. In liquid medium, after the same incubation time, no interaction between predator and prey was observed. The three isolates of *S. praedatoria* were able to penetrate *S. cerevisiae* cells. Lachance and Pang [7] reported the requirement for actual cell contact for the occurrence of predation. Predation was monitored for 48 h in YNB without amino acids agar plates, during which time we observed an increase in the number of collapsed prey cells and abundant growth of the predatory strain. The use of amino acid-free medium was justified by the fact that *Saccharomycopsis* species share a deficiency in sulphate utilization, such that the absence of an organic sulphur source in the medium was expected to stimulate predatory activity. Penetration of prey cells could be observed over at least 48 h. Further studies are necessary to characterize the ability of *S. praedatoria* to kill other yeast species and explore its potential for biotechnological applications.

DESCRIPTION OF *SACCHAROMYCOPSIS PRAEDATORIA* A.R.O. SANTOS, BARROS, BATISTA, G.F.L. SOUZA, ALVARENGA, ABEGG, T.K. SATO, HITTINGER, LACHANCE & ROSA SP. NOV.

Saccharomycopsis praedatoria (prae.da.to'ri.a L. fem. adj. *praedatoria*, in reference to the predatory abilities of the species).

After 3 days on YM agar at 25°C growth is dull, tannish-white and butyrous to mycelial. Abundant true mycelium and blastoconidia are observed. Budding cells are ellipsoidal or elongate, 2.3–4.0×5.1–9.4 µm. Hyphae and pseudohyphae are observed on 5% malt agar, YM agar, 2% malt agar and V8 media after 1–2 days. Asci and spores are observed on 2% malt agar and V8 sporulation media after 4 days of incubation at 25°C. Asci are persistent, spheroidal, borne laterally or terminally on hyphae, and occur singly. Each ascus formed only one ascospore. Ascospores are spheroidal or ovoid and have an equatorial or subequatorial ledge (Fig. 2). Fermentation of glucose is negative. Assimilation of carbon compounds: glucose, sucrose, maltose, cellobiose (slow), L-sorbose, D-xylose, ethanol, glycerol, erythritol, ribitol, D-mannitol, D-glucitol, succinate, D-glucosamine (weak), xylitol and 2-propanol. No growth occurs on inulin, galactose, raffinose, melibiose, lactose, trehalose, melezitose, soluble starch, salicin, L-rhamnose, L-arabinose, D-arabinose, D-ribose, methanol, galactitol, *myo*-inositol, DL-lactate, citrate, D-gluconate, *N*-acetyl-D-glucosamine and hexadecane. Assimilation of nitrogen compounds: positive for lysine, negative for nitrate and nitrite. Growth in amino-acid-free medium is positive. Growth at 37 °C is negative. Growth on YM agar with 10% sodium chloride and medium with 50% glucose and 0.5% yeast extract is negative. Acid production is weak. Starch-like compounds are not produced. In 100 µg ml^{-1} cycloheximide, growth is positive. Urease activity is negative. Diazonium blue B reaction is negative.

The habitat is soil and rotting wood collected in Itacoatiara municipality, Amazonas state, Brazil. The holotype of *Saccharomycopsis praedatoria* sp. nov., CBS 16589^T, is preserved in a metabolically inactive state in the CBS Yeast Collection of the Westerdijk Fungal Biodiversity Institute, Utrecht, Netherlands. An isotype of *Saccharomycopsis praedatoria* sp. nov., UFMG-CM-Y6632, was deposited in the Collection of Microorganisms and Cells of the Federal University of Minas Gerais (Coleção de Microrganismos e Células da Universidade Federal de Minas Gerais, UFMG), Belo Horizonte, Minas Gerais, Brazil. It was isolated from soil samples collected in an Amazonian biome site of the municipality of Itacoatiara, Amazonas state. The MycoBank number is MB849369. The GenBank/EMBL/DDBJ accession numbers for ITS-5.8S region and the D1/D2 domains of the large subunit rRNA gene sequences of strain UFMG-CM-Y6632 are OQ641694 and OM321353, respectively. The Whole Genome Shotgun project of the authentic strain *S. praedatoria* UFMG-CM-Y6991 has been deposited at DDBJ/ENA/GenBank under accession JASJSC000000000. The version described in this paper is version JASJSC010000000.

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Conflicts of interest

The authors declare that there are no conflicts of interest.

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