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Sarcinomyces sideticae, a new black yeast from historical marble monuments in Side (Antalya, Turkey)

HACER B. SERT[1,2]*, HÜSEYIN SÜMBÜL[2] and KATJA STERFLINGER[1]

[1]*University of Natural Resources and Applied Life Sciences, Austrian Centre of Biological Resources and Applied Mycology (ACBR), Muthgasse 18, A1190 Vienna, Austria*
[2]*Department of Biology, Faculty of Arts and Sciences, Akdeniz University, TR-07058 Antalya, Turkey*

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A new species of *Sarcinomyces*, a melanized fungus with meristematic development, is described. On the basis of small subunit and internal transcribed sequence regions of ribosomal DNA sequencing, the new species was accommodated in the anamorph genus *Sarcinomyces* (Herpotrichiellaceae, Chaetothyriales) close to *S. petricola*. © 2007 The Linnean Society of London, *Botanical Journal of the Linnean Society*, 2007, **154**, 373–380.

ADDITIONAL KEYWORDS: Herpotrichiellaceae – phylogeny – rock-inhabiting fungi – taxonomy.

INTRODUCTION

In recent years, the interest in microfungi inhabiting the surface of stone monuments has increased considerably. Most of the fungi found on rock in arid and semi-arid environments belong to the form-group of so-called 'meristematic fungi' that are characterized by slowly expanding cauliflower-like colonies, reproducing by isodiametric enlargement of subdividing cells. Usually, these fungi have thick, multilayered cell walls, in which melanin is deposited (De Leo & Urzi, 2002; Selbmann *et al*., 2004). Some species also exhibit yeast stages. As the fungi isolated from stone and monuments in the Mediterranean have an *in situ* morphology similar to or even the same as that of fungi on desert rocks, described by Staley, Palmer & Adams (1982), the term 'microcolonial fungi' (MCF) is also applied to them. MCF are commonly isolated from marble and other calcareous rock types in nature and on monuments (Turian, 1977; Staley *et al*., 1982; Taylor-George *et al*., 1983; Wollenzien *et al*., 1995; Sterflinger & Krumbein, 1997), but also from plants (Middelhoven & de Hoog, 1997) and even from hypersaline environments (Zalar, de Hoog & Gunde Cimerman, 1999). They are the most harmful microorganisms associated with the biodeterioration of monuments (De Leo & Urzi, 2002). All of these taxa are able to endure extreme environmental conditions (Wollenzien *et al*., 1995; Sterflinger, 1998). Because of their very similar morphology, the correct identification of MCF is quite difficult using morphological methods. They have therefore been identified by sequencing the small subunit (SSU) and internal transcribed spacer (ITS) regions of ribosomal DNA (rDNA) (Sterflinger, 2000). Their phylogeny is quite diverse, being assigned to three different ascomycete orders: Dothideales, Chaetotyriales, and Pleosporales (Sterflinger, de Hoog & Haase, 1999).

In this paper, a new species of *Sarcinomyces*, *Sarcinomyces sideticae*, is described. The type strain was isolated from the temple of Apollo in Side (Antalya, Turkey) (Fig. 1), and identical strains were isolated from four different locations in Turkey: Side (Syedra), Termessos, Perge, and Trebenna.

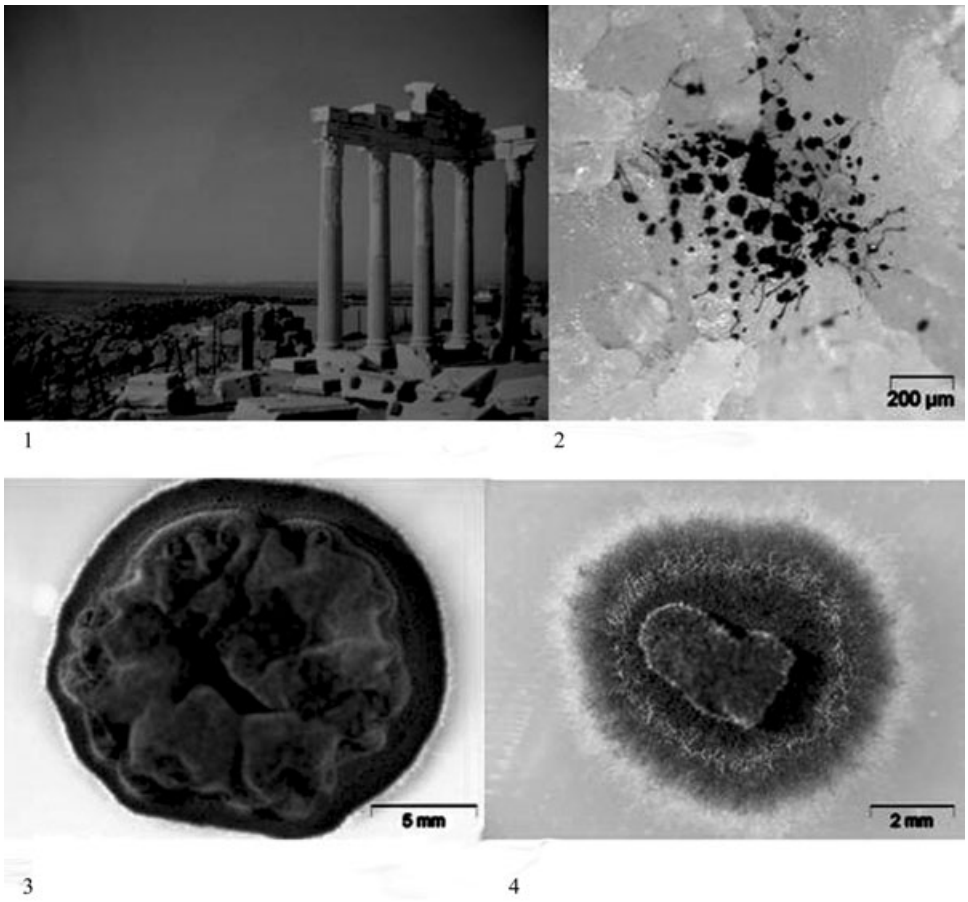
MATERIAL AND METHODS

SAMPLING AND MORPHOLOGICAL CHARACTERIZATION

Marble samples were taken, transferred to paper bags, and stored at room temperature. The fungi were isolated from the stone samples with a stereomicroscope by picking fungal colonies using needles (following Sterflinger & Krumbein, 1995). The black colonies

*Corresponding author. E-mail: hacersert@yahoo.de

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Figures 1–4. Fig. 1. The temple of Apollo from which samples were taken. Fig. 2. Macro-photograph of microcolonies on marble surface. Fungal growth after 1 month of incubation. Fig. 3. On malt extract agar. Fig. 4. On czapek agar.

(Fig. 2) were transferred to Petri dishes and two different media were used: (1) 2% malt extract agar (20 g malt extract, 1.0 g peptone, 20 g glucose, 20 g agar in 1 l of water); (2) dichloran rose bengal agar (Merck, Darmstadt, Germany). The plates were incubated at room temperature. The resulting colonies were picked up and purified by one to several transfers onto malt extract agar and czapek agar (Merck). For morphological characterization, mounts of the mycelium were prepared and observed with a light microscope.

The strains were conserved in the Austrian Centre of Biological Resources and Applied Mycology (ACBR) culture collection for further investigation.

DNA extraction

About 1 cm^2 of mycelium of 30-day-old cultures was transferred to a 1.5-ml Eppendorf tube containing 500 µl of lysing buffer and 200 µl of glass beads (425–600 mm; Merck). The mixture was shaken in a cell disrupter (Thermo Savant FastPrep, FP120, Holbrook, NY, USA) at full speed for 3 min. After incubation for 1 h at 65 °C, the mixture was shaken again at full speed for 3 min and then centrifuged for 15 min at 16 100 *g*. Subsequently, the supernatant was transferred to a new Eppendorf tube. RNAse (2.5 µl) was added, and the mixture was incubated for 1.5 h at room temperature. Finally, the DNA was prepared at 1 : 150 dilution for use in polymerase chain reactions (PCRs).

Polymerase chain reactions

Amplification was performed in 50-µl volumes containing 12.6 µl of template DNA, 30.57 µl of distilled water, 5.5 µl of buffer (1.1 µl $MgSO_4$, 2.75 µl dNTP), 0.35 µl of each primer, and 0.44 µl Taq DNA polymerase (Genekraft, Münster, Germany). NSO (TATCTGGTTGATCCTGCC) and ITS4 (TCCTCCG CTTATTGATATGC) primers were used. Samples were amplified through 40 cycles in an MJ Research PTC 200 thermocycler (MJ Research, Watertown, MA, USA) as follows: denaturation (94 °C, 30 s), annealing (55 °C, 30 s), extension (72 °C, 1 min), and final exten-

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sion (72 °C, 5 min). Amplicons were electrophoresed in 1.2% agarose gels (SeaKem LE Agarose, Cambrex Bio Science, Rockland, ME, USA) containing ethidium bromide for 0.5 h at 120 V in TAE buffer [40 mM Tris, 20 mM acetic acid, 1 mM ethylenediaminetetraacetic acid (EDTA), pH 8.3], and photographed for further analyses. The PCR products were purified using the Qiaquick PCR Purification Kit (Qiagen, Hilden, Germany).

Sequencing reaction

The cycle sequencing reactions were performed in 20-µl volumes containing 10 µl of distilled water, 6 µl of buffer (Big Dye Buffer), 2 µl of Big Dye RR Mix (Applied Biosystems, Nieuwerkerk a/d, Ijssel, The Netherlands), 1 µl of PCR product, and 1 µl of primer. The sequencing primers are listed in Table 1. Amplification was performed in an MJ Research PTC 200 thermocycler as follows: 96 °C for 30 s, 50 °C for 15 s, and 60 °C for 4 min (25 cycles). The products were purified using an Amersham Bioscience AutoSeq G-50 Purification Kit (Amersham Biosciences, Freiburg, Germany). Sequencing was performed on an ABI Prism automatic sequencer (Applied Biosystems, Foster City, CA, USA). Sequence assembly was performed using the Seqman program (Dnastar Inc., Madison, WI, USA). The sequences were then compared with the database of the National Center for Biotechnology Information (NCBI), Bethesda, MD, USA (BLAST search, http://www.ncbi.nlm.nih.gov/BLAST/). Sequences were deposited in the EMBL databank (Cambridge, http://www.ebi.ac.uk).

Table 1. List of sequencing primers and their positions

Primer	Sequence (5′–3′)	Corresponding position in 18S rDNA
NSO	TATCTGGTTGATCCTGCC	2–20
18/8	GTTGATAGGGCAGAAA	301–317
18/4	CTGCCCTATCAACTTT	305–321
18/20	GAATTACCGCGGCTGCTG	546–564
18/10	AAACGTCCTTGGCAAAT	942–959
18/1203	GAGTTTCCCCGTGTTGAG	1185–1203
18/11	CTTCCGCAGGTTCA	1776–1790
ITS4	TCCTCCGCTTATTGATATGC	26S
18/2	GGTAATTCCAGCTCCAATA	576–595
18/5	AGGTGAAATTCTTGGATT	897–915
18/1184	GACTCAACACGGGGAAACTC	1184–1204
ITS1	TCCGTAGGTGAACCTGCGG	1796–1815

Alignment and phylogenetic analysis

A preliminary automatic alignment was generated using Meg Align (Dnastar Inc.). On this basis, a more precise alignment was made manually using Clustal X (NCBI). The phylogenetic tree was constructed with the TREECON software package (Van de Peer & de Wachter, 1994) using the neighbour-joining method (Saitou & Nei, 1987) with Jukes & Cantor (1969) correction. One hundred bootstrap replicates were used for analysis.

RESULTS

Sarcinomyces sideticae was isolated from eight samples taken at four different sites in Turkey: Side, Termessos, Perge, and Trebenna (Table 2). Their identity was proven by morphological characters and on the basis of ITS I, ITS II, and 5.8S similarity, as described later.

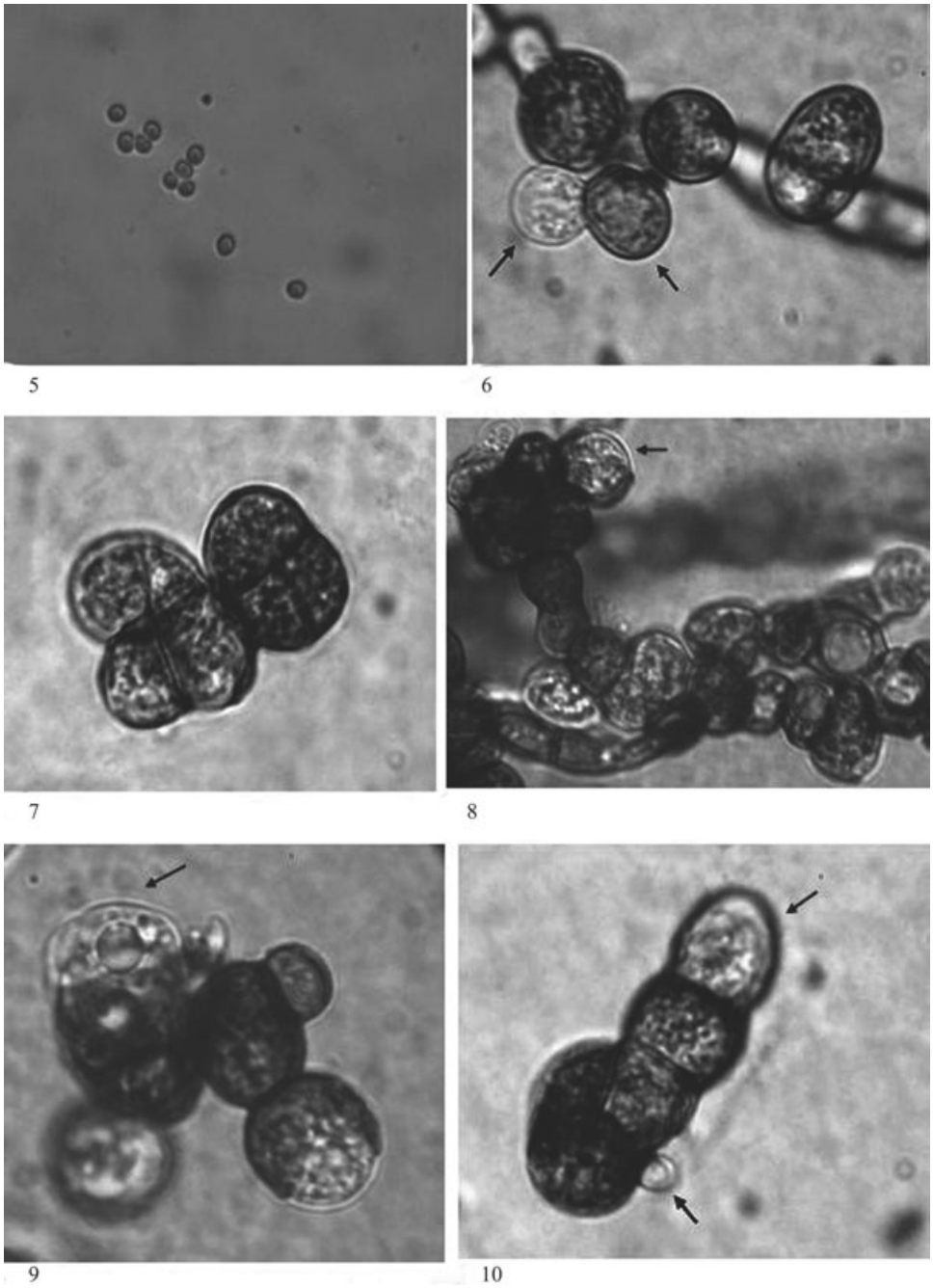
Colony morphology

Colonies on malt extract agar attaining about 20 mm in diameter in 4 weeks; dark grey to black, dry, initially soft, later hard; mature colonies consisting of pale grey aerial mycelium, cerebriform with age; margin sharp, slightly lobed (Fig. 3). Colonies on czapek agar attaining up to 10 mm in diameter in 4 weeks; soft, initially black, later becoming white to pale grey

Table 2. Strains of ***Sarcinomyces sideticae***, and places and monuments from which cultures were isolated

Strain	Place of sample	Monument
MA 4760, AJ972809 (Holotype)	Side	Temple of Apollo
MA 4629, AJ972810	Side	Eros sarcophagus
MA 4620, AJ972813	Perge	The marble relief (at the front of the theatre's stage)
MA 4563, AJ972814	Trebenna	The door of big grave
MA 4787, AJ972815	Trebenna	The small grave
MA 4665, AJ972811	Termessos	Temple of Artemis-Hadrian
MA 4770, AJ972816	Termessos	Gymnasium
MA 4660, AJ972812	Termessos	Necropolis

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Figures 5–10. Figs 5, 6. Yeast-like young cells (Fig. 5, ×1800; Fig. 6, ×3000). Fig. 7. Cells subdivided by septa (×3000). Fig. 8. Hyphal formation in 1-month-old culture (×3000). Fig. 9. Cells with disarticulation (×3000). Fig. 10. Mature conidia (×3000).

aerial mycelium; flat; margin fimbriate and irregular (Fig. 4).

MICROSCOPY

Young cells hyaline to olivaceous, single or in groups, smooth, thin- to thick-walled, 2–5 μm in diameter (Fig. 5), enlarging to 7–10 μm (Fig. 6). Later developing one or more oblique septa, becoming cells, which are pale brown, smooth, and thick-walled, ellipsoidal to spherical, about 12 μm in diameter (Fig. 7). Budding multilateral (Figs 6, 10). Initial elongated hyphae consisting of hyaline to olivaceous, thin- and smooth-walled cells about 4–8 μm wide and 7–15 μm long. Mature hyphae consisting of pale to dark brown to olivaceous, thin- to thick-walled cells about 12 μm wide

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and 14 μm long; gradually developing several transverse, longitudinal, and oblique septa; the individual cells finally arise by disarticulation. Cracks or splits occur in the outer cell walls (Figs 8–10).

DNA ANALYSIS

The taxonomic and phylogenetic position of *S. sideticae* was clarified on the basis of SSU and ITS regions of rDNA sequencing data. Eight morphologically similar strains of *S. sideticae* from four different locations were clustered according to their ITS I/5.8S/ITS II rDNA sequences with a strain that was isolated from calcareous rock on Mallorca by Ruibal *et al*. in 2004 (EMBL accession number: AY559335; data available at http://www.ncbi.nlm.nih.gov). Three strains (MA 4787, MA 4770, MA 4563) had 99% homology and two strains (MA 4665, MA 4660) had 98% homology with the strain from Mallorca. The holotype (MA 4760) and two other strains (MA 4629, MA 4620) had 92% similarity with the same strain. The 18S rDNA sequences of *S. sideticae* and *S. petricola* were found to differ in ten positions, corresponding to an 18S rDNA similarity of 99% (Table 3). Table 4 shows the morphological differences between *S. sideticae* and *S. petricola*.

Table 3. Differences in 18S rDNA sequences between the two species ***Sarcinomyces sideticae*** and *S. petricola*

Position	***S. sideticae***	*S. petricola*
45	C	T
201	G	A
269	T	C
543	G	A
577	G	T
932	G	R
1368	C	T
1718	G	C
1735	T	–
1736	G	–

A neighbour-joining tree based on 34 near-complete SSU rDNA sequences and, as an outgroup, *Saccharomyces cerevisiae* is presented in Figure 11. From SSU phylogeny data, *S. sideticae*, together with *S. petricola,* should belong to the Dothideales (Sterflinger *et al*., 1999). The results of sequencing of the ITS rDNA domain are presented in Figure 12. *S. sideticae* and identical strains clustered with the strain from Mallorca (AY559335). They were separate from *S. crustaceus*, *S. phaeomuriformis*, and *S. petricola*.

DISCUSSION

The genus *Sarcinomyces* was described by Lindner in 1898 for the strongly melanized species *S. crustaceus* Lindner and for the hyaline *S. albus* Lindner (Sigler, Tsuneda & Carmichael, 1981). Neither was designated as the type species. Clements & Shear (1931) listed only *S. crustaceus*. Because no type material remains, the identity of *S. albus* is uncertain (Sigler *et al*., 1981). *Sarcinomyces* species described to date have been found on several substrates. *S. crustaceus* was isolated from wood, *S. phaeomuriformis* Tad. Matsumoto, A.A. Padhye, Ajello & McGinnis from infected tissue, and *S. petricola* Wollenz. & de Hoog, as well as *S. sideticae*, from antique marble monuments in the Mediterranean area. *Sarcinomyces* species are phylogenetically distant (Sterflinger *et al*., 1999) and the genus is heterogeneous (Sigler *et al*., 1981). *S. sideticae* differs from all described species of *Sarcinomyces* in colony morphology, and, in particular, from *S. petricola* in the size of individual cells, young budding cells, and colony, and in mycelial growth and the amount of yeast cells (Table 4). Initially, colonies of *S. petricola, S. phaeomuriformis*, and *S. crustaceus* are slimy, buttery, and glossy (Sigler *et al*., 1981; Matsumoto *et al*., 1986; Wollenzien *et al*., 1997). In contrast, colonies of *S. sideticae* are soft, but never slimy. Colonies on malt extract agar are

Table 4. Morphological differences between ***Sarcinomyces sideticae*** and *S. petricola* (*S. petricola* data taken from Wollenzien *et al*., 1997)

Characteristic	*S. petricola*	***S. sideticae***
Colony feature	Slimy	Initially soft, later hard, not slimy
Colony diameter on malt extract agar	20 mm (in 2 months)	20 mm (in 1 month)
Colony diameter on czapek agar	10 mm (in 2 months)	10 mm (in 1 month)
Yeast cells	Preponderant	Not preponderant
Young budding cells	4.5–5.5 μm, finally 7–13 μm	2–5 μm, finally 12 μm
Hyphae	Present in old cultures	Present in old and young cultures
Hyphae	With limited growth	Most marked
Cells of hyphae	5 × 10 μm	Initially, 4–8 × 7–15 μm; mature, 12–14 μm

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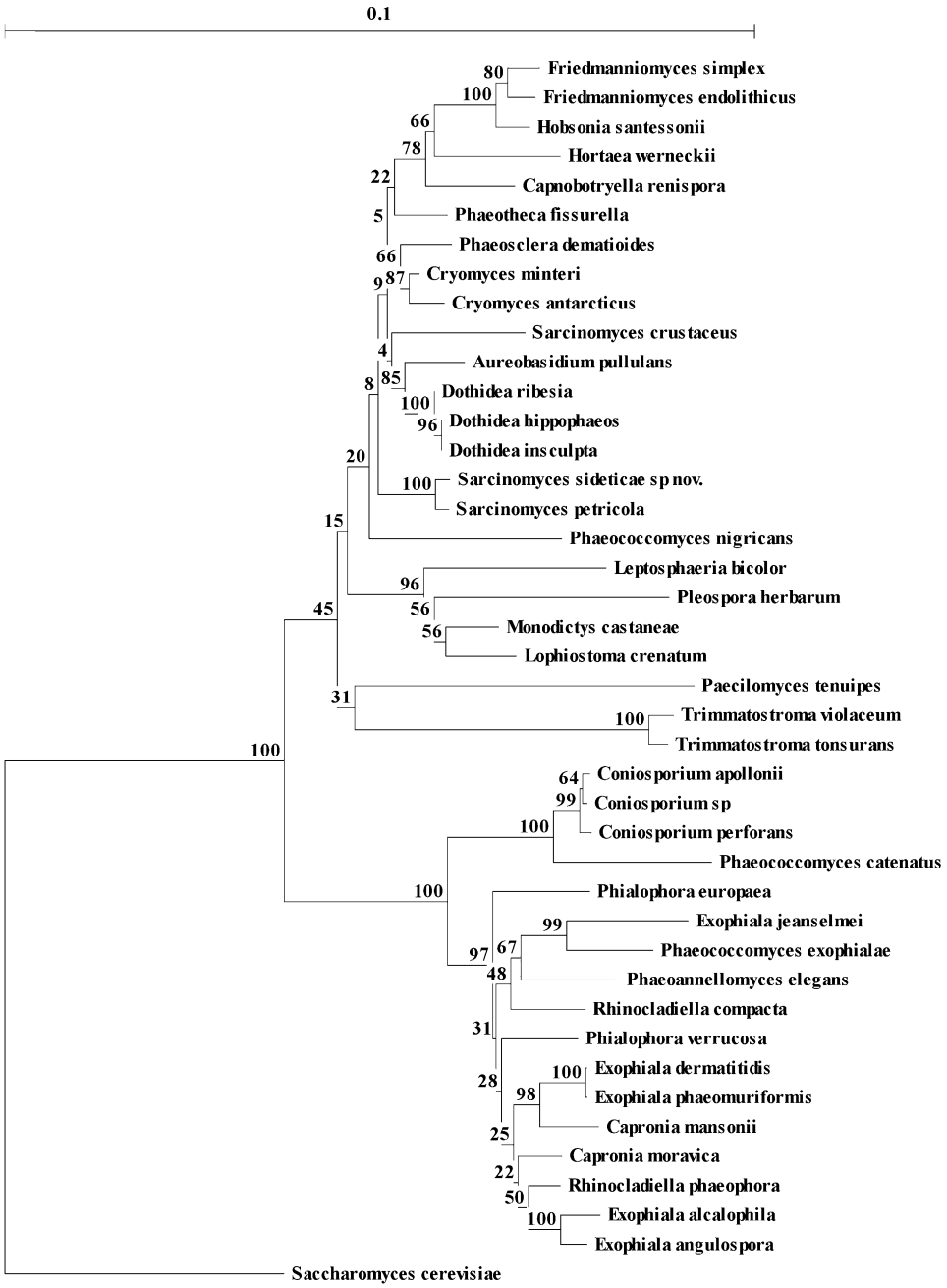


Figure 11. Consensus tree of 18S rDNA of 34 fungal species belonging to the ascomycete orders Dothideales, Pleosporales, and Chaetothyriales, *Saccharomyces cerevisiae* was used as outgroup.

Coniosporium Link-like, but SSU and ITS I, II/5.8S sequences show that the strain is clearly distinct from *Coniosporium* (Figs 11, 12). In many respects, the development and morphology of *Phaeococcomyces chersonesos* Bogomolova & Minter are similar to those of species of *Sarcinomyces*, and it is closest to *S. petricola* (Bogomolova & Minter, 2003). *S. sideticae* is also considered to be close to *S. petricola*. Mycelial growth in *P. chersonesos* was most marked on media, as in *S. sideticae*. This contrasts with *S. petricola*, where mycelial growth is very limited. Cells of hyphae are larger for *S. sideticae* than for *S. petricola and P. chersonesos*. In *P. chersonesos*, hyphae never disarticulate into individual cells, there is no obvious meristematic growth, and no bursting of the outer cell wand layer is observed. However, all of these features occur in the development of *S. sideticae* and *S. petricola*.

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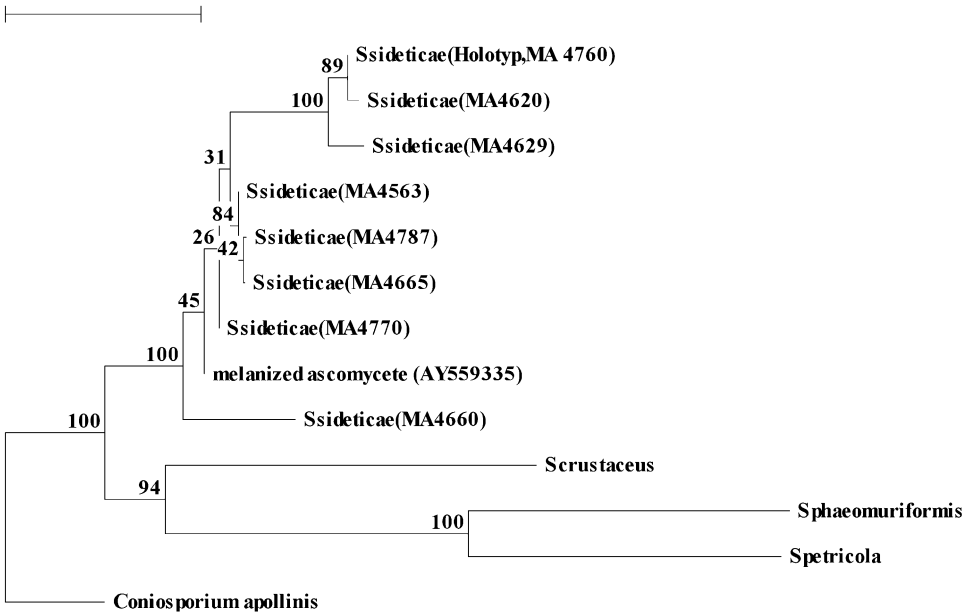


Figure 12. Consensus tree of 5.8S/ITS I and II rDNA of ***Sarcinomyces sideticae*** and identical strains (*Coniosporium apollinis* was used as outgroup.)

The masses of sclerotic cells formed by *S. sideticae* are morphologically reminiscent of the genus *Phaeotheca* Sigler *et al*. However, *Phaeotheca* produces endoconidia (de Hoog, Beguin & Batenburg-van de Vegte, 1997), which have not been observed in *Sarcinomyces*. Gradual enlargement of cell packets and final falling apart into individual cells and bursting of the outer cell wall of mature conidia are typical developmental characteristics of *Sarcinomyces*. Species of the meristematic genus *Sarcinomyces* have hitherto been defined on the basis of morphological, developmental, and molecular criteria. *S. petricola* was assessed on the basis of SSU restriction fragment length polymorphism (RFLP) data. Later, the identities of *S. phaeomuriformis*, *S. crustaceus*, and *S. petricola* were established using 18S/ITS I–II/5.8S rDNA sequence data. The analysis of ITS rDNA of the black yeast *Exophiala dermatitidis* (Kano) de Hoog revealed a close phylogenetic relationship with *S. phaeomuriformis*. As most strains of *S. phaeomuriformis* have a yeast-like phenotype corresponding to the anamorph genus *Exophiala* Kano, a new combination in *Exophiala* was proposed of *Exophiala phaeomuriformis* (Matsumoto, Padhye, Ajello & McGinnis) Matos, Haase & de Hoog (Matos *et al*., 2003). According to the SSU phylogenetic tree, the holotype (selected strain from cluster) is close to *S. petricola*. However, the phylogenetic tree based on 5.8S/ITS I–II sequencing shows that the strains of *S. sideticae* isolated in this study are phylogenetically distinct from the other *Sarcinomyces* species described to date. The sequencing of SSU is suitable for placement into the right classes, whereas ITS I is a taxonomic tool for species identification (de Hoog *et al*., 1999; Sterflinger, in press). The 5.8S and part of the ITS II region can close the gap between the species level (ITS I) and higher taxonomic levels, although the 5.8S gene sometimes indicates a higher heterogeneity than the ITS I region (de Hoog *et al*., 1999). Both *S. petricola* and *S. sideticae* are widely separated from *S. crustaceus* and *Exophiala phaeomuriformis* (former *S. phaeomuriformis*). The SSU phylogenetic trees published so far suggest a close relationship of the type species *S. crustaceus* to the Herpotrichiellaceae. However, its position is always solitary, and thus the exact phylogeny remains unclear. As a consequence, a revision of the genus *Sarcinomyces* based on its natural taxonomy is necessary.

CONCLUSIONS

The identity of *S. sideticae* as a new species was established by sequencing SSU and ITS regions of rDNA. The rDNA sequences did not show a degree of similarity to any sequence in GenBank that would have allowed it to be assigned to one of the existing species.

SARCINOMYCES SIDETICAE SERT & STERFLINGER, SP. NOV.

Coloniae in agaro maltoso 20 mm diam post 28 dies, atroschistaceae vel atrae, aridae, initio molles postea durae, margine acutae, leviter lobatae; cellulae juve-

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nales hyalinae vel olivaceae, socatae solum vel in circulis, parietes laeves et tenues vel crassi, 2–5 µm diam dein amplificantes usque 7–10 µm diam. Postea unum vel multa obliqua septa efficientes, cellularescentes, brunneas, parietes laeves et crassos, elipsoideas vel sphaericas, 12 µm diam. Gemmatio multilateralis. Hyphae elongatae hyalinae olivaceae; cellulae laevibus et tenuibus parietibus, 4–8 µm in latitudine et 7–15 µm in longitudine. Hyphae maturae brunneae vel olivaceae, tenuibus et crassis parietibus; cellulae 12 µm in latitudine et 14 µm in longitudine, gradatim septa multa transversalia, longitudinalia et obliqua efficientes, denique cellulas singulas orientes liberation. Habitat in templo Apollois in urbe Sidae.

Holotype: (MA 4760, AJ972809), in collectione ACBR, Vienna, Austria, et in collectione CBS, The Netherlands; isolatus ex Marmora, templa Apollo, Side/Antalya/Turkey.

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