Geotrichum bryndzae sp. nov., a novel asexual arthroconidial yeast species related to the genus Galactomyces

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Ten strains of an asexual arthroconidial yeast species were isolated from Bryndza, a traditional Slovak artisanal sheep cheese, which was manufactured from raw milk during a 4-month summer production period at two Slovakian sites (the northern Ružomberok and the central-southern Tisovec areas). Sequence comparison of the D1/D2 domains of the large-subunit rRNA gene revealed that this yeast represents a novel species of the genus Geotrichum, which contains anamorphs of the ascogenous genus Galactomyces, for which the name Geotrichum bryndzae sp. nov. is proposed (type culture CCY 16-2-1T = NRRL Y-48450T = CBS 11176T). The novel species is most closely related to Geotrichum silvicola NRRL Y-27641T, although yeasts with identical or very similar sequences have been found throughout the world.

The taxonomy of the arthroconidial ascomycetous genus Geotrichum Link: Fr. (Hemiascomycetes) is still being developed, although these yeast-like fungi have been studied quite extensively by conventional taxonomy as well as by DNA sequence comparisons (de Hoog et al., 1986; Smith et al., 2000; Naumova et al., 2001; Smith & Poot, 2003; de Hoog & Smith, 2004). Geotrichum represents the anamorphic state of species of the genera Dipodascus Lagerheim and Galactomyces Redhead & Malloch (de Hoog et al., 1998a, b), as demonstrated by sequence divergence of the rRNA subunits (Kurtzman & Robnett, 1998; Ueda-Nishimura & Mikata, 2000). Until 1998, the genus Geotrichum contained 11 species, five of which have their teleomorph in the genus Dipodascus and two in the genus Galactomyces, while the remaining four species have no known sexual state (de Hoog et al., 1998a, b). Since 1998, several revisions have been suggested and novel species have been proposed (Naumova et al., 2001; de Hoog & Smith, 2004). Less closely related Dipodascus species from the so-called group 2 clade were renamed Magnusiomyces, with the anamorph for this genus being Saprobysaete (de Hoog & Smith, 2004).

Kurtzman & Robnett (1998) determined that domains 1 and 2 (D1/D2) (~600 nt) of the large-subunit rRNA gene are sufficiently variable to resolve individual biologically defined species. They also reported the sequences of all known ascomycetous yeasts, and Fell et al. (2000) published the D1/D2 sequences of known basidiomycetous yeasts. From these extensive data, Kurtzman & Robnett (1998) deduced simple rules, which generally defined strains showing 6 or more non-contiguous substitutions (1%) as likely to represent separate species (Kurtzman, 2006). Currently, the only exception to this prediction is among interfertile strains of Clavispora lisitaniae, which are unusually polymorphic in a 90 bp region of the D2 domain (Lachance et al., 2003).

Recently, DNA sequence comparison has allowed the description of two novel species, Geotrichum silvicola (Pimenta et al., 2005) and Geotrichum vulgare (Wuczkowski et al., 2006).

During a survey of yeasts and fungi associated with Bryndza, a traditional Slovak artisanal sheep cheese, we isolated ten strains of asexual arthroconidial yeasts...
identified by conventional taxonomy as *Galactomyces/Geotrichum* strains. These yeasts were found in all Bryndza samples collected from two dairies located in different geographical regions during the summer of 2003 (June–September). Sequence comparison of the D1/D2 domains of the large-subunit rRNA gene revealed that these isolates belong to the same novel *Geotrichum* species (Laurencík et al., 2008), related to *Geotrichum silvicola* (Pimenta et al., 2005).

### Isolation and characterization of yeasts

The strains described in this study were isolated from samples of Brynda collected from two dairies, one located in Ružomberok, in the north of Slovakia (49° 04′ 45″ N 19° 18′ 09″ E; altitude 464 m), and the other in Tisovec, in central-southern Slovakia (48° 34′ 31″ N 19° 57′ 04″ E; altitude 310 m). Monthly samples were taken during June–September 2003, 14 days after clothing, and they were transported immediately to the laboratory, maintained at 4 °C and analysed in triplicate within 24 h. Detailed isolation procedures were described by Laurencík et al. (2008). Yeasts were characterized by standard methods (Yarrow, 1998) and identified using the keys of Kurtzman & Fell (1998) and Barnett et al. (2000). Their ability to form ascii was examined on sporulation media [Gorodkowa agar, 5 % malt extract agar, cornmeal agar, McClary’s acetate agar and yeast sporulation medium (0.1 % yeast extract, 5 % malt extract agar, cornmeal agar, McClary’s cerevisiae)].

### DNA sequence analysis

Cultivation, DNA extraction and PCR were carried out as described by Laurencík et al. (2008). Briefly, the divergent D1/D2 domain (nucleotides 63–642 for *Saccharomyces cerevisiae*) at the 5′ end of the rRNA gene of the cytoplasmic large ribosomal subunit was amplified by PCR with primers NL1 (5′-GCATATCAATAAGCGGAGGAAAAG) and NL4 (5′-GGTCCGTTTTCGAGACGG) as described by Kurtzman & Robnett (1998). To obtain clear sequences, PCR products were cloned in the pCR-Blunt II-TOPO vector of the Zero Blunt TOPO PCR Cloning kit (Invitrogen) according to the manufacturer’s instructions.

Mitochondrial DNA (mtDNA) was prepared by a modification of the original protocol described by Defontaine et al. (1991). Parts of the gene for the small rRNA subunit (*rns*) were amplified by two sets of primers, SSU1 (5′-CTATCGCAGCTCCGTTAATAC) plus SSU2 (5′-GGA-TATCGAATTAAATAACATGCCTCCACTG) and SSU3 (5′-CAGTGGGAGCTGTTAATTCGATAATCC) plus SSU5 (5′-CAAGTTCCCTACAGTAACTGTATTTCACATT), in 36 PCR cycles of denaturation at 94 °C for 1 min, annealing at 52 °C for 1 min and extension at 72 °C for 2 min.

Individual PCR products and those cloned in plasmids were purified with the Novagen SpinPrep Gel DNA kit or Qiagen Plasmid Mini kit (Qiagen). Purified DNA was sequenced directly with one of the amplification primers (or sequencing primers −21M13F or −48M13R) using an Applied Biosystems BigDye Terminator v3.1 cycle sequencing kit and ABI3100-Avant Genetic Analyzer (Applied Biosystems). Sequences were edited in CHROMAS version 1.45 and compared with the NCBI database (http://www.ncbi.nlm.nih.gov/) by the BLASTn program (Altschul et al., 1990, 1997).

The sequences were aligned with the CLUSTAL W multiple sequence alignment program included in the CLUSTAL_X 1.8 package (Thompson et al., 1997). Rooted phylogenetic trees were constructed with the neighbour-joining method of the CLUSTAL_X 1.8 package. The stability of individual branches was assessed by the bootstrap method (Felsenstein, 1988), and numbers given at nodes are scores with which a given internode appeared in 1000 bootstrap replicates.

The number of nuclei was examined by DAPI staining, according to the specific fluorescence pattern as previously described (Marinoni et al., 1999), using a fluorescent microscope equipped with a DAPI optical filter.

### Classification and ecology

Typical characteristics for the members of *Galactomyces/Dipodascus/Geotrichum* clade and also for the novel strains are the assimilation of D-glucose, D-galactose, L-sorbose, glycerol, D-lactate, succinate and ethanol as carbon sources. Some differences were observed when the novel species was compared with *Galactomyces geotrichum*. The novel species does not use ribitol or D-mannitol. In order to separate the novel species from *Geotrichum silvicola*, its closest relative, assimilation of D-glucitol and D-glucosamine can be used; *Geotrichum silvicola* assimilates D-glucitol and does not assimilate D-glucosamine.

The anamorphic species of the genus *Geotrichum* can be distinguished from their teleomorphs in the genera *Dipodascus* and *Galactomyces* by their inability to form ascii. However, typical ascii were not found after cultivation on the most common yeast sporulation media. In contrast, *Galactomyces geotrichum* NRRL Y-17569T produced a number of spherical ascii, each containing a single spore which can be seen on DAPI staining (not shown).

The large-subunit rRNA gene D1/D2 domain sequence was analysed for five of the ten novel isolates. Three strains provided identical sequences and the other two isolates had single and double nucleotide polymorphisms in different positions. The DNA polymorphism was confirmed by sequencing of PCR products cloned in pCR-Blunt II-TOPO. Sequence comparison with the GenBank database revealed 12 nucleotide differences in a 545 bp sequence from *Galactomyces geotrichum* NRRL Y-17569T and 16 substitutions in comparison with *Galactomyces* sp. NRRL Y-6418 (Kurtzman & Robnett, 1998). Additionally, the DNA sequence exhibited variation in 18 nucleotides from...
the sequence of the type strain of the recently described species *Geotrichum vulgare* (Wuczkowski et al., 2006) and 6 substitutions in 542 nucleotides from the sequence of the type strain of *Geotrichum silvicola* (Pimenta et al., 2005).

When the rate of divergence and the inability to form ascii are considered together, the isolate found in Bryndza is most likely an anamorphic form of a novel *Geotrichum* species.

Phylogenetic analysis of the *Dipodascus* clade (Kurtzman & Robnett, 1998) involving the novel species supported this conclusion, especially when the high bootstrap values show clear separation on the phylogenetic tree for all the lineages (Fig. 1). The novel species belonged to a clade of several *Galactomyces* species. Kurtzman & Robnett (1998) suggested that there is no basis for maintaining the separate genera *Galactomyces* and *Dipodascus*, as they are phylogenetically intertwined. However, Naumova et al. (2001) have disagreed because of the common mating type system and the high DNA–DNA reassociation.

A high degree of divergence was also shown by two sequences obtained from mitochondrial DNA (rns gene), where 12 substitutions in the 504 bp amplified segment and 12 substitutions in the second 350 bp PCR product were found when the sequences of strain CCY 16-2-1 T and 12 substitutions in the 504 bp amplified segment where 12 substitutions in the 504 bp amplified segment were found when the sequences of strain CCY 16-2-1 T and 12 substitutions in the 504 bp amplified segment were found when the sequences of strain CCY 16-2-1 T were aligned with those of *Galactomyces geotrichum* (GenBank accession numbers EU429455 and EU429456) and *Geotrichum vulgare* (Pimenta et al., 2006) and 6 substitutions in the 250 bp PCR product were found when the sequences of strain CCY 16-2-1 T were aligned with those of *Galactomyces geotrichum* (GenBank accession numbers EU429455 and EU429456) and *Geotrichum vulgare* (Pimenta et al., 2006) and 6 substitutions in the 250 bp PCR product were found when the sequences of strain CCY 16-2-1 T.

*Galactomyces*/*Geotrichum* species are quite ubiquitous since they are involved in biodegradation and depollution. They are recognized as an integral part of the microbiota of some food products. In particular, *Geotrichum candidum* is naturally present in raw milk (Desmasures et al., 1997) and it has long been accepted to be an important component of the microbiota of soft cheeses such as Camembert and semi-fresh goat’s and ewe’s milk cheeses (reviewed by Boutrou & Guéguen, 2005). Yeasts with the same D1/D2 sequence as the novel strains identified in Bryndza cheese have been found in Asia among cow rumen microbiota (uncultured fungus clone FE24) and also in Chinese koji (daqu) (GenBank accession no. DQ912852; not shown in Fig. 1). Conspecific strains (with minor divergences in the sequence) are preserved in the Chinese Industry Culture Collection (GenBank accession no. DQ912846) and among microbes degrading fats and oils in Vietnam (DQ377646).

On the basis of the results presented here, a novel species of the genus *Geotrichum* is described to accommodate these strains from Bryndza cheese. *Geotrichum bryndzae* sp. nov.

**Latin diagnosis of Geotrichum bryndzae Sulo, Laurencík, Poláková, Minárik and Sláviková sp. nov.**


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**Fig. 1.** Phylogenetic tree of the *Dipodascus* clade containing the novel species *Geotrichum bryndzae*. Neighbour-joining tree based on nucleotide sequences of the D1/D2 region in the 26S rRNA gene of the novel *Geotrichum* species and its relatives from the *Dipodascus* clade (Kurtzman & Robnett, 1998). The tree also includes the recently described species *Geotrichum vulgare* (Wuczkowski et al., 2006) and *Geotrichum silvicola* (Pimenta et al., 2005). Branch lengths are proportional to nucleotide differences and numbers at nodes are frequencies of a given branch appearing in 1000 bootstrap replications (frequencies under 50 % not given). The outgroup in this analysis was *Schizosaccharomyces pombe* NRRL Y-12796T. Bar, 2 % sequence divergence.
CCY 16-2-1<sup>T</sup> (=NRRL Y-48450<sup>T</sup> =CBS 11176<sup>T</sup>), collectione zymotica Culture Collection of Yeasts in the Institute of Chemistry, Slovak Academy of Sciences.

Description of Geotrichum bryndzae Sulo, Laurenčík, Poláková, Minárík and Sláviková sp. nov.

Geotrichum bryndzae (brynd’zae. N.L. gen. n. bryndzae of Bryndza, a traditional Slovak artisanal raw sheep milk cheese, the source of isolation of the first strains).

After 7 days on malt extract-yeast extract agar at 25 °C, colonies are white, flat, dry and powdery to finely hairy. Arthroconidia are abundantly present (Fig. 2). The hyphae are 3–7 μm wide with early disarticulation into cubic arthroconidia containing mostly three or four nuclei. Arthroconidia are 5.8–6.6 μm wide and 6.6–13.2 μm long. Abundant true mycelium and arthroconidia are formed on slide cultures with potato dextrose agar after 1 week. Glucose is not fermented. The following carbon compounds are assimilated: D-glucose, D-galactose, D-xyllose, L-sorbose (weak), D-gluucosamine (weak), glycerol, 2-keto-D-glucurate (weak), DL-lactate, succinate, citrate (weak), ethanol, propane-1,2-diol and butane-2,3-diol. No growth on D-ribose, L-arabinose, D-arabinose, L-rhamnose, maltose, 3,3'-trehalose, cellobiose, salicin, arbutin, melibiose, sucrose, lactose, raffinose, melezitose, inulin, starch, erythritol, ribitol, xylitol, L-arabinotol, D-mannitol, glucitol, galactitol, myo-inositol, D-glucono-1,5-lactone, 5-keto-D-gluconate, D-glucurate, D-glucurionate or methanol. Ethylamine and cadaverine are assimilated, but not nitrate, nitrite or lysine. Growth in a vitamin-free medium is positive. Exhibits good growth at 28 °C, weak and variable growth at 37 °C and no growth at 42 °C. There is also no growth in 50% glucose. Growth occurs at 0.01% cycloheximide, while growth at 0.1% is variable. Urease activity is negative; does not produce starch or extracellular amyloid compounds.

The type strain is CCY 16-2-1<sup>T</sup> (=NRRL Y-48450<sup>T</sup> =CBS 11176<sup>T</sup>), which is deposited in the Culture Collection of Yeasts in the Institute of Chemistry, Slovak Academy of Sciences, Bratislava, Slovakia. The Mycobank accession number is MB 512675.

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References


