Taxonomic studies on the genus Cystofilobasidium: description of Cystofilobasidium ferigula sp. nov. and clarification of the status of Cystofilobasidium lari-marini

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A new species of the genus Cystofilobasidium is described as Cystofilobasidium ferigula sp. nov. The new taxon represents the teleomorphic stage of Cryptococcus ferigula and was obtained in mating experiments using three strains deposited in the Portuguese Yeast Culture Collection (mating types A1) and a recent isolate (mating type A2). Cystofilobasidium ferigula is characterized using an integrated approach encompassing morphological studies, investigation of the ultrastructure of the septal pore, a comparative study of physiological traits, determination of the DNA base composition, DNA reassociation experiments and PCR fingerprinting. During the course of this study, a close similarity of microsatellite-primed PCR fingerprints was detected between Cystofilobasidium lari-marini and Cystofilobasidium capitatum. DNA-DNA reassociation experiments gave high homology values, which indicates that Cystofilobasidium lari-marini must be regarded as a synonym of Cystofilobasidium capitatum.

Keywords: heterobasidiomycetes, basidiomycetous yeasts, systematics, Cystofilobasidiales, Cystofilobasidium ferigula sp. nov.

INTRODUCTION

The heterobasidiomycetous genus Cystofilobasidium Oberwinkler et Bandoni (Oberwinkler et al., 1983) was created to accommodate two teliospore-producing yeasts previously classified in Rhodosporidium Banno, namely Cystofilobasidium bisporidii (Fell, Hunter et Tallman) Oberwinkler et Bandoni and Cystofilobasidium capitatum (Fell, Hunter et Tallman) Oberwinkler et Bandoni. Members of the genus Cystofilobasidium produce Filobasidium-like basidia, i.e. holobasidia each having a narrow central region and a swollen apex (Oberwinkler et al., 1983), whereas in Rhodosporidium the basidia are tubular and transversely septate. At present, the genus Cystofilobasidium includes four species: three are pink-coloured and one is cream-coloured. The pigmented species are the two mentioned above and Cystofilobasidium infirmominiatum (Fell, Hunter et Tallman) Hamamoto, Sugiyama et Komagata (Hamamoto et al., 1988), also transferred from Rhodosporidium. More recently, Cystofilobasidium lari-marini (Saëz et Nguyen) Fell et Statzell-Tallman (cream-coloured) was transferred from Leucosporidium Fell, Statzell, Hunter et Phaff (Fell & Statzell-Tallman, 1992).

The order Cystofilobasidiales (Fell et al., 1999) was proposed on the basis of studies of 26S rDNA sequences. This order includes two teleomorphic genera, Cystofilobasidium and Mrakia Yamada et Komagata, the anamorphic genus Udeniomyces Nakase et Takematsu and three species of Cryptococcus Vuillemin, viz. Cryptococcus aquaticus (Jones et Slooff) Rodrigues de Miranda et Weijman, Cryptococcus ferigula (corrig.) Saëz et Rodrigues de Miranda and Cryptococcus macerans (Frederiksen) Phaff et Fell. According to Fell et al. (1999), the Cystofilobasidiales clade includes two subclades, the Mrakia subclade and the Cystofilobasidium subclade. The latter group includes all known species of Cystofilobasidium and also Cryptococcus ferigula and Cryptococcus macerans.

Abbreviation: CMA, corn meal agar; UPGMA, unweighted pair group method using arithmetic averages.

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Cryptococcus ferigula is a pink yeast originally found in the oral cavity of several wild animals kept in captivity (Saëz & Rodrigues de Miranda, 1988). This report presents the description of the sexual state of Cryptococcus ferigula and the consequent proposal of a new species of the genus Cystofilobasidium. Our studies also revealed that Cystofilobasidium lari-marini should be considered as a synonym of Cystofilobasidium capitatum.

METHODS

Yeast cultures. The list of strains used in this study, and relevant information, is shown in Table 1.

Morphological and physiological characterization. Physiological and biochemical characterization was performed according to the techniques described by Yarrow (1998). Additional assimilation tests were performed using aldaric acids and aromatic compounds as described by Fonseca (1992) and Sampaio (1994), respectively. All assimilation tests were performed twice, in separate experiments. The results of the 78 tests selected by Sampaio & Fonseca (1995) were used to calculate the overall similarity of physiological and biochemical profiles, employing numerical taxonomy methods (the data matrix is available upon request). The similarity between strains was estimated using the simple-

matching coefficient and cluster analysis was performed using the UPGMA (unweighted pair-group method using arithmetic averages) algorithm (Sneath & Sokal, 1973). These analyses were computed using the NTSYS-pc software package, version 2.0 (Rolf, 1998). For microscopy, cultures were grown at room temperature on YM agar (Yarrow, 1998) or on corn meal agar (CMA) and studied with phase-contrast optics.

Ultrastructure. For transmission electron microscopy, samples were fixed overnight in 2 % glutaraldehyde in 0·1 M sodium cacodylate buffer at pH 7.2. After six transfers in 0.1 M sodium cacodylate buffer, the material was post-fixed in 1% osmium tetroxide in the same buffer for 2 h in the dark, washed in distilled water and stained in 1% aqueous uranyl acetate for 1 h in the dark. After five washes in distilled water, samples were dehydrated in acetone, using 10 min changes at 25, 50, 70 and 95 % (v/v), and three times in 100% acetone. The material was embedded in Spurr's plastic (Spurr, 1969). Serial sections (65–75 nm) were cut with a Reichert-Jung Ultracut E (Leica) equipped with a diamond knife. Sections were mounted on Formvar-coated, single-slot, copper grids, stained with lead citrate (Reynolds, 1963) at room temperature for 3-5 min and washed again with water. The thin sections were examined at 80 kV with a Zeiss EM 109 transmission electron microscope.

Determination of DNA base composition and DNA reassociation experiments. For DNA isolation, strains were

Table 1. List of strains studied in this work

Culture collections are abbreviated as: IGC, Portuguese Yeast Culture Collection, FCT-UNL, Caparica, Portugal; CBS, Centraalbureau voor Schimmelcultures, Yeast Division, Delft, The Netherlands; FO, personal collection of F. Oberwinkler, University of Tübingen, Germany; ZP, personal collection of J. P. Sampaio.

Species	Strain	Strain origin	Isolation source	Observations
Cryptococcus macerans	IGC 2869 ^T	CBS 2206 ^T	Dew-retted flax straw, Denmark	
Cryptococcus macerans	IGC 4482		Flower of Cineraria sp., Oeiras, Portugal	
Cryptococcus macerans	IGC 4737		Grasshopper, Sintra, Portugal	
Cystofilobasidium bisporidii	IGC 4415 ^T	CBS 6346 ^T	Seawater, Antarctic Ocean	Mating type A1B1
Cystofilobasidium capitatum	IGC 4418 ^T	CBS 6358 ^T	Zooplankton, Antarctic Ocean	Self-sporulating
Cystofilobasidium capitatum	IGC 4309	FO 31572.a	Gleba of <i>Phallus impudicus</i> , Tübingen, Germany	Self-sporulating
Cystofilobasidium capitatum	IGC 5626	ZP 317	Trifolium sp. leaf infected with rust, Sesimbra, Portugal	Self-sporulating
Cystofilobasidium capitatum	IGC 5627	ZP 327	Contaminant of MYP agar plate, Caparica, Portugal	Self-sporulating
Cystofilobasidium ferigula	IGC 5359 [™]	CBS 7202 ^T	Dead male <i>Papio papio</i> (baboon), Paris Zoological Gardens, France	Mating type A1
Cystofilobasidium ferigula	IGC 4410	CBS 7201	Rhea americana (rhea), Paris Zoological Gardens, France	Mating type A1
Cystofilobasidium ferigula	IGC 4410-I		_	Colourless variant of IGC 4410
Cystofilobasidium ferigula	IGC 5540	CBS 6954	Sawdust (locality of isolation unknown)	Mating type A1
Cystofilobasidium ferigula	IGC 5628	ZP 322	Contamination of home-made sauerkraut, Caparica, Portugal	Mating type A2
Cystofilobasidium infirmominiatum	IGC 3955 [™]	CBS 323^{T}	Air, Japan	Mating type A1
Cystofilobasidium infirmominiatum	IGC 4414	CBS 2204	Deep-frozen vegetables, The Netherlands	Mating type A2
Cystofilobasidium lari-marini	IGC 4530 ^T	CBS 7420 ^T	Larus marinus (Great black-backed gull), France	Self-sporulating

Table 2. Physiological characterization of strains of Cystofilobasidium ferigula

Growth is scored as: +, positive; -, negative; D, delayed; D, weak. All four strains gave positive results for utilization of the following compounds: D-glucose, D-glucose, D-gluconic acid, D-glucosamine, sucrose, maltose, methyl D-glucoside, melibiose, lactose, raffinose, melezitose, inulin, soluble starch, erythritol, galactitol, D-lactic acid, succinic acid, D-tartaric acid, m-tartaric acid, mucic acid, methanol, vanillyl alcohol, veratryl alcohol, vanillic acid, veratric acid, ferulic acid, syringic acid, sinapic acid, cinnamic acid, benzoic acid, D-hydroxybenzoic acid, D-hydroxybenzoic acid, D-hydroxybenzoic acid, protocatechuic acid, catechol, gallic acid, salicylic acid, gentisic acid, D-coumaric acid, caffeic acid, phenol and guaiacol. All four strains gave the same results for the following nitrogen compounds (responses are in parentheses): potassium nitrate D-sodium nitrite D-sodium nitrite D-sodium nitrite D-sodium additional tests (responses are in parentheses): growth in vitamin-free medium D-sodium D-south with D-sodium D-south at 30 D-south at 35 D-sodium nitrite D-south at 35 D

Characteristic	IGC 5359 ^T	IGC 4410	IGC 5540	IGC 5628	
Utilization of:					
D-Ribose	DW	DW	_	DW	
D-Xylose	+	D	D	+	
D-Arabinose	+	+	_	-	
α,α-Trehalose	+	DW	DW	+	
Glycerol	_	-, DW	_	_	
Ribitol	_	_	-	-, D	
Xylitol	_	_	-	-, DW	
D-Glucitol	+	D	D	+	
Citric acid	DW	_	D	D	
L-Malic acid	_	-, +	_	_	
Growth with 0.01 % cycloheximide	_	_	_	D	

grown for 3–4 d at 22 °C in shaken YM broth (initial pH 8). Cells were ruptured using a hydraulic cell press and the DNA was purified using the method of Britten *et al.* (1970). The nuclear DNA base composition was determined by following the method of Marmur & Doty (1962) with a Gilford Response UV-VIS spectrophotometer and its Thermal Programming software with nDNA from *Candida parapsilosis* (Ashford) Langeron *et* Talice IGC 2545° (= CBS 604°) (G+C content = 40·2 mol%) as a reference. For DNA–DNA reassociation experiments, the same instrument was used and the methods of Seidler & Mandel (1971), as modified by Kurtzman *et al.* (1980), were followed.

PCR fingerprinting. Cultures grown on MYP agar were suspended in 500 μ l lysing buffer (50 mM Tris/HCl, 250 mM NaCl, 50 mM EDTA, 0·3 % SDS, pH 8) and glass beads (425–600 μ m; Sigma) equivalent to a volume of 200 μ l were added. After being vortexed for 3 min, the tubes were incubated for 1 h at 65 °C. The suspensions were then centrifuged for 30 min at 4 °C. Nucleic acids were precipitated during 24 h at -20 °C with a 0·1 vol 3 M sodium acetate and 2 vols absolute ethanol. Finally, the DNA was washed with ethanol (70%), vacuum-dried and then resuspended in TE (100 mM Tris/HCl, pH 8, 100 mM EDTA).

The primer (GTG)₅ (Meyer *et al.*, 1993), synthesized by Pharmacia Amersham Biotech, was used for the microsatellite-primed PCR experiments. PCR reactions were performed in 25- μ l reaction volumes containing 1 × PCR buffer (Pharmacia Amersham Biotech), 2 mM each of dATP, dCTP, dGTP and dTTP (Promega), 0·8 μ M primer, 10–15 ng genomic DNA and 1 U *Taq* DNA polymerase

(Pharmacia Amersham Biotech). Amplification was performed in a Uno II Thermal Cycler (Biometra) and consisted of an initial denaturation step at 95 °C for 5 min, followed by 40 cycles of 45 s at 93 °C, 60 s at 50 °C and 60 s at 72 °C and then a final extension step of 6 min at 72 °C. A negative control, in which DNA was replaced by sterile distilled water, was also included. Amplified DNA fragments were separated by electrophoresis in 1.4% agarose gel (Gibco), in 0.5 × TBE (Tris/borate/EDTA) buffer at 90 V for 3.5 h and stained with ethidium bromide. On each gel, a molecular size marker was used for reference (λDNA cleaved with HindIII and ΦX174 DNA cleaved with HaeIII; Pharmacia Amersham Biotech). DNA banding patterns were visualized under UV transillumination and images were obtained using a Kodak Digital Science EDA 120 system and the Kodak Digital Science 1D Image Analysis software. DNA banding patterns were analysed using the GELCOMPAR software package, version 4.1 (Applied Maths). Similarities among isolates were estimated using the Dice coefficient and the clustering was based on UPGMA.

RESULTS AND DISCUSSION

A pink yeast strain (IGC 5628), isolated by us from home-made sauerkraut, was identified (on the basis of standard yeast identification tests) as *Cryptococcus ferigula*. Crossing experiments performed on CMA revealed that IGC 5628 was sexually compatible with the type strain of this species. The teleomorph of *Cryptococcus ferigula* is described as a new species of the genus *Cystofilobasidium*.

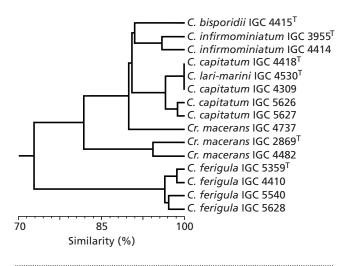


Fig. 1. Phenogram of Cystofilobasidium (C.) and Cryptococcus (Cr.) macerans based on overall similarity (simple-matching coefficient) and cluster analysis (UPGMA) of 78 physiological tests.

Characterization of *Cystofilobasidium ferigula* sp. nov.

A mycelium with clamp connections forms 2 d after inoculation, and large numbers of teliospores can be detected after 1 week at room temperature (20–22 °C). Germination of teliospores requires a resting period. Good results were obtained by harvesting the teliospores from 1-month-old cultures and soaking them in demineralized water for 6 weeks at 4 °C. The soaked agar cubes containing the teliospores were transferred to 2% water agar and germination was observed after 2 d at room temperature.

Nutritional and biochemical profiles are given in Table 2. The nutritional characterization of the four strains of *Cystofilobasidium ferigula* corresponds to published data (Barnett *et al.*, 1990). However, three discrepant results were found. In our study, glycerol gave negative results with most strains, citric acid was utilized by three strains and L-lysine was utilized by all strains. Moreover, of the 76 assimilation tests per-

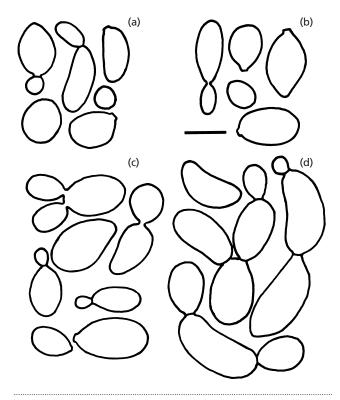


Fig. 2. Line drawings of yeast cells of *Cystofilobasidium* ferigula strains IGC 5359^{T} (a), IGC 4410 (b), IGC 5540 (c) and IGC 5628 (d) grown on YM agar for 1 week at 25 °C. Bar, 5 μ m.

formed, seven gave variable results. The utilization of L-malic acid was considered variable for IGC 4410, since, in four determinations, positive results were recorded twice and negative results were also recorded twice. In spite of the discrepant results, the four strains of *Cystofilobasidium ferigula* formed a distinct cluster in the overall comparison of physiological data (Fig. 1).

Physiological differences relevant to the other species in the *Cystofilobasidium* subclade are shown in Table 3.

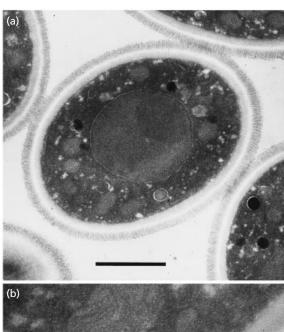
Micromorphological differences were found between the four *Cystofilobasidium ferigula* isolates (Fig. 2).

Table 3. Relevant physiological differences between the species of the subclade Cystofilobasidium

C., Cystofilobasidium.

Characteristic	C. ferigula	C. bisporidii	C. infirmominiatum	C. capitatum	C. lari-marini	Cryptococcus macerans
Utilization of:						
Erythritol	_	_	_	_	_	+
L-Malic acid	-*	+	+	+	+	+
L-Tartaric acid	_	_	+	_	_	_
Ethylamine	_	+	+	+	+	+
Cadaverine	_	+	+	+	+	+
Growth at 30 °C	+	_	_	_	_	_

^{*} Variable for strain IGC 4410.



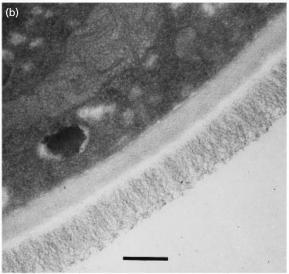


Fig. 3. Transmission electron micrographs of *Cystofilobasidium* ferigula (IGC 5359^T × IGC 5628) grown for 1 month on CMA. Note that the yeast cells have a layer of fine fibrils at the surface. Bars: $1 \mu m$ (a) and $0.2 \mu m$ (b).

Cells of strains belonging to mating type A1 were normally smaller than those of strain IGC 5628 (mating type A2). Moreover, cells of IGC 5628 were slightly curved. Transmission electron microscopy revealed that the yeast cells had a layer of fine fibrils at the surface (Fig. 3).

The G+C content of the nuclear DNA of strain IGC 5359^{T} was $67\cdot0\pm0.40$ mol% (six determinations) and that of strain IGC 5628 was $66\cdot4\pm0.12$ mol% (six determinations). The homology value determined in DNA–DNA reassociation experiments with the two strains ranged between 87 and 95% (three determinations).

A method of PCR fingerprinting based on the microsatellite DNA primer (GTG)₅ was used to evaluate the relationships among *Cystofilobasidium ferigula* strains.

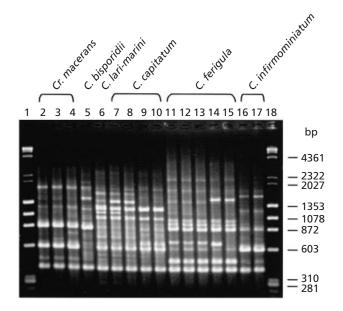


Fig. 4. Microsatellite-primed PCR fingerprints of Cystofilobasidium (C.) and Cryptococcus (Cr.) macerans obtained with primer (GTG)₅. Lanes: 1 and 18, λDNA cleaved with HindIII/ΦX174 DNA cleaved with HaelII marker; 2–4, Cryptococcus macerans IGC 2869^T, IGC 4482 and IGC 4737; 5, Cystofilobasidium bisporidii IGC 4415^T; 6, Cystofilobasidium lari-marini IGC 4530^T; 7–10, Cystofilobasidium capitatum IGC 4418^T, IGC 4309; IGC 5626 and IGC 5627; 11–15, Cystofilobasidium ferigula IGC 5359^T, IGC 4410, IGC 4410-I, IGC 5540 and IGC 5628; 16–17, Cystofilobasidium infirmominiatum IGC 3955^T and IGC 4414.

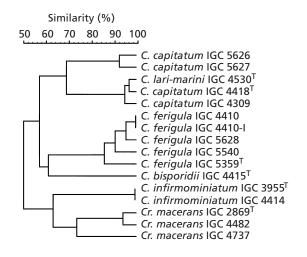


Fig. 5. Dendrogram of *Cystofilobasidium* species and *Cryptococcus macerans* based on the analysis of the PCR fingerprints obtained with primer (GTG)₅, the Dice coefficient and the UPGMA cluster method.

Other strains belonging to the genus *Cystofilobasidium* and to *Cryptococcus macerans* were also tested using this approach. The PCR patterns obtained are depicted in Fig. 4, and their respective clustering, based on the Dice coefficient, is shown in Fig. 5.

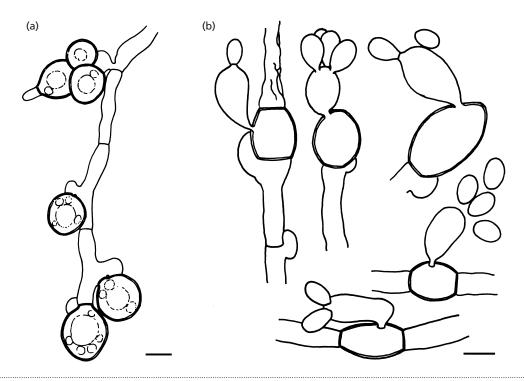


Fig. 6. Line drawings of *Cystofilobasidium ferigula* showing (a) a hypha with lateral and terminal teliospores (IGC 5359^T × IGC 5628) after 1 month on CMA and (b) germinated teliospores with basidia and basidiospores (IGC 5359^T × IGC 5628 and IGC 4410 × IGC 5628). Bars, 5 μm.

Two types of basidial morphology can be distinguished in Cystofilobasidium. In Cystofilobasidium capitatum. Cystofilobasidium bisporidii and Cystofilobasidium larimarini, the basidia are elongated. The capitate apical swelling is separated from the teliospore by a tubular structure measuring up to 80 µm in Cystofilobasidium capitatum (Fell et al., 1973; Oberwinkler et al., 1983), up to 140 µm in Cystofilobasidium bisporidii (Fell et al., 1973) and up to 106 µm in Cystofilobasidium larimarini (Fell & Statzell-Tallman, 1992). The other basidial type is present in Cystofilobasidium infirmominiatum and in the new species, Cystofilobasidium ferigula. In Cystofilobasidium infirmominiatum, the basidia are usually pyriform (Fig. 18 of Fell et al., 1973), with the large base attached to the teliospore, and basidial length does not exceed 14 µm (Fell et al., 1973). In Cystofilobasidium ferigula, basidia are normally cylindrical and their maximum length is 12 μm (Fig. 6). It has been reported that the species belonging to the first group occasionally produce short basidia, which can resemble those of the second group (Fig. 12 of Fell et al., 1973). However, the occurrence of long basidia has never been observed in Cystofilobasidium infirmominiatum or Cystofilobasidium ferigula. The short basidial type of Cystofilobasidium is similar to the basidia produced by species of *Mrakia*, both in shape and in size (Fig. 12 of Fell et al., 1969 and Fig. 336 of Fell & Statzell-Tallman, 1998).

In addition to basidial morphology, other traits support the assignment of the new species to Cystofilobasidium. Cystofilobasidium ferigula and the other species in the genus assimilate inositol, glucuronate, nitrate and nitrite, possess a CoQ 8 system (Fell et al., 1999) and have xylose in the cell walls (Fell et al., 1999). Moreover, Cystofilobasidium ferigula does not utilize any of the aromatic compounds tested (Table 2). The incapacity to assimilate aromatic compounds was observed for the vast majority of species of the Cystofilobasidiales (Sampaio, 1999). The three known exceptions are Cystofilobasidium capitatum, Cystofilobasidium lari-marini and Cryptococcus huempii (Ramírez et González) Roeijmans, van Eijk et Yarrow, which were able to assimilate caffeic acid (Sampaio, 1999). Furthermore, the hyphal septa of Cystofilobasidium ferigula have dolipores without parenthesomes (Fig. 7). This septal pore type is normally interpreted as a retained primitive characteristic and is also present in Cystofilobasidium capitatum (Oberwinkler et al., 1983), Cystofilobasidium lari-marini (Suh & Sugiyama, infirmominiatum 1993), Cystofilobasidium Mrakia frigida (Suh et al., 1993). In Cystofilobasidium ferigula, cisternae of the endoplasmic reticulum were sometimes found in the vicinity of the septal pore (Fig. 7). In contrast to the parenthesomes, these cisternae do not have an exact position in relation to the septal pore and lack an additional internal layer.

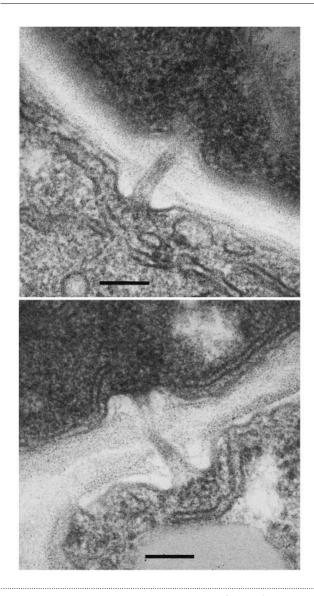


Fig. 7. Transmission electron micrographs of *Cystofilobasidium ferigula* (IGC 5359^T × IGC 5628) grown for 1 month on CMA, showing dolipores without parenthesomes. Note that cisternae of endoplasmic reticulum are located in the neighbouring areas of the pores. Bars, 0·1 μm.

At the molecular level, phylogenetic studies using 26S rDNA sequences indicate a close relationship between *Cystofilobasidium ferigula* (*Cryptococcus ferigula*) and the remaining species of *Cystofilobasidium* (Fell *et al.*, 1999).

The microsatellite-primed PCR fingerprinting method using primer (GTG)₅ proved to be a useful approach for differentiating most species of *Cystofilobasidium* (Figs 4 and 5). Moreover, the three strains of *Cryptococcus macerans* were grouped in one cluster (Fig. 5), which contradicts the heterogeneity of the species suggested in the analysis of phenotypic data (Fig. 1). During this study, a non-pigmented variant of strain *Cystofilobasidium ferigula* IGC 4410 was detected, purified and maintained as IGC 4410-I. The PCR-

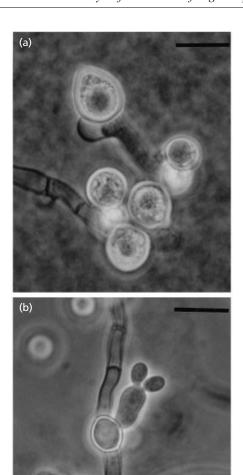


Fig. 8. Micrographs of *Cystofilobasidium ferigula* showing (a) 2-week-old teliospores on CMA (IGC 5359^T \times IGC 5628) and (b) a germinated teliospore with a basidium and two basidiospores (IGC 4410 \times IGC 5628). Bars, 10 μ m.

fingerprinting banding profiles validated the origin of IGC 4410-I as a non-pigmented variant of IGC 4410 (Fig. 4). Moreover, this non-pigmented variant was also sexually compatible with IGC 5628. The exception to the good species separation was Cystofilobasidium lari-marini, which clustered among the strains of Cystofilobasidium capitatum (Fig. 5). In addition, the banding profile of Cystofilobasidium lari-marini was identical to the pattern obtained for the type strain of Cystofilobasidium capitatum (Fig. 4). These results suggested conspecificity between the two species; in order to test this hypothesis, the G+C content of the nuclear DNA was determined and DNA-DNA reassociation experiments were carried out using both type strains. Cystofilobasidium capitatum had a G+C content of 60.0 ± 0.61 mol % (five determinations) and Cystofilobasidium lari-marini had a value of 60·2± 0.33 mol% (five determinations). The homology

values obtained ranged between 85 and 100% (three determinations), which confirms that *Cystofilobasidium lari-marini* must be regarded as a synonym of *Cystofilobasidium capitatum*.

In spite of different culture pigmentation, a close relationship had been observed between Cystofilobasidium capitatum and Cystofilobasidium lari-marini in molecular phylogenetic studies using 26S rDNA sequences (Fell et al., 1999). Moreover, Cystofilobasidium capitatum and Cystofilobasidium lari-marini are also very similar with respect to basidial morphology (Fell & Statzell-Tallman, 1992), septal pore ultrastructure (Suh & Sugiyama, 1993) and nutritional profiles (Table 3 and Fig. 1). Culture pigmentation must therefore be considered to be variable in Cystofilobasidium capitatum, since typical isolates of this species are orange in colour, whereas IGC 4530 has cream-coloured colonies. Pigmented yeast species can sometimes give rise to colourless variants, as was reported for Rhodosporidium toruloides Banno (Joo et al., 1988) and as observed in the present study with strain IGC 4410-I of Cystofilobasidium ferigula.

Latin diagnosis of *Cystofilobasidium ferigula* Sampaio, Gadanho *et* Bauer sp. nov.

Hyphae hyalinae (3–3·5 μm in diametro), septis fibulatis. Teliosporae laterales, terminales vel intercalares, fibulatae, in culturis duorum mensium subglobosae ad plus minusve dacryoideae, 7–11 × 7–12 μm si terminales vel laterales, elongatiores (6–8 × 8–13 μm) si intercalares, aggregatae demum cinnamomeae, basidiis ovoideis ad cylindraceis (4–7 × 7–12 μm) germinant. Basidiosporae sessiles, plerumque in parte apicali basidii oriuntur, gemmis germinant.

Typus depositus in collectionis Portuguese Yeast Culture Collection, FCT-UNL, Caparica, *Lusitania* (IGC 5359^T).

Description of *Cystofilobasidium ferigula* Sampaio, Gadanho *et* Bauer sp. nov.

Anamorphic stage: *Cryptococcus ferigula* (nom. corrig.) Saëz *et* Rodrigues de Miranda 1988 (spelled incorrectly in the original publication as *Cryptococcus feraegula*).

Hyphae hyaline (3–3·5 µm in diameter), with clamp connections. Teliospores lateral, terminal or intercalary on the mycelium and subtended by a clamp connection. Teliospores in 1-month-old cultures are subglobose to slightly dacryoid (Figs 6a and 8a), 7–11 × 7–12 µm when terminal or lateral, more elongated (6–8 × 8–13 µm) when intercalary, formed in large groups that become orange-brown in colour. Upon germination, teliospores originate ovoidal to cylindrical basidia (4–7 × 7–12 µm) (Figs 6b and 8b). One to four sessile subglobose basidiospores (3–3·5 × 4–5 µm) are formed, normally on the apical portion of the basidia (Fig. 6). Basidiospores germinate by budding.

The type strain of *Cystofilobasidium ferigula*, strain IGC 5359^T (mating type A1), has been deposited in the Portuguese Yeast Culture Collection, FCT-UNL, Caparica, Portugal.

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