

ALFREDO VIZZINI, TOMASO LEZZI, ENRICO ERCOLE, MAURO CITTADINI, MARCO CONTU

*HEBELOMA PAMPHILIENSE* IS A MEMBER OF THE  
TUBARIA FURFURACEA CLADE (AGARICALES, TUBARIACEAE)

**Abstract**

*Based on molecular data Hebeloma pamphiliense is showed to be an albinotic form of a species of the Tubaria furfuracea clade.*

**Riassunto**

*Sulla base di dati molecolari viene dimostrato che Hebeloma pamphiliense è una forma albina di una specie del complesso facente capo a Tubaria furfuracea.*

**Key words:** Basidiomycota, Agaricomycetes, albinotic taxa, ITS sequences, molecular phylogeny, taxonomy.

**Introduction**

The genus *Hebelomina*, typified by *H. domardiana* Maire, was established by MAIRE (1935) for pale-coloured *Hebeloma*-like fungi with whitish lamellae, white spore-print and smooth spores. So far, seven species have been described in this genus (HUIJSMAN, 1946, 1978; ALESSIO & NONIS, 1977; NATARAJAN & RAMAN, 1980, 1983; DESSI & CONTU, 1993; GENNARI, 2002; VESTERHOLT, 2005; FRAITURE & HAYOVA, 2006; CITTADINI ET AL., 2008). Most of them are extremely rare or even known only by the type specimens. Morphologically, the described species are heterogeneous, terricolous or lignicolous and the taxonomic position of the genus and its species was long debated (HUIJSMAN, 1978; NEVILLE & ROUX 1997; FRAITURE & HAYOVA, 2006) even though preliminary data indicated that *Hebelomina* is an artificial assemblage. In particular, the phylogenetic analyses by MONCALVO ET AL. (2002) have shown that the lignicolous *Hebelomina neerlandica* Huijsman is an albinotic *Gymnopilus* P. Karst., close to *G. penetrans* (Fr.) Murrill; Vesterholt (2005) considered the terricolous *H. domardiana* a white-spored *Hebeloma*. Consequently, the genus *Hebelomina* has been recently included in *Hebeloma* (Fr.) P. Kumm. (VESTERHOLT 2005) as subsection *Hebelomina* (Maire) Beker, U. Eberh. & Vesterh. of section *Denudata* and *H. domardiana* recombined in *Hebeloma*. Accordingly, CITTADINI ET AL. (2008) transferred on the basis of only morphological data *Hebelomina neerlandica* and *H. pallida* Dessi & Contu in *Gymnopilus*, *Hebelomina mediterranea* A. Gennari in *Hebeloma* and described a new species in the “*Hebelomina* complex” as *Hebeloma pamphiliense* Cittadini, Lezzi & Contu.

After collecting new specimens in the type area and re-evaluating the original material we have decided to infer the phylogenetic position of *Hebeloma pamphiliense* based on a ITS sequence analysis. Specimens of *Tubaria furfuracea* (Fr.) Gillet found not so far from the type area, were also sequenced.

**Materials and methods***DNA extraction, amplification and sequencing*

Genomic DNA was isolated from 10 mg of a dried herbarium specimen from three collections (see TAB. 1), by using the DNeasy Plant Mini Kit (Qiagen, Milan Italy) according to the

manufacturer's instructions. Universal primers ITS1F/ITS4 were used for the ITS region amplification (WHITE *ET AL.*, 1990; GARDES & BRUNS, 1993). Amplification reactions were performed in a PE9700 thermal cycler (Perkin-Elmer, Applied Biosystems) following VIZZINI *ET AL.* (2014). The PCR products were purified with the AMPure XP kit (Beckman) and sequenced by MACROGEN Inc. (Seoul, Republic of Korea). The sequences were submitted to GenBank ([www.ncbi.nlm.nih.gov/genbank](http://www.ncbi.nlm.nih.gov/genbank)) and their accession numbers are reported in FIG. 1 and TAB. 1.

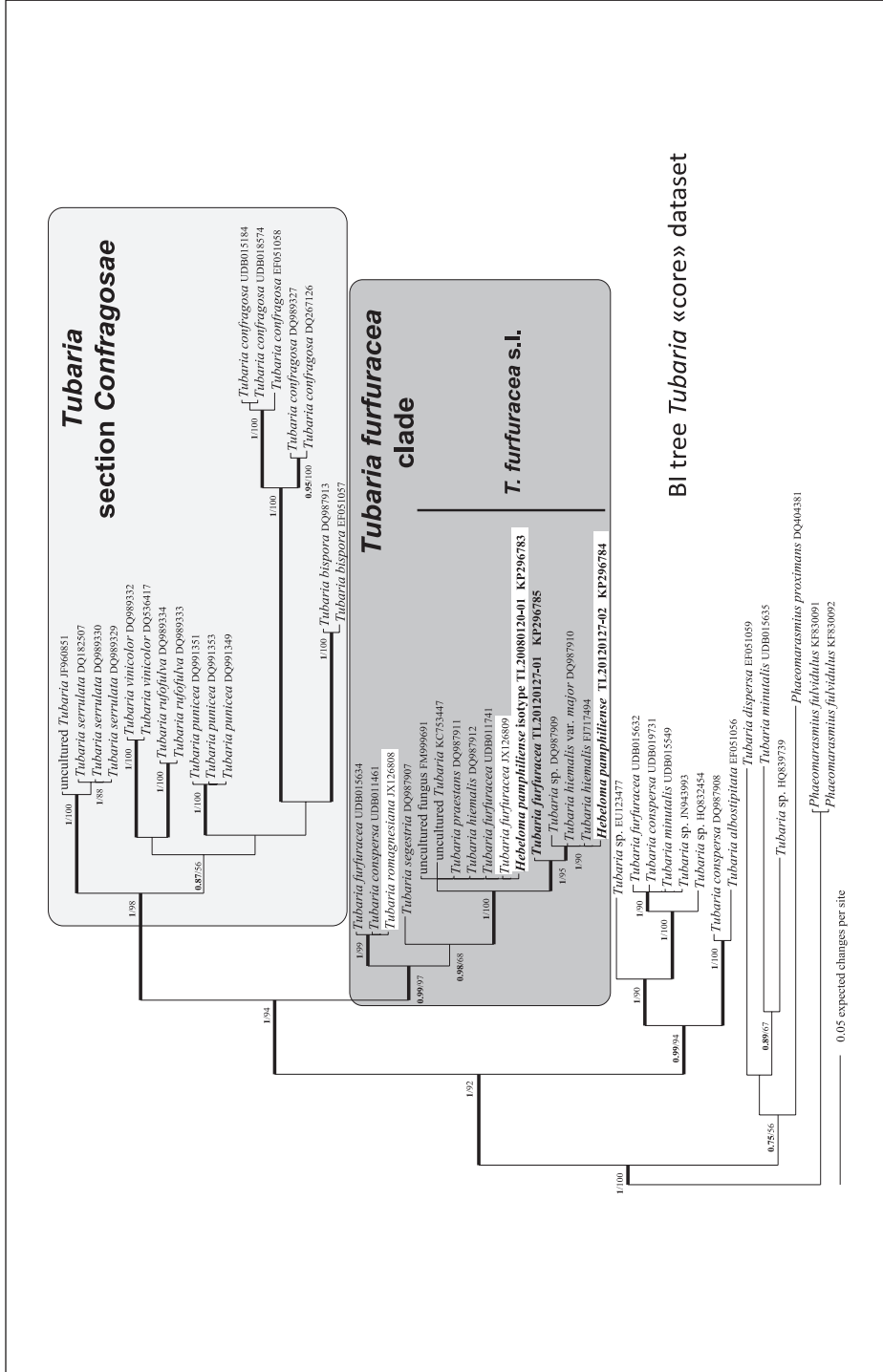
**Table 1.** Features of the sequenced collections

TAXON	COLLECTION DATA	ITS-GENBANK ACC. NUMBERS	SPORE DIMENSIONS ( $\mu\text{m}$ )	CHEILO-CYSTIDIA (FORM AND DIMENSION) ( $\mu\text{m}$ )	ELEMENTS OF THE HYMENOPHORAL TRAMA ( $\mu\text{m}$ )
<i>Hebeloma pamphiliense</i>	Isotype, Italy, Rome, Villa Pamphili, on <i>Quercus ilex</i> debris, 20 Jan 2008, leg. T. Lezzi, TL20080120-01	KP296783	6.6-8.3 $\times$ 4.8-6.4	Mainly capitate, 25-32 $\times$ 4.5-6.5	$\times$ 4.0-9.1
<i>Hebeloma pamphiliense</i>	Italy, Rome, Villa Pamphili, on <i>Quercus ilex</i> debris, 27 Jan 2012, leg. T. Lezzi, TL20120127-02	KP296784			
<i>Tubaria furfuracea</i>	Italy, Rome, Villa Pamphili, on <i>Quercus ilex</i> debris, 27 Jan 2012, leg. T. Lezzi, TL20120127-01	KP296785	6.7-7.4 $\times$ 4.0-5.1	Mainly capitate, 37-49 $\times$ 6.7-9.5	$\times$ 4.1-8.5

#### Sequence alignment and phylogenetic analysis

The sequences obtained in this study were checked and assembled using Geneious v.5.3 (DRUMMOND *ET AL.*, 2010). A preliminary BLAST search showed *Hebeloma pamphiliense* is a member of the genus *Tubaria* (W.G. Sm.) Gillet. Consequently, sequences were combined with published *Tubaria* ITS rDNA sequences selected from GenBank and UNITE (<http://unite.ut.ee>) databases on the basis of the greatest similarity based on BLASTsearch, outcomes of a recent phylogenetic study focused on *Tubaria* (MATHENY *ET AL.*, 2007), and subsequent phylogenetic analysis (preliminary trees not shown).

The alignment was generated using MAFFT (KATOHI *ET AL.*, 2002) with default conditions for gap openings and gap extension penalties. The alignment was then imported into MEGA v.5.0 (TAMURA *ET AL.*, 2011) for manual adjustment. Best-fit models were estimated by both the Akaike information criterion (AIC) and the Bayesian information criterion (BIC) with jModelTest 0.1.1 (POSADA, 2008) to provide a substitution model for the alignment. Phylogenetic analyses were performed using the Bayesian Inference (BI) and Maximum Likelihood (ML) approaches. Following MATHENY *ET AL.*, (2007), *Phaeomarasmium fulvidulus* Singer and *P. proximans* (A.H. Sm. & Hesler) Singer were chosen as outgroup species. The BI was performed with MrBayes 3.1.2

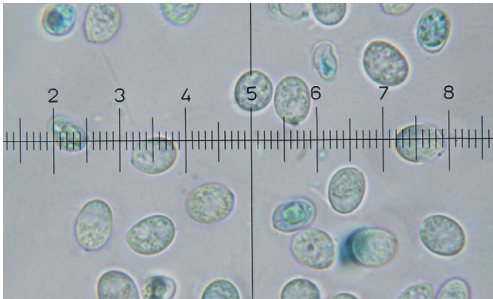


**Fig. 1.** Bayesian phylogenetic tree from the ITS1-5.8S-ITS2 sequence alignment of *Tubaria* species, with *Phacomarasmius subtidulus* and *P. proximus* as outgroup taxa. BPP values (in bold)  $\geq 0.75$  and MLB values  $\geq 50\%$  are shown on the branches. Thickened branches indicate Bayesian posterior probability  $>0.95$  and ML bootstrap support  $>90\%$ . For each sequence taxon name and Genbank/UNITE number are given. In bold, albino collections are highlighted in white and marked by an asterisk.

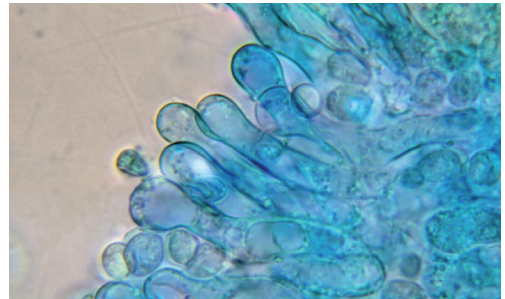


*Hebeloma pamphiliense* (TL20120127-02).

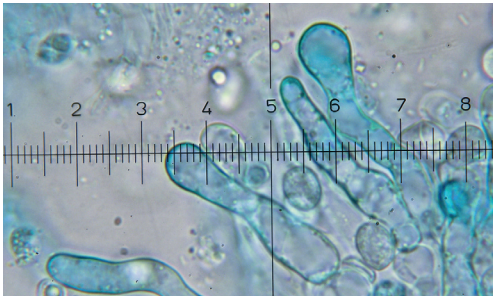
Photo by Tomaso Lezzi



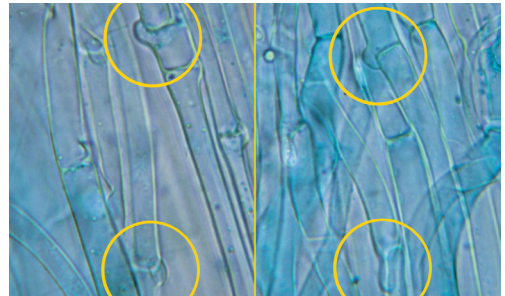
*Hebeloma pamphiliense* (TL20120127-02). Spores.  
Photo by Tomaso Lezzi



*Hebeloma pamphiliense* (TL20120127-02). Cheilocystidia.  
Photo by Tomaso Lezzi



*Hebeloma pamphiliense* (TL20120127-02). Cheilocystidia.  
Photo by Tomaso Lezzi



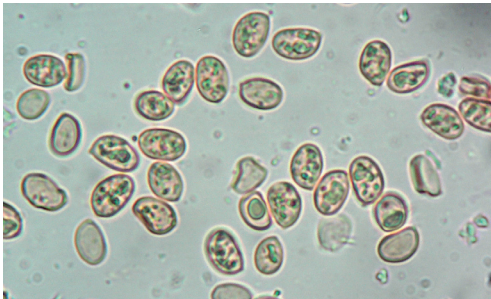
*Hebeloma pamphiliense* (TL20120127-02). Clamp connections.  
Photo by Tomaso Lezzi



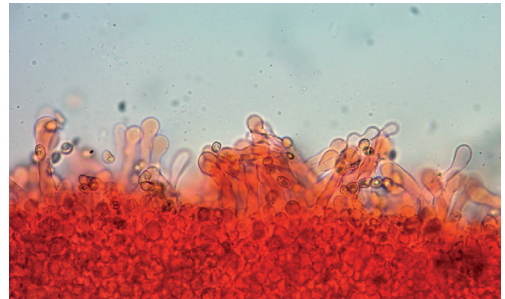


*Tubaria furfuracea* (TL20120127-01).

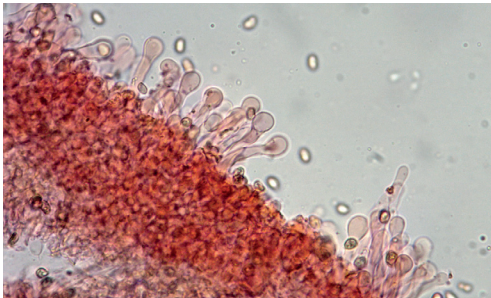
Photo by Tomaso Lezzi



*Tubaria furfuracea* (TL20120127-01). Spores (1000×).  
Photo by Tomaso Lezzi



*Tubaria furfuracea* (TL20120127-01). Cheilocystidia (400×).  
Photo by Tomaso Lezzi



*Tubaria furfuracea* (TL20120127-01). Cheilocystidia (400×).  
Photo by Tomaso Lezzi



*Tubaria furfuracea* (TL20120127-01). Lamellar hyphae (400×).  
Photo by Tomaso Lezzi

(HUELSENBECK & RONQUIST, 2001) with four incrementally heated simultaneous Monte Carlo Markov Chains (MCMC) run over 10 million generations, under GTR+ $\Gamma$  evolutionary model. Trees were sampled every 1 000 generations resulting in an overall sampling of 10 001 trees; the first 2 500 trees were discarded as “burn-in” (25%). For the remaining trees, a majority rule consensus tree showing all compatible partitions was computed to obtain estimates for Bayesian Posterior Probabilities (BPP). ML estimation was performed through RAxML v.7.0.4 (STAMATAKIS, 2006) with 1 000 bootstrap replicates (FELSENSTEIN, 1985) using the GTRGAMMA algorithm to perform a tree inference and search for a good topology. Support values from bootstrapping runs (MLB) were mapped on the globally best tree using the “-f a” option of RAxML and “-x12345” as a random seed to invoke the novel rapid bootstrapping algorithm. Only BPP values over 0.75 and MLB over 50% are reported in the resulting tree (Fig. 1). Pairwise % identity values of ITS sequences were calculated using MEGA 5.10 (TAMURA ET AL., 2011).

## Results

Both Bayesian and Maximum likelihood analyses produced the same topology; therefore, only the Bayesian tree with both BPP and MLB values is shown (FIG. 1). The ITS data matrix comprises a total of 48 sequences (including 36 from GenBank and 9 from UNITE). In the obtained Bayesian phylogenetic tree (FIG. 1), our three collections (TL20080120-01, TL20120127-01 and TL20120127-02) fall in a well-supported clade (hereafter designed as *T. furfuracea* s.l.; BPP = 1; MLB = 100) in the *Tubaria furfuracea* clade (BPP = 0.99; MLB = 97). The sequences of the *T. furfuracea* s.l. clade share a pairwise % identity value of 98.7. The clade is sister (BPP = 0.98, MLB = 68) to a *T. segestria* sequence (DQ987907).

## Discussion

*Hebeloma pamphiliense* is a *Tubaria*

*Hebeloma pamphiliense* was established on morphological basis on the ground of collections from the Villa Pamphili Park (Rome); it is apparently terricolous but growing on *Quercus ilex* debris and cupules (CITTADINI ET AL., 2008). The phylogenetic analysis (FIG. 1) highlighted that *H. pamphiliense* is a *Tubaria*. The genus *Tubaria* (*Tubariaceae* Vizzini) is polyphyletic and heterogeneous. The number and the identity of the species belonging to this very difficult complex is still debated and the taxonomic problems have still to be solved (MATHENY ET AL., 2007). In their phylogenetic analysis, MATHENY ET AL. (2007) recovered two major groups in the *Tubaria* core, viz. *Tubaria* section *Confragosae* (Singer) Matheny and the *Tubaria furfuracea* complex.

The first group, recognized as a strongly monophyletic clade, encompasses *T. bispora* Matheny, P.-A. Moreau, M.A. Neves & Vellinga, *T. confragosa* (Fr.) Harmaja, *T. punicea* (A.H. Sm. & Hesler) Ammirati, Matheny & P.-A. Moreau, *T. rufofulva* (Cleland) D.A. Reid & E. Horak, *T. serrulata* (Cleland) Bougher & Matheny and *T. vinicolor* (Peck) Ammirati, Matheny & Vellinga; the group is distinguished morphologically from the other species of *Tubaria* by darker yellowish brown spore prints and resistance of spore walls to collapse in microscopic mounts MATHENY ET AL. (2007). The development of the partial veil is variable and ranging from an evanescent cortina to a membranous annulus. The second group, the *Tubaria furfuracea* complex, forming an unresolved polytomy in the Bayesian analysis by MATHENY ET AL. (2007), is distinguished mainly by the lighter spore prints (ochraceous) and spore walls that fail to revive (appearing collapsed) for some spores in microscopic mounts. Species in this group usually do not produce an annulus and include collections named *T. conspersa* (Pers.) Fayod, *T. furfuracea*, *T. hiemalis* Romagn. ex Bon, *T. hiemalis* var. *major* Bon & Trimbach, *T. pallidospora* J.E. Lange, *T. praestans* Romagn. ex E. Horak & P.-A. Moreau, *T. segestria* (Fr.) Boud. sensu Romagnesi, *Tubaria* sp., and “*Phaeomarasmius*” sp. Gates 0006.

The ITS sequences of the two *Hebeloma pamphiliense* collections (isotype included) and of the normally brown-pigmented *Tubaria* collection found about 200 m far from the type area

(TAB. 1) matched well those of the *Tubaria furfuracea* s.l.: *T. furfuracea*, *T. hiemalis*, *T. hiemalis* var. *major* and *T. praestans* (FIG. 1).

The taxonomy of *Tubaria furfuracea* s.l. is very puzzling because of the lack of detailed molecular studies; almost all recent studies are based on morphological characters (ARNOLDS, 1982; BON, 1992; VOLDERS, 2002). ARNOLDS (1982) recognized three species: *Tubaria furfuracea* s.s. with evident velar remnants present at the pileus margin, spores (6.0)6.5–9.0(11) × (4.0)4.5–5.5(6.5) μm, ellipsoid to ellipsoid-oblong, sometimes slightly constricted apically, cheilocystidia (30)34.5–53 × 4.5–7.5(9.5) μm, subcylindrical to slightly ventricose, at apex not to rather swollen, and (6.0)8.5–20(26) μm wide hymenophoral trama hyphae; *T. hiemalis* with scarce velar remnant, slightly larger spores (6.7)7.0–9.5(10.5) × 4.5–5.5(6.0) μm, usually distinctly apically swollen (capitate) cheilocystidia, (5)8.0–18(20) μm wide hymenophoral trama hyphae, and winter fructification; and *T. romagnesiana* Arnolds with distinct velar remnants at pileus margin, shorter spores [(5.8)6.0–8.2(8.5) × 4.0–5.2(5.5) μm], cylindrical or slightly ventricose cheilocystidia without a swollen to subcapitate apex, and only ± 4.0–10(14.5) μm wide hymenophoral trama hyphae. The same species concept was followed by BON (1992) and HORAK (2005).

VOLDERS (2002) after thorough morphological studies, considered all three species conspecific. However, he distinguished two infraspecific taxa without distinctly capitate cheilocystidia, viz. *T. furfuracea* var. *furfuracea* with (8)10–20(30) μm wide trama hyphae and 6.5–9(11) × 4.5–5.5(6.5) μm large spores and var. *furfuracea* f. *romagnesiana* (Arnolds) Volders with 4–10(15) μm wide trama hyphae and rather thick-walled, 6–8 × 4–5 μm large spores, and var. *hiemalis* (Romagn. ex Bon) Volders with 10–20(30) μm wide trama hyphae, 7–10(11) × 4.5–5 μm large spores and distinctly capitate cheilocystidia.

VESTERHOLT (2012) considered all three species as phenotypic expressions of *T. furfuracea* s.l. without recognizing infraspecific taxa.

In the analysis of the nrLSU sequences by AIME ET AL. (2009), *T. furfuracea* and *T. hiemalis* are conspecific.

According to our analysis (FIG. 1) *T. furfuracea*, *T. hiemalis*, *T. hiemalis* var. *major* and *T. praestans* seem to be conspecific (they share a pairwise % identity value of 98.7) whereas *T. romagnesiana* and *T. segestria* sensu Romagnesi occupy an independent position.

Morphologically, our three collections share with *T. furfuracea* var. *hiemalis* the capitate cheilocystidia and with var. *furfuracea* the spore size, see Cittadini ET AL. (2008) and TAB. 1.

### The albinotic *Tubaria*

Albinotic entities belonging to the genus *Tubaria* (sometimes labeled as “*Leucotubaria*”, see BENDIKSEN, 1980) are only rarely described in the literature (BENDIKSEN, 1980; ANTONÍN ET AL., 2012). *Tubaria hololeuca* Kühner ex E. Horak & P.-A. Moreau is the only white coloured *Tubaria* species formally described from Europe (BON, 1992; VOLDERS, 2002; HORAK & MOREAU, 2004). It is characterized by very pale and small largely ellipsoid spores, 5.5–6.5 × 4.5–5 μm (tetrasporic basidia) up to 7(7,8) × 5.5 (bisporic basidia) and cylindrical to lageniform cheilocystidia.

BENDIKSEN (1980) described an albinotic form of *T. furfuracea* from Norway which shows morphological features exactly superimposable to those present in our collections (capitate cheilocystidia *T. hiemalis*-like and 6.5–8.5 × 4.5–5.5 μm spores *T. furfuracea*-like). ANTONÍN ET AL. (2012), based on morphological and molecular data attributed a first albinotic collection from Norway (O 370700N-Bendiksen 191/79, Oslo, Grorud, Groruddammen, on soil, 18 Aug. 1979, leg. E. Bendiksen, cited in BENDIKSEN, 1980) to *T. furfuracea* (see sequence JX126809, FIG. 1) and a second one from the Czech Republic to *T. romagnesiana* (see sequence JX126808, FIG. 1). The Norwegian collection is contaxic with the isotype collection of *Hebeloma pamphiliense*.

According to our analysis, albinotic forms seem to be restricted to the *T. furfuracea* clade so far, and are apparently not described for the section *Confragosae*.



## Conclusions

The *Hebelomina* genus (habit) is highly polyphyletic. Molecular analysis by MONCALVO *ET AL.* (2002) has shown that *Hebelomina neerlandica* is a *Gymnopilus*. Those authors extend however prematurely their conclusions to the whole genus *Hebelomina*. VESTERHOLT (2005) considered the type species, *Hebelomina domardiana*, a *Hebeloma*. Finally, our analysis highlighted that *Hebeloma pamphiliense*, formally ascribed to *Hebeloma* sect. *Denudata* subsect. *Hebelomina*, is an albinotic form of a taxon in *Tubaria furfuracea* s.l.

### Author's addresses

ALFREDO VIZZINI, ENRICO ERCOLE

Dipartimento di Scienze della Vita e Biologia dei Sistemi, Università di Torino,  
Viale P.A. Mattioli 25, I-10125 Torino, Italy.

E-mail: alfredo.vizzini@unito.it

TOMASO LEZZI - CSM AMINT

Via Filopanti, 2 - 00152 - Roma (RM).

E-mail: tomaso@spyrograph.it

MAURO CITTADINI

Viale Luigi Mascherpa, 21 - 00144 - Roma (RM).

E-mail: mauro.cittadini@alice.it

MARCO CONTU

Via Marmilla 12, 07026 – Olbia (OT) (Italia).

E-mail: contumarco1@gmail.com

## References

- AIME C., VILA J. & MOREAU P.-A. – 2009: *Crepidotus subfulviceps* comb. nov., a stipitate *Crepidotus* from temperate North America and Europe. *Mycotaxon* 110: 283-287.
- ALESSIO C.L. & NONIS U. – 1977: *Una specie quasi sconosciuta: Hebelomina microspora* Huijsman. *Micol. Ital.* VI(3): 15-19.
- ANTÓNÍN V., KRAMOLIŠ J. & TOMŠVOVŠKY M. – 2012: *Two collections of albinotic forms of Tubaria* (Basidiomycota, Agaricales, Inocybaceae). *Czech Mycol.* 64(2): 197-208.
- ARNOLDS E. – 1982: *Ecology and coenology of macrofungi in grasslands and moist heathlands in Drenthe, the Netherlands. Part 2. Autecology, part 3. Taxonomy.* J. Cramer, Vaduz.
- BENDIKSEN E. – 1980: *An albino Tubaria furfuracea*. *Norw. J. Bot.* 27(4): 203-206.
- BON M. – 1992: *Clé monographique des espèces galero-naucorioïdes*. *Doc. Mycol.* 21(84): 1-89.
- CITTADINI M., LEZZI T. & CONTU M. – 2008: *Hebeloma pamphiliense, una nuova specie a spore ialine e amiloidi appartenente al complesso Hebelomina*. *Boll. Ass. Micol. Ecol. Romana* 73-74: 5-23.
- DESSI P. & CONTU M. – 1993: *Una nuova specie di Hebelomina dalla Sardegna meridionale*. *Micol. e Veget. Medit.* 7(2): 101-106.
- DRUMMOND A.J., ASHTON B., BUXTON S., CHEUNG M., COOPER A., DURAN C., FIELD M., HELED J., KEARSE M., MARKOWITZ S., MOIR R., STONES-HAVAS S., STURROCK S., THIERER T. & WILSON A. – 2010: *Geneious v5.3*. Available from <http://www.geneious.com/>
- FELSENSTEIN J. – 1985: *Confidence limits on phylogenies: an approach using the bootstrap*. *Evolution* 39: 783-791.
- FRAITURE A. & HAYOVA V. – 2006: *Hebelomina neerlandica, a new species for Ukraine and considerations about the genus Hebelomina*. *Acta Mycologica* 41(2): 177-188.
- GARDES M. & BRUNS T.D. – 1993: *ITS primers with enhanced specificity for basidiomycetes – application to the identification of mycorrhizae and rusts*. *Mol. Ecol.* 2: 113-118.
- GENNARI A. – 2002: *Una nuova specie di Hebelomina dall'Italia. Chiave per la determinazione delle specie sinora descritte*. *Riv. Micol.* 45(4): 311-318.



- HORAK E. – 2005: *Röhrlinge und Blätterpilze in Europa*. Elsevier, München.
- HORAK E. & MOREAU P.-A. – 2004: *Les "Naucoria" nouveaux de la Flore Analytique (Alnicola, Flammulaster, Tubaria)*. – Bull. Soc. mycol. Fr. 120(1-4): 215-237.
- HUELSENBECK J.P. & RONQUIST F. – 2001: *MrBayes: Bayesian inference of phylogeny*. Bioinformatics 17: 754-755.
- HUIJSMAN H.S.C. – 1946: *Hebelomina microspora nov. spec.* Rev. Mycol. (Paris) 11: 31-33.
- HUIJSMAN H.S.C. – 1978: *Hebelomina microspora and reflexions on Hebelomina as a genus*. Persoonia 9: 485-490.
- KATO H., MISAWA K., KUMA K. & MIYATA T. – 2002: *MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform*. Nucl. Acids Res. 30: 3059-3066.
- MAIRE R. – 1935: *Un nouveau genre d'Agaricacées*. Bull. Soc. Hist. Nat. Afrique du Nord 26: 13-14.
- NATARAJAN K. & RAMAN N. – 1980: *South Indian Agaricales*, 13. Kavaka 8: 69-72.
- NATARAJAN K. & RAMAN N. – 1983: *South Indian Agaricales*. Bibl. Mycol. 89. J. Cramer, Vaduz.
- NEVILLE P. & ROUX P. – 1997: *Hebelomina neerlandica Huijsman. Première récolte française et deuxième station connue d'un très rare Agaricomycetidae*. Bull. Féd. Myc. Dauphiné-Savoie 144: 35-46.
- MATHENY P.B., VELLINGA E.C., BOUGHER N.L., CESKA O., MOREAU P.-A., NEVES M.A. & AMMIRATI J.F. – 2007: *Taxonomy of displaced species of Tubaria*. Mycologia 99(4): 569-585.
- MONCALVO J.-M., VILGALYS R., REDHEAD S.A., JOHNSON J.E., JAMES T.Y., AIME M.C., HOFSTETTER V., VERDUIN S., LARSSON E., BARONI T.J., THORN R.G., JACOBSSON S., CLÉMENÇON H. & MILLER O.K. – 2002: *One hundred and seventeen clades of euagarics*. Mol. Phylogenet. Evol. 23: 357-400.
- POSADA D. – 2008: *jModeltest: phylogenetic model averaging*. Mol. Biol. Evol. 25: 1253-1256.
- STAMATAKIS A. – 2006: *RAxML-VI-HPC: Maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models*. Bioinformatics 22: 2688-2690.
- TAMURA K., PETERSON D., PETERSON N., STECHER G., NEI M. & KUMAR S. – 2011: *MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods*. Mol. Biol. Evol. 28: 2731-2739.
- VESTERHOLT J. – 2005: *The genus Hebeloma. Fungi of Northern Europe 3*. Narayana Press, Gylling.
- VESTERHOLT J. – 2012: *Tubaria (W.G. Sm.) Gillet*. In: KNUDSEN H. & VESTERHOLT J. (eds.), *Funga Nordica*. Nordsvamp, Copenhagen, pp. 974-976.
- VIZZINI A., ERCOLE E. & VOYRON S. – 2014: *Lepiota sanguineofracta (Basidiomycota, Agaricales), a new species with a hymeniform pileus covering from Italy*. Mycol. Progr. 13: 683-690.
- VOLDERS J. – 2002: *Het genus Tubaria in Vlaanderen*. Sterbeekia 21-22: 3-28.
- WHITE T.J., BRUNS T.D., LEE S. & TAYLOR J. – 1990: *Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics*. In: Innis M.A., Gelfand D., Sninsky J., White T. (eds), *PCR Protocols, a guide to methods and applications*. Academic, Orlando, pp. 315-322.