

Chapter 7

The Puberulum Group Sensu Lato (Whitish Truffles)

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7.1 Introduction

Tuber species in the Puberulum group sensu lato (s.l.) produce small and light-colored ascomata with alveolate-reticulated ascospores. Members of this group are commonly called “whitish truffles” (Zambonelli et al. 2000a), in order to distinguish them from the most precious species *Tuber magnatum* Pico (the Italian white truffle). Puberulum group s.l. is the most widely distributed group and has the highest species richness within *Tuber* genus (Bonito et al. 2010a). Its members have been found all over the Northern Hemisphere associated with angiosperm and/or gymnosperm in a wide range of habitats: from the northern boreal forests of Europe and North America to the semiarid environments of Mexico and North Africa. Moreover, unclassified members of the Puberulum group were also found as ectomycorrhizas (ECMs) in the Southern Hemisphere (Bonito et al. 2010b). The Puberulum group s.l. includes commercially valuable species which are becoming increasingly popular in the marketplace. The most noteworthy species is *Tuber borchii* Vittad. (“bianchetto” truffle) which, actually, is cultivated outside its native areas and the extent of its plantations is increasing around the world. Actually, it is successfully cultivated in New Zealand and Australia, and, more recently, it has also been introduced in the USA (Zambonelli et al. 2015). *Tuber gibbosum* Harkn.

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(Oregon spring white truffle) and *Tuber oregonense* Trappe, Bonito and P. Rawl. (Oregon winter white truffle) are well appreciated in North America, but the efforts to cultivate them are in their infancy (Lefevre 2012). The potential culinary value of all the other whitish truffles has to be investigated yet.

The term “*Puberulum*” was used for the first time by Knapp (1950) to group together the *Tuber* species forming ascomata with smooth, papillate or rough surface, soft texture, and globose asci bearing an early-disappearing stalk and reticulate ascospores. Furthermore, the author define a *Puberulum* group A including nine species (*Tuber puberulum* Berk. & Broome, *Tuber albidum* Pico, *Tuber michailowskianum* Bucholtz, *Tuber rapaeodorum* Tul. & C. Tul., *T. borchii*, *Tuber maculatum* Vittad., *Tuber mougeotii* Quéll., *Tuber asa-foetida* Lesp., and *Tuber lacunosum* Mattir.) with small-meshed (<10 µm) and regularly reticulate ascospores and a *Puberulum* group B consisting of three species (*Tuber dryophilum* Tul. & C. Tul., *Tuber foetidum* Vittad., and *T. magnatum*) with large-meshed (>10 µm) and irregularly reticulate ascospores. Thereafter, taxonomic relationships of the whitish truffle species have been debated for decades by many other European mycologists. Based on the spore dimension and morphology, Gross (1987) identified a *Puberulum* “cluster” within the white truffle species with small-sized ascomata, which included *T. borchii* var. *sphaerosperma* Malençon (= *T. puberulum* var. c), *T. puberulum* (=var. b), *Tuber murinum* R. Hesse (= *T. puberulum* var. a), *Tuber exiguum* R. Hesse, and *T. borchii*. Montecchi and Lazzari (1987) reported a redundant increase of species within the *Puberulum* group and accepted as valid only *T. borchii*, *T. rapaeodorum*, *T. dryophilum*, *T. maculatum*, *T. puberulum*, and *T. foetidum*. As time passes, the validity of some of these species was questioned, and new European species were included within the *Puberulum* group such as *Tuber oligospermum* (Tul. & C. Tul.) Trappe (Riousset et al. 2001) and *Tuber cistophilum* P. Alvarado, G. Moreno, Manjón, Gelpi & J. Muñoz (Alvarado et al. 2012).

The recent studies on molecular phylogeny of truffles have significantly improved the taxonomy of *Puberulum* group s.l., unraveling most of the phylogenetic affiliations within it. For example, Jeandroz et al. (2008) demonstrated that *T. magnatum* is phylogenetically well differentiated from the whitish truffles and belongs to the *Aestivum* group. On the contrary, many Asiatic and American species have been recently added to the *Puberulum* group s.l. (Wang et al. 2007, 2013; Jeandroz et al. 2008; Bonito et al. 2010a; Guevara et al. 2013).

Based on recent insight, we can consider as whitish truffles the *Tuber* species forming fruiting bodies with the following general features (Fig. 7.1):

Ascomata: hypogeous, small (commonly <5 cm in diameter), solid, and firm; globose or sub-globose, sometimes lobed; whitish at first becoming pale yellowish to yellow-brown or reddish-brown; surface smooth or finely pubescent, rarely with minute and flat warts (*T. foetidum*)

Peridium: pseudoparenchymatous or plectenchymatous; yellow or darker toward the surface, otherwise white/hyaline

Dermatocystidia: cylindrical or needle with septa when present; hyaline or yellowish

Gleba: whitish at first becoming grayish-brown to yellowish-brown, marbled with branching white veins arising from different points on the peridium

Asci: globose to ovate with 1–4 (–5) spores, thin-walled, sessile or short stipitate

Ascospores: hyaline at first becoming yellow-brown or reddish-brown at maturity, bearing an alveolate reticulum 3–6 µm deep

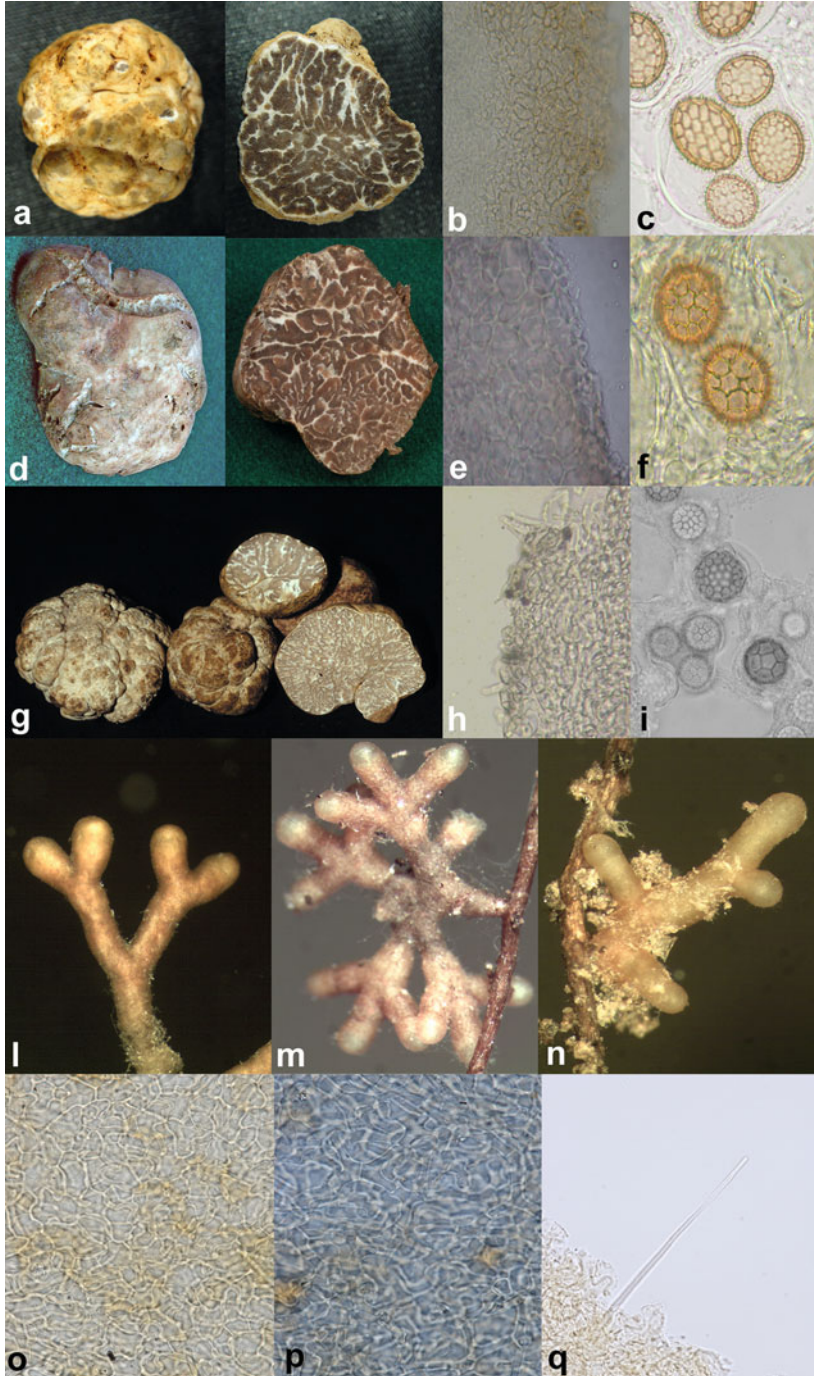


Fig. 7.1 Ascomata, peridium, and spores of *T. borchii* (a, b, c), *T. dryophilum* (d, e, f), and *T. oligospermum* (g, h, i). Mycorrhizas of whitish truffles with *P. nigra*, *A. unedo*, and *Q. robur*

The large amount of molecular data deposited in the public sequence repositories have represented a great resource to study the relationships among whitish truffle species but their analysis also revealed inconsistencies and contradictions. Indeed, part of the misidentified entries have been generated from the difficulties in identifying the whitish truffle ascomata because only few taxonomic informative traits of peridium and spores are available for species identification. However, most of the conflicting entries are from European species described before the twentieth century because the poor quality of the original descriptions led to disagreement among taxonomists and a different application of the species concepts (Jeandroz et al. 2008; Zambonelli et al. 2012). Then, the poor quality of the oldest holotypes in herbarium collections made often difficult to obtain reference DNA sequences useful to solve these controversies. Considering also that *Puberulum* group s.l. contains the highest number of insufficiently identified taxa and most of the diversity within *Tuber* genus (Bonito et al. 2010a), it remains the most controversial group of truffle species.

This chapter aimed to investigate the phylogenetic relationships and the diversity within *Puberulum* group s.l. based on the recent findings and the screening of the internal transcribed spacer (ITS) rDNA sequences available in GenBank database. We attempted to select an ITS reference sequence and, consequently, to assess the current extent of misidentified entries for each whitish truffle species. Finally, we reported the geographical distribution and intraspecific variability of each member of the *Puberulum* group s.l. as well as the description of mycorrhizas formed by these fungi.

7.2 Phylogeny of the *Puberulum* Group s.l.

Halász et al. (2005) were the first to explore the phylogenetic relationships within *Puberulum* group, validating the distinction among *T. rapaeodorum*, *T. foetidum*, *T. maculatum*, *T. borchii*, and *T. puberulum*. Wang et al. (2007) and Jeandroz et al. (2008) sorted members of this group in four subclades, including new species from Europe, Asia, and North America. Later, Bonito and colleagues (2010a) separated the whitish truffle species in two different clades, *Puberulum* and *Maculatum*, accounting for 37 (25 undescribed) and 19 (12 undescribed) species, respectively, all around the world. A third closely related lineage, the *Gibbosum* clade, was identified by only four species from North America. More recently, this latter phylogenetic reconstruction was also confirmed by the analysis of three different individual loci (28S large subunit rDNA, elongation factor 1-alpha, RNA polymerase II) in addition to the common ITS rDNA-based phylogeny, and

Fig. 7.1 (continued) (l, m, n). Puzzle-like (o) and puzzle-like bearing a hyphal net (p) mantles and cystidia (q) of whitish truffles

it was estimated that the most recent common ancestors of *Puberulum*, *Maculatum*, and *Gibbosum* clades diverged 65, 67, and 27 Mya, respectively (Bonito et al. 2013).

Actually (date of accession 18 January 2015), about 800 ITS1-5.8S-ITS2 rDNA complete sequences (>400 bp) attributable to the *Puberulum* group s.l. are deposited in GenBank. To retrieve all the sequences (identified and insufficiently identified) belonging to this group of truffles, three reference sequences were selected for each clade (*Puberulum*, *Maculatum*, and *Gibbosum*) and BLAST against GenBank nucleotide database adjusting to 1000 the “max target sequences” parameter. The output sequences of each clade were aligned together by Muscle in MEGA6 (<http://www.megasoftware.net/>, Tamura et al. 2013), and those of poor quality and short length as well as the redundant entries were removed by the datasets. A provisional neighbor-joining tree was then generated for each of the three dataset for identifying and removing the sequences belonging to other *Tuber* lineages after Bonito et al. (2010a). We assumed 97% ITS sequence similarity as threshold for phylotype definition and species approximation. Phylotypes were defined based on a similarity matrix constructed using MEGA6. Sequences with a *p*-distance < 3% were grouped into the same phylotype. The 3% is commonly accepted as global cutoff values for intraspecific variation in fungi (Nilsson et al. 2008; Smith et al. 2007) and in *Tuber* spp. (Bonito et al. 2013) although it is unable to discriminate cryptic species of whitish truffles (Bonuso et al. 2010; Wang et al. 2013). For some species of the *Maculatum* clade, we adopted a more stringent threshold for species definition after the work of Guevara et al. (2013) on North American truffles. We defined a reference ITS sequence for each described species of the *Puberulum* group s.l. according to one of the following criteria (listed in order of priority) (Table 7.1, second column): (1) sequences from holotypes considered by the “ITS RefSeq Target Loci project” (Schoch et al. 2014); (2) sequences from holotypes characterized in various scientific works; and (3) sequences from specimens in which characters are congruent with those reported by Pegler et al. (1993), Astier (1998), Zambonelli et al. (2000b), Montecchi and Sarasini (2000), Rioussset et al. (2001), and Ceruti et al. (2003).

The validity of the reference sequences selected for *T. borchii* and *T. maculatum* is supported by the analysis carried out by Mello et al. (2000) which amplified some neotypes of “Vittadini original” collections with the species-specific primer pairs TBA–TBB (Mello et al. 1999) and TmacI–TmacII (Amicucci et al. 1998), respectively.

The ITS sequence divergence of each phylotype was measured by *p*-distance in MEGA6, using either the correctly identified or misidentified sequences as well as the unidentified sequences. Mean and max values of *p*-distance are reported in Table 7.1.

It has not been possible to assign reference ITS sequences to *T. asa* and *T. sphaerospermum* because, in our opinion, their genetic and morphological identity is still controversial. All sequences from GenBank identified as *T. asa* (1) and *T. sphaerospermum* (5) clustered within our *T. oligospermum* phylotype (<3% diversity).

Table 7.1 List of the described species within the *Puberulum* group sensu lato (*Puberulum*, *Maculatum*, and *Gibbosum* clades)

<i>Tuber</i> species (reference)	Ref. Seq.	GB Seq.	Id Seq.	Un Seq.	≠Species name	<i>p</i> -distance max/mean	≠ITS
Puberulum clade							
<i>T. anniae</i> (Colgan and Trappe 1997)	NR 119860 (1)	46	9	29	<i>T. pacificum</i> (7), <i>T. puberulum</i> (1)	0.034/0.013	
<i>T. borchii</i> (Vittadini 1831)	FJ554490 (3)	126	87	26	<i>T. maculatum</i> (1), <i>T. puberulum</i> (12)	0.036/0.012	13
<i>T. californicum</i> (Harkness 1899)	HM485351 (3)	7	5	2		0.004/0.001	
<i>T. cistophilum</i> (Alvarado et al. 2012)	NR119983 (1)	16	12	4		0.015/0.005	
<i>T. dryophilum</i> (Tulasne and Tulasne 1845)	AF003917 (3)	44	4	17	<i>T. melanosporum</i> (1), <i>T. puberulum</i> (11), <i>T. borchii</i> (9), <i>T. oligosporum</i> (2)	0.024/0.011	2
<i>T. latissporum</i> (Chen and Liu 2007)	NR119620 (1)	4	1	3		0.005/0.003	
<i>T. tijiangense</i> (Fan et al. 2011b)	KF805727 (2)	7	1	4	<i>T. microsphaerosporum</i> (1), <i>T. borchii</i> var. <i>sphaerosporum</i> (1)	0.013/0.008	
<i>T. liui</i> (Xu 1999)	DQ898182 (3)	1	1	0			
<i>T. oligosporum</i> (Trappe 1979)	KF021624 (3)	14	8	1	<i>T. sphaerosporum</i> (4), <i>T. asa</i> (1)	0.024/0.012	28
<i>T. pacificum</i> (Trappe and Castellano 2000)	HM485378 (3)	9	5	3	<i>Choironyces abvolatus</i> (1)	0.024/0.014	5
<i>T. pseudo-sphaerosporum</i> (Fan and Yue 2013)	KF744063 (2)	1	1	0			
<i>T. zhongdianense</i> (He et al. 2004)	NR119621 (1)	3	3	0		0.005/0.003	
<i>T. panzhihuanense</i> (Deng et al. 2013)	NR120126 (1)	13	12	1		0.001/0.000	
<i>T. sphaerosporum</i> (Gilkey 1939)	HM485390 (3)	4	4	0		0.008/0.006	
<i>T. huizeanum</i> (Fan et al. 2012b)	JQ910651 (2)	2	2	0		0.003/0.003	
<i>T. alboubilicum</i> (Li et al. 2014)	KJ742702 (2)	1	1	0			
<i>T. puberulum</i> (Berkeley and Broome 1846)	AJ969626 (2)	25	8	17		0.009/0.004	31
<i>T. separans</i> (Gilkey 1916)	HM485387 (3)	20	5	15		0.029/0.002	0
<i>T. pseudomagnatum</i> (Fan and Cao 2012)	NR111718 (1)	2	1	0	<i>T. liyuatum</i> (1)		
<i>T. sinosphaerosporum</i> (Fan et al. 2012c)	JX092086 (2)	2	0	0			

Maculatum clade		90	13	53		0.016/0.007	14
<i>T. maculatum</i> (Vittadini 1831)	AF003919 (3)				<i>T. rapaeodorum</i> (21), <i>T. borchii</i> (2), <i>T. dryophyllum</i> (1)		
<i>T. scruposum</i> (Hesse 1891)	DQ011845 (3)	14	4	10		0.018/0.007	12
<i>T. lauryi</i> (Guevara et al. 2013)	NR119862 (1)	13	6	7		0.020/0.008	
<i>T. rapaeodorum</i> (Tulasne and Tulasne 1843)	DQ011850 (3)	8	3	5		0.007/0.003	22
<i>T. shearii</i> (Murrill 1920)	HM485389 (3)	3	2	1			
<i>T. foetidum</i> (Vittadini 1831)	AJ557544 (3)	15	5	10		0.003/0.009	
<i>T. whetstoneae</i> (Frank et al. 2006)	NR119864 (1)	12	5	7		0.026/0.013	
<i>T. walkeri</i> (Guevara et al. 2013)	JF419265 (2)	9	7	2		0.021/0.015	
<i>T. beyerlei</i> (Guevara et al. 2013)	NR119866 (1)	2	0	2		0.005/0.005	
<i>T. guevarai</i> (Guevara et al. 2013)	JF419251 (3)	5	3	2		0.011/0.006	
<i>T. castilloi</i> (Guevara et al. 2013)	NR119865 (1)	19	6	13		0.031/0.014	
<i>T. miquihuanense</i> (Guevara et al. 2013)	NR119868 (1)	26	2	19	<i>T. rapaeodorum</i> (1), <i>T. scruposum</i> (3), <i>T. mexicanum</i> (1)	0.030/0.014	
<i>T. mexicanum</i> (Guevara et al. 2013)	NR119867 (1)	13	7	5	<i>T. miquihuanense</i> (1)	0.026/0.014	
<i>T. bomiense</i> (Su et al. 2013)	KC517480 (2)	3	0	3		0.00/0.00	
<i>T. microverrucosum</i> (Fan et al. 2012b)	JN870099 (3)	2	0	1	<i>T. liyuanum</i> (1)		
<i>T. linsdalei</i> (Gilkey 1954)	HM85370 (2)	2	1	1			
Gibbosum clade							
<i>T. bellisporum</i> (Bonito et al. 2010b)	NR121354 (1)	3	3	0		0.004/0.004	
<i>T. castellanoi</i> (Bonito et al. 2010b)	NR121355 (1)	4	4	0		0.002/0.001	
<i>T. gibbosum</i> (Harkness 1899)	FJ809868 (3)	13	11	2		0.014/0.003	
<i>T. oregonense</i> (Bonito et al. 2010b)	NR121356 (1)	14	14	0		0.002/0.001	

Reference sequence (Ref. Seq.), number of sequences in GenBank: total (GB Seq.), date of accession 18/01/2015), correctly identified (Id. Seq.), unidentified (Un. Seq.), misidentified [\neq species name, number (between brackets) of entries with same ITS phylogroup but differently named; \neq ITS, number of entries with same name but different ITS phylogroup] and intraspecific diversity (p -distance, mean, and max values calculated in MEGA6 software) are reported for each species

T. asa was considered synonym of *T. oligospermum* by Alvarado et al. (2012), but they were regarded as true species by other authors which, instead, considered *T. lacunosum* synonym of *T. asa* (Ceruti 1960; Montecchi and Sarasini 2000; Rioussset et al. 2001; Ceruti et al. 2003).

Tuber sphaerospermum has been promoted to the rank of species only recently by Roux (2006) but it was firstly identified as *T. borchii* var. *sphaerosperma* by Malençon (1973). The original description of its ascomata reported regularly spherical spores and a pseudoparenchymatous peridium. *Tuber oligospermum* shows the same spore morphology but a plectenchimatous peridium as described by Ceruti et al. (2003) who examined a syntype of the Mattiolo herbarium.

No ITS sequences are available in GenBank for the American truffle species *Tuber guzmanii* Trappe and Cázares, *Tuber irradians* Gilkey, and *Tuber levissimum* Gilkey which were included within the *Puberulum* group by Bonito et al. (2010a) based on the sequence of their LSU rDNA gene.

7.3 Unreliability of the ITS Accessions and Unknown Species

Several studies have questioned the taxonomic reliability of the entries in public sequence databases, demonstrating that more than 10 % of the identified ITS sequences from fungi have been incorrectly annotated (Bridge et al. 2003; Nilsson et al. 2006). Despite the efforts recently made by the scientific community to improve the quality and the interpretation of database submissions (Tedesoo et al. 2011; Nilsson et al. 2012), compromised annotations still hamper the correct interpretation of the molecular data of some fungal taxa. Among these, whitish truffles account for a significant number of incorrect annotations.

GenBank ambiguities have been revealed in two different ways with respect to each reference entry: (1) entries with the same ITS sequence but differently named (Table 7.1, column 6) and (2) entries with the same name but with ITS sequence clustering in a different phylotype (Table 7.1, column 8). According to our criteria of analysis, we found 83 ambiguous entries (31 % of total identified sequences belonging to the *Puberulum* group s.l.) in the first case and 127 ambiguous entries (47 % of total) in the second case. Erroneous annotations were found in 10 out of 38 described whitish truffle species represented by at least one GenBank entry (Table 7.1). The highest number of misidentified entries has been found for *T. puberulum*, *T. maculatum*, *T. oligospermum*, *T. rapaeodorum*, *T. dryophilum*, and *T. borchii* (Table 7.1). More than 75 % of the sequences identified as *T. puberulum* (31 out of 39), *T. oligospermum* (28 out of 36), and *T. rapaeodorum* (22 out of 25) fall into other phylotypes in addition to that of the respective reference sequence (Table 7.1, columns 4 and 8). On the contrary, *T. maculatum* and *T. dryophilum* show the highest number of sequences (24 and 23, respectively) erroneously accessioned under other whitish truffle species (Table 7.1, column 6).

The reliability of the recent described Asiatic species *Tuber polyspermum* (Fan et al. 2011a) and *Tuber microsphaerosporum* (Fan et al. 2012a) must be verified because they are both represented by a single ITS sequence clustering within the *Tuber lijiangense* L. Fan and J. Z. Cao phylotype. Likewise, the unique sequence identified as *T. murinum* (JF261371) is similar to those of the *Tuber beyerlei* Trappe, Bonito, and Guevara holotype. The validity of *T. murinum* was debated for a long time, and, recently, it has been ignored by taxonomists (Ceruti et al. 2003).

Also the number of insufficiently identified sequences attributable to described species of the Puberulum group s.l. is remarkable. In fact, 42 % (249 out of 594) of the sequences of these species are mainly from ECMs or soil clones with the highest values registered in *T. maculatum* (53 out of 90) and *Tuber anniae* W. Colgan & Trappe (29 out of 46).

Based on the sequences from mycorrhiza, soil clone and unidentified ascomata deposited in GenBank, Bonito et al. (2010a) added 25 and 12 putative undescribed species to the Puberulum and Maculatum clades, respectively. A number of these unknown phylotypes have been recently identified and their ascomata characterized (Guevara et al. 2013). Our analysis found a total of 53 unidentified phylotypes in the Puberulum (43) and Maculatum (10) groups, whereas no unidentified species were revealed for the Gibbosum group. Most of these unidentified phylotypes appeared only recently in GenBank (later than Bonito et al. 2010a), and 18 out of 53 are only represented by one sequence.

7.4 Phylogeography

Whitish truffles represent the most widely distributed group of species in the world although many of them appear to have a native distribution range restricted to continental or subcontinental scale. Indeed, truffle cultivation, forestry, and nursery trade have contributed to introduce a number of whitish truffle species into novel habitats (Barroetaveña et al. 2005; Hall et al. 2007; Bulman et al. 2010; Wang et al. 2013). However, to date, the number of species shared between continents is still low (six for both Puberulum and Maculatum groups).

7.4.1 *Puberulum* Clade

Puberulum clade is the most abundant and ubiquitous clade of whitish truffle species, with members distributed across Europe, Asia, North America, South America, and northern Africa (Fig. 7.2). A new unidentified species belonging to the Puberulum group was also found in Argentina analyzing ITS sequences from ECMs of *Nothofagus* spp. and *Salix humboldtiana* Willd. natural stands (Bonito et al. 2013). Based on the sequence metadata, all described species from Asia and America have been found only in China (11 species), the USA (*Tuber californicum* Harkn.; *Tuber pacificum* Trappe, Castellano, and Bushnell; *Tuber sphaerosporum*

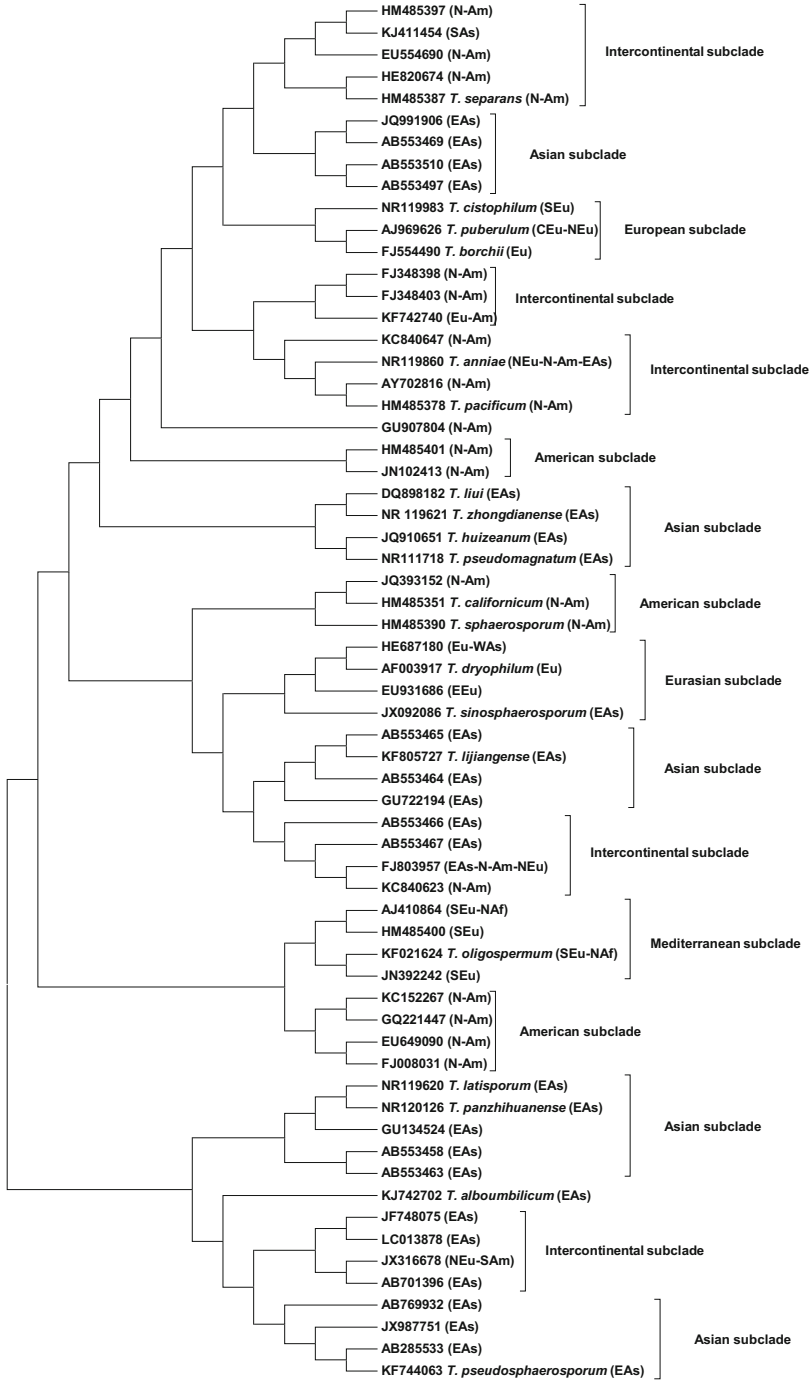


Fig. 7.2 Neighbor-joining tree (*p*-distance) of described and undescribed species of *Puberulum* clade. Accessions without the species name are referred to undescribed *Tuber* species. The bootstrap consensus tree was inferred from 100 replicates. Branches corresponding to partitions

Gilkey), or both the USA and Mexico (*Tuber separans* Gilkey). However, the number of entries attributable to these species is probably still too low to determine their entire range of distribution. On the contrary, four out of five species are widespread in Europe and have been also found in Iran (*T. dryophilum* and *T. puberulum*) and Morocco (*T. oligospermum*) or are cultivated around the world (*T. borchii*). According to the current metadata, *T. cistophilum* is only present in the Iberian Peninsula, and as *T. oligospermum*, it might be a species confined to the Western Mediterranean areas, with a preference for acid soils (Alvarado et al. 2012). The higher intraspecific diversity within *T. oligospermum* than *T. cistophilum* is probably due to the different range of collection sites. *Tuber oligospermum* has also been found outside the Iberian Peninsula, and its ITS sequences are grouped in two subclades, the first distributed in Morocco, Portugal, and Spain and the second in Sardinia (Italy) and Spain. On the contrary to the latter two species, the phylotype identified by us as *T. puberulum* almost grows in the northern temperate areas of middle Europe, from France and England to Poland and Czech Republic. To date, no molecular evidence of this species in Italian and Iberian Peninsulas as well as in the south Balkans or Scandinavia has been found.

Tuber borchii and *T. dryophilum* are ubiquitous in Europe and share the same distribution range and, often, also the same habitat (Iotti et al. 2010). Both species grow in cold-temperate to Mediterranean regions, from Iberian to Balkan Peninsulas (Hall et al. 2007). They are commonly found in calcareous sub-alkaline soils but can also colonize host species in acid soils (Peintner et al. 2007; Lancellotti and Franceschini 2013). ITS sequences of *T. borchii* are also from nonnative countries (the USA, British Columbia, New Zealand) probably due to increased cultivation of this truffle or introduced host plants. *Tuber borchii* is the whitish truffle mostly represented in GenBank with more than 120 entries, and our analysis revealed highest diversity within *Puberulum* group s.l. Its ITS variation is distributed between two main subclades, considered as cryptic species by Bonuso et al. (2010). Collections of the first group (clade I of Bonuso's work) are distributed mainly throughout Italy, whereas the second group (clade II) is ubiquitous in Europe. A significant genetic diversity was also found in *T. dryophilum* and the analysis of ITS sequence from 44 entries distinguished 6 subclades without any geographic structure. However, most of the diversity was found in Italy which might represent the area of diversification for this species.

Tuber anniae is the species of the *Puberulum* group with the largest geographical distribution. Its ascomata and ECMs have been mainly found in the coldest region of the Northern Hemisphere, but there is evidence for introduction of this species also in New Zealand (Bulman et al. 2010) and Hawaii (Hynson et al. 2013). Wang et al. (2013) considered *T. anniae* a species complex composed by three distinct



Fig. 7.2 (continued) reproduced in less than 50 % bootstrap replicates are collapsed. Evolutionary analyses were conducted in MEGA6. *Am* America, *N-Am* North America, *SAm* South America, *EAs* East Asia, *SAs* South Asia, *WAs* West Asia, *Eu* Europe, *NEu* North Europe, *SEu* South Europe, *CEu* Central Europe, *EEu* East Europe

clades not supported by distinct morphological differences of their ascomata. Members of the clade I have been only found in North America, whereas clades II and III represent geographically disjunct phylotypes, which both include sequences from Europe and North America (Wang et al. 2013). *Tuber anniae* has been recently found also in northern Japan (Hashimoto et al. 2012) to form symbiosis with *Betula ermanii* Cham., a tree species widespread also in Russian, Korea, and China (Li and Skvortsov 1999). So, this species complex could have a wider distribution range than previously supposed.

With respect to Bonito et al. (2010a), we found 23 additional unidentified phylotypes within *Puberulum* clade, mostly from East Asia. Two unidentified phylotypes (*Tuber* sp. 33 and *Tuber* sp. 29 from Bonito's work) have been recently described as *Tuber pseudosphaerosporum* L. Fan (Fan and Yue 2013) and *T. lijiangense* (Fan et al. 2011b).

7.4.2 *Maculatum* Clade

Maculatum clade includes ten described species found exclusively in North America (*Tuber shearii* Harkn.; *Tuber lauryi* Trappe, Bonito & Guevara; *Tuber whetstonense* J. L. Frank, D. Southw. & Trappe; *Tuber walkeri* Healy, Bonito & Guevara; *T. beyerlei*; *Tuber guevarai* Bonito & Trappe; *Tuber castilloi* Guevara, Bonito & Trappe; *Tuber miquihuanense* Guevara, Bonito & Cázares; *Tuber mexiusanum* Guevara, Bonito & Cázares, and *Tuber linsdalei* Gilkey) and four described species from Europe (*T. maculatum*, *Tuber scruposum* R. Hesse, *T. rapaeodorum*, *T. foetidum*) rarely found also in Asia (Fig. 7.3). In general, intra-specific ITS diversity of European species is lower than American species.

Within *Maculatum* group, *T. maculatum* was the phylotype with the highest number of ITS entries which are grouped in six main subclades. Members of these subclades share a similar geographic range of distribution, from the Netherlands to Iran and from Italy to Finland. A unique sequence from China forms an additional basal subclade which might represent a native Asiatic cryptic species of *T. maculatum* (GU134516). Our analysis revealed also the introduction of *T. maculatum* in Canada, the USA, and New Zealand.

Tuber maculatum ascomata can be easily confused with those of *T. rapaeodorum* and our analysis confirmed the taxonomic difficulties in distinguishing between these species (Table 7.1). According on our criteria for species selection, *T. rapaeodorum* should be only present in East Europe and South Caspian region.

Tuber scruposum was found in the same areas where *T. rapaeodorum* grow as well as in central Europe (Italy, Germany, and Austria). Its ITS sequences are grouped in two subclades which do not show any geographic structure. The reference sequence selected for *T. scruposum* correspond to the *Tuber* sp. 37 (*scruposum* 1) phylotype after Bonito et al. (2010a) which is phylogenetically distinct from *Tuber* sp. 40 (*scruposum* 2), found both in North America and Europe. ITS diversity between these two phylotypes (>7%) does not seem

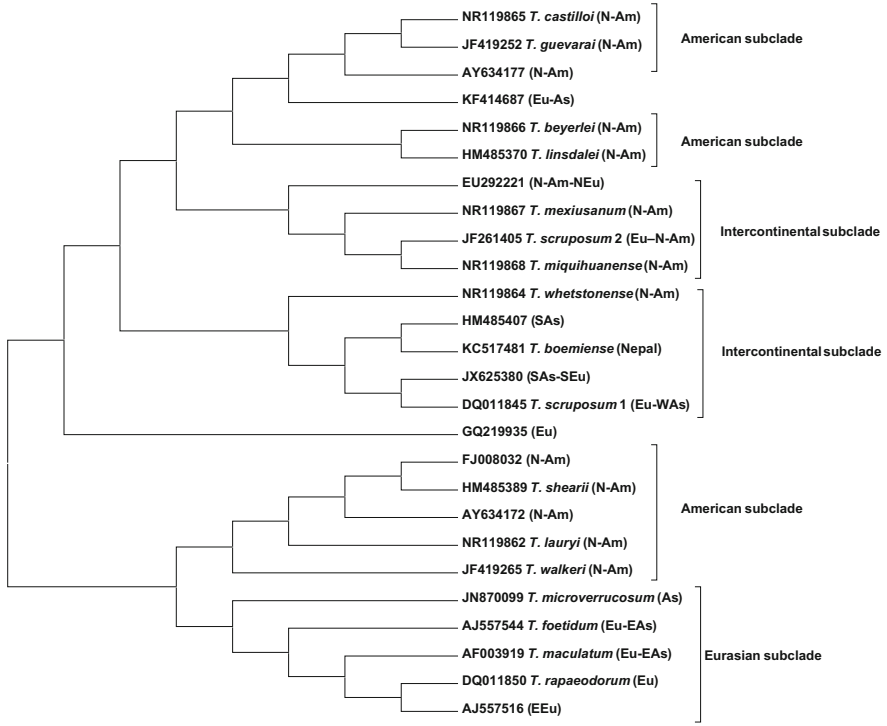


Fig. 7.3 Neighbor-joining tree (p -distance) of described and undescribed species of *Maculatum* clade. Accessions without the species name are referred to undescribed *Tuber* species. The bootstrap consensus tree was inferred from 100 replicates. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. Evolutionary analyses were conducted in MEGA6. *N-Am* North America, *As* Asia, *EAs* East Asia, *SAs* South Asia, *WAs* West Asia, *Eu* Europe, *NEu* North Europe, *SEu* South Europe, *EEu* East Europe

supported by evident differences in morphology of their ascomata. In fact, Badalyan et al. (2005) classified as *T. scruposum* the ascomata of both species collected in an oak-hornbeam forest near Dilijan (Armenia).

With respect to Bonito et al. (2010a), our analysis revealed only one new unidentified phylotype from ECMs collected in a *T. magnatum* truffle ground located in South Italy (Leonardi et al. 2013). Two unidentified phylotypes (*Tuber* sp. 39 and *Tuber* sp. 45 from Bonito's work) and other four new species have been recently described by Guevara et al. (2013).

7.4.3 *Gibbosum* Clade

Gibbosum clade includes only four described species (*T. gibbosum*, *Tuber bellisporum* Bonito & Trappe, *Tuber castellanoi* Bonito & Trappe, and *T. oregonense*). All 34 analyzed ITS sequences have been obtained by ascomata or

ECMs collected in western North America. Montecchi and Sarasini (2000) and Pomarico et al. (2007) reported *T. gibbosum* ascomata from Emilia-Romagna (northern Italy) and Basilicata (Southern Italy), respectively, but evidences for these collections are not available in GenBank database. This truffle species was probably introduced in Italy together with *Pseudotsuga menziesii* (Mirb.) Franco, a nonnative European tree present in both collection sites. Species of the *Gibbosum* clade are characterized by a low intraspecific ITS variation (Table 7.1), and unlike the other *Tuber* lineages, they appear to be exclusively associated with Pinaceae hosts (Bonito et al. 2010b; Bonito et al. 2013). Five years after Bonito et al. (2010a), also our analysis did not reveal unidentified phylotypes within *Gibbosum* clade.

7.5 Mycorrhizas

Many species of the *Puberulum* group s.l. have been proven to form ECMs with a wide range of host plants either in greenhouse or in the field. Mycorrhizas of *T. borchii* have been synthesized and described on a wide range of host plants: *Pinus strobus* L. (Scannerini and Palenzona 1967), *Pinus pinea* L. (Zambonelli et al. 1995), *Pinus radiata* D. Don (Duñabeitia et al. 1996), *Quercus robur* L. (Fontana et al. 1992; Boutahir et al. 2013), *Quercus pubescens* Willd. (Zambonelli et al. 1993), *Quercus suber* L. (Zambonelli and Branzanti 1989), *Tilia platyphyllos* Scop. (Granetti et al. 1995; Sisti et al. 1998), *Corylus avellana* L. (Zambonelli and Branzanti 1984; Fontana et al. 1992; Rauscher et al. 1996), *Populus* sp. (Fontana and Palenzona 1969), *Castanea sativa* Miller (Zambonelli and Branzanti 1989), *Alnus cordata* (Loisel.) Desf. (Zambonelli and Branzanti 1989), *Carya illinoensis* (Wangenh.) K. Koch (Benucci et al. 2012), and *Arbutus unedo* L. (Lancellotti et al. 2014). ECMs of *T. puberulum* on *Picea abies* Karst. (Blaschke 1988), *T. maculatum* on *Ostrya carpinifolia* Scop. (Zambonelli et al. 1999), *T. oligospermum* on *Quercus cerris* L. (Bencivenga et al. 1997), and *Q. robur* (Boutahir et al. 2013) have also been synthesized. In natural condition whitish truffles have been found in association with a broad host range, including both gymnosperm and angiosperm (Kovács and Jakucs 2006; Iotti et al. 2010; Leonardi et al. 2013). Whitish truffles are also susceptible to orchid colonization (Tešitelová et al. 2012).

ECMs established by the whitish truffle species share a common morphology and only little differences could be detected in some anatomical characters (Fig. 7.1). However, these differences are usually wide even within the same species and partially overlap between species of whitish truffles. Unramified ends are commonly club-shaped, straight, yellow ochre (younger tissues) to brown (older tissues), with a smooth or spiny surface. The mantle is pseudoparenchymatous with roundish to epidermoid cells, sometimes covered by a hyphal network, and the cystidia, when present, are needle-shaped, straight, or slightly bent, hyaline with a blunt tip and one basal septa (sometimes 2). Emanating hyphae are rare, septate, hyaline, without clamps, and not frequently ramified. Rhizomorphs have never been found.

Characters useful to discriminate ECMs of different whitish truffles can be only found in cystidia and mantle cells although the shape of mantle cells can slightly vary depending on the strain and the host plant (Giomaro et al. 2000). Kovács and Jakucs (2006) confirmed this statement analyzing ECMs formed by different species of the *Puberulum* group s.l. in natural conditions. For example, cystidia of *T. oligospermum* show a frequent basal inflation which can be used to discriminate ECMs of this species (Bencivenga et al. 1997; Boutahir et al. 2013). *Tuber maculatum* ECM differs from those of *T. borchii* for the shorter cystidia (Zambonelli et al. 1999).

7.6 Conclusions

The *Puberulum* group s.l. is the phylogenetic group inside the genus *Tuber* having the greatest genetic and species diversity, not supported by a similar variability in morphology of ascomata, ECM, or mycelia. Most of the whitish truffle species are difficult to differentiate morphologically and the number of cryptic species within this group is probably high. As a consequence, these species are often misidentified or insufficiently identified in GenBank, and, so, caution has to be exercised in interpreting the BLAST results for the molecular identification.

This context led to confusion among researchers who are concerned with the study of these truffles. Moreover, being some whitish truffles of high economic importance, this confusion may have negative effects on truffle market and cultivation. In fact, in many parts of Italy and throughout Europe, the precious species *T. borchii* is very often confused with other *Tuber* species in the *Puberulum* group s.l. such as *T. maculatum*, *T. dryophilum*, and *T. puberulum* which have poor culinary quality (Montecchi and Sarasini 2000). Misidentification of *T. borchii* ascomata may produce ecological and economic problems when alien or nontarget species are used to inoculate the seedlings for truffle cultivation.

We aim that reference sequences and morphological considerations reported in this chapter will help in research and practical studies on whitish truffles and will be a starting point for developing shared species concepts.

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