## Chapter 5 State of the Art of the Research on *Boletus edulis*

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### 5.1 Introduction

The genus Boletus belongs to the family Boletaceae, order Boletales, and consists of a complex of ectomycorrhizal fungal species. A large number of plants are suitable hosts: Fagales, Fagaceae (Castanea, Castanopsis, Fagus, Lithocarpus, Quercus) and Betulaceae (Carpinus, Corylus, Betula, Ostrya, Populus); Malvales, Malvaceae (Tilia) and Cistaceae (Cistus); Malpighiales, Salicaceae (Salix); Ericales, Ericaceae (Arctostaphylos); and Pinales, Pinaceae (Abies, Keteleeria, Picea, Pinus, Tsuga) (Olivier et al. 1997; Águeda et al. 2006; Mello et al. 2006). Among many sections, the section Boletus Singer (=Edules Fr. 1838) known as "porcini" is a conspicuous group of wild, edible mushrooms (Singer 1986; Murat et al. 2008; Sitta and Floriani 2008). Their reported distribution throughout the Northern Hemisphere was mostly limited to the sampling of European species. Nevertheless, they are popular in Europe and are becoming an economic resource North America also (Arora 2008). A global geographic sampling together with the selection of four loci—the fast-evolving in nuclear internal transcribed spacer (Fig. 5.1), the nuclear large subunit of the ribosome, the largest subunit of the nuclear gene encoding RNA polymerase II, and the mitochondrial ATPase subunit 6-has allowed Dentinger et al. (2010) to trace the molecular phylogenetics of these mushrooms. On this basis authors could recognize 18 reciprocally monophyletic species, show the monophyly of porcini, and expand their known distribution to Australia and Thailand. However, this global analysis did not consider Boletus pinetorum, a new species described using both morphological and molecular analysis by Korhonen et al. (2009) who focused on section Boletus in Fennoscandia.

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Fig. 5.1 Phylogram of the best maximum likelihood tree using *Boletus* ITS sequences. Clades that correspond to species are *shaded* and labeled with the specific epithet on the *right*. Geographic range of each species is indicated at *right*. Figure reprinted by "Molecular Phylogenetics and Evolution," 57, Dentinger et al., Molecular phylogenetics of porcini mushrooms (*Boletus* section *Boletus*), 2010, with permission from Elsevier

Many attempts to cultivate edible boletes have been made (Hall et al. 1998). This practice mostly concerned species belonging to *B. edulis* sensu lato (s.l.), such as *Boletus edulis* Bull.: Fr. sensu stricto (s.s.), *B. aereus* Bull.: Fr., *Boletus pinophilus* Pilát & Dermek, and *Boletus aestivalis* (Paulet) Fr. (Fig. 5.2). These fruiting bodies are in high demand; these mushrooms have a pleasant flavor and texture and are used in huge quantities for the production of dried mushroom soups. Preparations of these dried mushrooms sometimes include different species even some not belonging to section *Boletus*, such as *Boletus violaceofuscus*. Although Helbling et al. (2002) report that *B. edulis* induces allergic IgE-mediated symptoms, no taxonomic indication is given concerning *B. edulis* (sensu stricto or sensu lato), so the identity of the specific mushroom culprit remains unclear. Therefore, specific primers have been designed within the internal transcribed spacer rDNA region for the unambiguous



Fig. 5.2 Pictures of *Boletus aestivalis* (a), *Boletus aereus* (b), *Boletus pinophilus* (c), and *Boletus edulis* (d). Photos by Alfredo Vizzini

detection of these five species (Mello et al. 2006). The availability of these primers represents a crucial resource for detecting these fungi. Next steps are focused toward the analysis of the genetic structure of these fungi, as well as the certification of mycelia to be used as inocula in long-term reforestation programs focused on increasing bolete production. The broad host range of *B. edulis* makes it a suitable species to be introduced with various host tree species during reforestation efforts.

# 5.2 From *Boletus edulis* Molecular Identification to Cultivation

Many researchers have synthesized ectomycorrhizae of the *B. edulis* species complex on various hosts (Froidevaux and Amiet 1975; Tozzi et al. 1980; Molina and Trappe 1982a, b; Ceruti et al. 1983–1984, 1985; Poitou et al. 1982; Duñabeitia et al. 1996). However, the identification of the mycelia obtained by strain isolation and used as inoculum could not be confirmed by molecular analysis nor could the identification of the synthesized ectomycorrhizae. Because of this and other problems, when seedlings inoculated with *Boletus* species have been outplanted, the ectomycorrhizae of *Boletus* sp. are quickly replaced by other ectomycorrhizal fungi, and fruiting body production has never been successful (Olivier et al. 1997; Meotto et al. 1999; Wang and Hall 2004). Only more recently, Águeda et al. (2008) were able to synthesize ectomycorrhizae of *B. aereus*, *B. edulis*, and *B. reticulatus* (=*B. aestivalis*) with *Cistus* sp. and to provide molecular identification of the fungal strains isolated from fruiting bodies. Controlled mycorrhization now seems feasible opening new perspectives on the cultivation of these commercial mushrooms, which

have been collected exclusively from the wild (Cannon and Kirk 2007). In addition, *B. edulis* is regarded as a species tolerant to salinity stress, an adaptation that should be selectively advantageous in reforestation ecosystems (Liang et al. 2007). In order to understand the adaptive mechanisms of *B. edulis* to salt stress, proteomics was used to study the global expression profile of proteins in response to this stress. When the *B. edulis* was exposed to salt stress conditions (4 % NaCl, w/v), proteomic changes included proteins related to multiple cellular processes (e.g., metabolisms, energy-related processes, DNA repair, cell cycle control, and stress tolerance) (Liang et al. 2007).

# 5.3 In Field Characterization of *Boletus edulis* Mycelium and Mycorrhizae

Tracking the dynamics of an ectomycorrhizal fungus is a difficult task because fruiting bodies do not reflect the distribution of underground mycelial networks (Dahlberg 2001). Generally, the first analyses on the distribution of an ectomycorrhizal fungus focused on the fruiting bodies, which were followed by analyses of the mycorrhizae and extraradical mycelium in the soil. Few studies have been conducted on the ecology of the *B. edulis* complex. A first description and molecular characterization of the ectomycorrhizae of B. edulis on Cistus ladanifer L. was made by Águeda et al. (2006) by sampling field ectomycorrhizae and soil rhizomorphs under the fruiting bodies of B. edulis. Mycorrhizae of B. edulis, B. aestivalis, and B. aereus on Castanea sativa were detected in the field by Peintner et al. (2007). These mycorrhizae were morphologically similar to each other and showed the anatomo-morphological features previously described on C. ladanifer, except the color, which was darker ochre. In this investigation, ectomycorrhizae of B. edulis s.l. and soil fungal communities were characterized by molecular methods in a habitat with high production of B. edulis s.l. fruiting bodies. The first outcome of this investigation was that large amounts of basidiomes result from abundant mycorrhizae, but rare mycelia. While Boletus fruiting bodies dominated the aboveground fungal community, Boletus mycelia were rare in the soil and had a scattered distribution (Peintner et al. 2007). This finding is in agreement with a study by Zhou et al. (2001) showing that amounts of subterranean mycelia and mycorrhizae are not always correlated to the number of fruiting bodies formed by them. It is known that fructification is affected by habitat characteristics and climatic conditions (Bonet et al. 2004; Pinna et al. 2010) and depends on the presence of mycelium in the soil. Thanks to the progress of real-time PCR techniques, a quantification of *B. edulis* extraradical mycelium in a Scots pine forest soil was carried out (De la Varga et al. 2011). In this work the productivity of fruiting bodies was not correlated either with the concentration of B. edulis mycelia in soil samples or with the abundance of B. edulis mycorrhizae, whereas a statistically significant positive correlation was detected between the concentration of mycelia of *B. edulis* in the soil samples and the presence of *B. edulis* mycorrhizae in these samples. The lack of correlation between the concentration of the mycelium in the soil and the productivity of fruiting bodies has also been shown in *T. melanosporum* orchards (Suz et al. 2008).

#### 5.4 Applications of *B. edulis*

While ecologists are interested in deciphering the lifestyle of boletes, the common mushroom B. edulis is also an object of research aimed to discover important properties in edible fungi (see also Chap. 18). Since fungi are the most productive biological sources of various primary and secondary metabolites, they have long been exploited by the pharmaceutical and food industries. Heleno et al. (2011), in a targeted analysis of metabolites in wild *Boletus* species, revealed an important source of proteins, carbohydrates, fatty acids (mainly linoleic acid), sugars (mainly mannitol and trehalose), and vitamins (tocopherols and ascorbic acid) in *B. edulis*, B. aereus, and B. reticulatus, as well as phenolic acids. The finding of various macronutrients favors the consumption of these species not only for their taste and aroma but also as source of nutrients. On the other hand, the presence of phenolic acids, which has been correlated to antioxidative properties, can be exploited by food and pharmaceutical industries. In addition, polysaccharides extracted from B. edulis have shown important antioxidative properties and might be employed as ingredients in healthy and functional food to alleviate the oxidative stress (Zhang et al. 2011). As result of recent investigations, a lectin with antitumoral properties has been found, opening new perspectives in research aimed at developing new drugs for cancer therapy (Bovi et al. 2011). 1-Octen-3-ol is a characteristic aroma compound produced by mushrooms, including *B. edulis*, and is often added as flavoring in processed products such as dehydrated soups (probably because of huge losses of 1-octen-3-ol during the preparation of these food products) (Zawirska-Wojtasiak 2004). De Pinho et al. (2008) correlated the pattern of volatiles with the overall aroma of 11 wild edible mushrooms and discovered that only B. edulis presented linoleic acid that, as all a long-chain unsaturated fatty acids, shows antibacterial activity and is used as antimicrobial food additive. While metabolites are the object of interest for industrial applications, few studies have investigated their biological role in nature, such as their role in the interactions with other fungi, bacteria, and plants. In this regard, Splivallo et al. (2011) examined specific aspects of volatile ecology and biology of other ectomycorrhizal mushroom highly appreciated for their special taste and aroma, the truffles. To date, more than 200 volatile organic compounds have been described from various truffle species, and the biosynthetic pathways/genes involved in volatile biosynthesis have been traced in the recently sequenced genome of *Tuber melano*sporum Vittad. (Martin et al. 2010).

In a recent survey aimed to investigate metallic elements in wild-grown mushrooms, the use of *B. edulis* has established a baseline measure of regional mineral status and heavy metal pollution (Falandysz et al. 2011). It is known that

mushrooms are involved in the biogeochemical cycling of metallic elements and metalloids, and there is interest in understanding the mechanisms involved in bioconcentration of metallic elements by mushrooms.

### 5.5 Conclusions

Among the sections of the genus *Boletus*, the species belonging to the *B. edulis* complex have received more attention because of their commercial use. The application of morphological and molecular methods has allowed the production of B. edulis certified mycelia, and consequently inocula, and in vitro mycorrhizae, but research in field is still in its infancy. Although the detection of mycorrhizae and extraradical mycelium is feasible, no conclusions can be given on how this fungus completes its life cycle in time and space or on the population size. More long-term studies are needed to elucidate the genetic structure of B. edulis. Recently the ultrahigh-throughput DNA sequencing (UHTS) has dramatically changed the nature of biological research. These new sequencing technologies provide a tremendous amount of DNA sequence data with reduced costs, effort, and time as compared to Sanger sequencing (Fox et al. 2009). Among the UHTS numerous applications, genome sequencing/resequencing is opening new perspectives through understanding the biology and ecology of fungi. The sequencing of the mycorrhizal genomes has just started. The first sequenced genome is that of the basidiomycete Laccaria bicolor (Maire) P. D. Orton followed by the genome of the ascomycete T. melanosporum (Martin et al. 2008, 2010). The comparison of genomic traits in the two ectomycorrhizal fungi clearly indicated that the evolution followed along different ways in ascomycetes and basidiomycetes. Since the availability of genome sequences from ecologically and taxonomically diverse fungi would allow comparative studies to understand the evolutionary mechanisms of symbiosis, the US Department of Energy Joint Genome Institute launched the Fungal Genomics Program (FGP) (Martin et al. 2011). This program scheduled the sequencing of the genomes of 25 mycorrhizal fungi that have been chosen on the basis of their different affiliations, types of symbiosis they establish, and host specificity (http://mycor.nancy.inra.fr/blogGenomes/?p=1334). The genomes of some of them [Amanita muscaria (L.) Lam., Cenococcum geophilum Fr., Hebeloma cylindrosporum Romagn., Laccaria amethystina Cooke, Oidiodendron maius G. L. Barron, Piloderma croceum J. Erikss. & Hjortstam, Paxillus involutus (Batsch) Fr., Pisolithus microcarpus (Cooke & Massee) G. Cunn., and Pisolithus arhizus (Scop.) Rauschert (= Pisolithus tinctorius) have been just sequenced and preliminary data presented at the first Mycorrhizal Genomics Workshop held in Nancy in September 2011. B. edulis genome sequencing will follow soon [together with that of Cantharellus cibarius Fr., Coltricia cinnamomea (Jacq.) Murrill, Cortinarius glaucopus (Schaeff.) Fr., Gymnomyces xanthosporus (Hawker) A. H. Sm., Lactarius quietus (Fr.) Fr., Meliniomyces bicolor Hambl. & Sigler, Paxillus rubicundulus P. D. Orton, Ramaria formosa (Pers.) Quél., Rhizoscyphus ericae (D. J. Read) W. Y. Zhuang & Korf, *Scleroderma citrinum* Pers., *Suillus luteus* (L.) Roussel, *Sebacina vermifera* Oberw., *Tomentella sublilacina* (Ellis & Holw.) Wakef., *Tricholoma matsutake* (S. Ito & S. Imai) Singer, *Tulasnella calospora* (Boud.) Juel, and *Terfezia boudieri* Chatin] allowing the identification of crucial genetic traits driving symbiosis and fruiting body development. This could, in the future, provide tools for the management of this precious fungus *in situ*.

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