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Draft Genome Sequence of *Tuber borchii* Vittad., a Whitish Edible Truffle

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ABSTRACT The ascomycete *Tuber borchii* (Pezizomycetes) is a whitish edible truffle that establishes ectomycorrhizal symbiosis with trees and shrubs. This fungus is ubiquitous in Europe and is also cultivated outside Europe. Here, we present the draft genome sequence of *T. borchii* strain Tbo3840 (97.18 Mb in 969 scaffolds, with 12,346 predicted protein-coding genes).

The whitish truffle (*Tuber borchii* Vittad.) is an ectomycorrhizal ascomycete ubiquitous in Europe growing from cold temperate to Mediterranean climates (1). *T. borchii* is found in subalkaline and acid soils associated with a wide range of hosts, including oak, poplar, strawberry, and pine trees (1, 2). Seedlings inoculated with *T. borchii* have been available since 1969 (3), and this species is also cultivated outside Europe in Australia, the United States, and New Zealand (4). Before the release of the genome sequence of the black truffle of Périgord (*Tuber melanosporum*) (5), *T. borchii* was the most studied truffle species, as it is amenable to laboratory manipulations (6).

Tuber borchii strain Tbo3840 was isolated from a fruiting body harvested in April 2010 at Guzzano (Pianoro) in central Italy. For the genome sequencing, the vegetative haploid mycelium was grown in liquid modified Woody plant medium (7) for 2 months at 22°C in the dark. DNA was extracted from 2 g of mycelium by using a modified cetyltrimethylammonium bromide (CTAB) protocol (8). The genome sequencing was performed using Pacific Biosciences RS II version C4 chemistry. The genome assembly was generated with Falcon version 0.4.2 (9), improved with FinisherSC version 2.0 (10), and polished with Quiver (11). Contigs shorter than 1,000 bp were excluded from the assembly. RNA was extracted from 40 mg of mycelium ground in liquid nitrogen with the RNeasy plant minikit (Qiagen, Hilden, German), according to the provider's recommendations, and using the RLC lysis buffer. The RNA quality and quantity were checked with the Experion RNA StdSens analysis kit (Bio-Rad, Hercules, CA). Three micrograms of RNA was used for RNA sequencing using the Illumina HiSeq 2500 platform and *de novo* assembled using Rnnotator (12). The genome was annotated using the JGI annotation pipeline (13, 14).

The nuclear genome assembly is 97.18 Mb long in 969 scaffolds (N_{50}, 0.19 Mbp), with 47.12% of repeated sequences (http://genome.jgi.doe.gov/Tubbor1). *T. borchii* has a reduced genome size compared to other truffle species, such as *Tuber aestivum* (145 Mb) (15), *Tuber magnatum* (192 Mb) (15), and *T. melanosporum* (125 Mb) (5). A total of 12,346 protein-coding genes were predicted, with an average length of 1,521 bp and 379 amino acids for genes and proteins, respectively. This number of gene models is higher than that in *T. melanosporum* (7,496 genes annotation version 1.0) (5) but similar

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to that of the closely related pezizomycete *Pyronema confluens* (13,367 genes) (16). As found in *T. melanosporum,* glycoside hydrolase 6 (GH6) and GH7 are absent from the *T. borchii* genome, confirming that ectomycorrhizal species have a reduced content of plant cell wall-degrading enzymes (5, 8). The haploid genome of *T. borchii* Tbo3840 exhibits the mating type locus MAT1-2-1 with HMG box (protein identification [ID] 1092840); the other mating type locus was not detected, as expected for a heterothallic species (6, 17).

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number NESQ00000000. The version described in this paper is version NESQ01000000. All of the sequences are also available at the JGI-DOE Mycocosm portal (13) (http://genome.jgi.doe.gov/Tubbor1).

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