UNIVERSITÀ DEGLI STUDI DELL'AQUILA

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Dipartimento di Medicina Clinica, Sanità Pubblica, Scienze della Vita e dell'Ambiente

Project I.S.A.T. (Innovative Sicilian Autochthonous Truffle): Report of the experimental analyses and results obtained

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State-of-the-art

Tuber aestivum is one of the truffle species with the greatest ecological adaptability and distribution on a continental scale. This species grows wild from Portugal (Santos-Silva & Brígido, 2024) to the southern coasts of the Caspian Sea in Iran (Jamali, 2017) and from the island of Gotland in southern Sweden (Wedén et al., 2004) to the Middle Atlas range in Morocco (Henkrar et al., 2023). Its presence is documented from sea level up to 1,600 m altitude, depending on latitude.

Its ecological plasticity allows it to be cultivated even in extreme environments, such as the boreal regions of Scandinavia (Shamekh et al., 2014), where other truffle species fail to develop. The fruiting period, at the continental level, covers almost the entire year depending on latitude and altitude, limited mainly by summer drought and winter frosts (Le Tacon, 2016). Optimal climatic conditions for T. aestivum include an average annual temperature between 6.8 and 11.5 °C and annual precipitation between 400 and 1,500 mm (with an optimum around 750 mm) (Molinier et al., 2016a). The average temperature of the coldest month rarely falls below 0 °C, while that of the warmest month is around 20 °C.

The effects of climate change on the distribution and productivity of *T. aestivum* are still not entirely clear, but recent studies indicate that higher summer temperatures reduce yield (approximately 20 % per additional degree) and threaten the survival of many local ecotypes (Steidinger et al., 2022).

With regard to soils, *T. aestivum* grows in a wide range of substrates, from sandy to loamy-clayey, but generally avoids excessively clayey soils (Robin et al., 2016). The optimum pH is around 7.5, although the species can also thrive in sub-acidic (pH 5.9) or alkaline (pH 8.5) soils, with highly variable lime contents but generally lower than those preferred by *T. melanosporum* and *T. magnatum*. In the natural forests where it grows, the organic matter content usually ranges between 5% and 10%,

but the species is also often cultivated in agricultural soils with values close to 0% (Robin et al., 2016).

The summer truffle represents a significant economic and ecological resource for Sicily, as highlighted in the study by Calvo et al. (2022) conducted in the Monti Sicani Regional Park. The presence of this species on the island has been documented since 1845, when it was first reported in Caltagirone, and has since been confirmed in numerous other localities. In Sicily, *Tuber aestivum* grows primarily in calcareous soils, in association with oak woods such as *Quercus ilex*, *Q. pubescens*, and *Q. virgiliana*. It prefers sub-humid Meso-Mediterranean bioclimates, though it has also been found in drier environments, such as the Cammarata area.

In recent years, summer truffle harvesting has assumed an increasingly important role in the local economy, particularly in Sicily's disadvantaged rural areas. With 278 active truffle hunters across the region, this activity provides a complementary source of income and a concrete opportunity to promote food and wine tourism. A significant step forward was taken with the approval of Regional Law No. 496 of 2020, which introduced specific regulations for the collection and marketing of truffles, establishing quantitative limits and making a license mandatory for gatherers. However, the lack of a structured market and reliable official data has so far hindered the sector's full development.

In this context, the geographical characterization of the Sicilian summer truffle represents a significant scientific and technical challenge. This is due to the high genetic variability of the *Tuber aestivum* species and the ecological complexity of its harvesting areas. The ability to objectively and reproducibly verify the Sicilian origin of this truffle—one of the most sought-after and marketed species worldwide—would pave the way for essential forms of protection and valorization, such as obtaining a Protected Geographical Indication (PGI) status. Such recognition would not only strengthen the product's competitiveness in the global market but also promote the sustainable development of the island's inland areas, enhancing Sicily's natural and cultural heritage.

Methodologies

Pre- and post-planting soil fungal community analysis

All soil samples subjected to physico-chemical parameter analysis[1], both pre- and post-planting, were freeze-dried for 3 days at -57 °C in a VirTis Benchtop freeze dryer to remove water and subsequently sieved (# mesh = 2 mm) to eliminate small gravel and organic fragments (roots, leaves, etc.). DNA

[1] The results generated by the accredited laboratory EcoLab (Avezzano, AQ) are provided in the appendix, while the IDs of the analyzed soil samples are listed separately (pagg. 10, 22). Evaluation and interpretation of the physico-chemical analyses are reported in the final technical-scientific document prepared by Prof. Giovanni Pacioni (Scientific Director, I.S.A.T.).

was extracted in triplicate from 250 mg of freeze-dried soil using the DNeasy PowerSoil Pro Kit (QIAGEN), following the manufacturer's instructions (Figure 1).

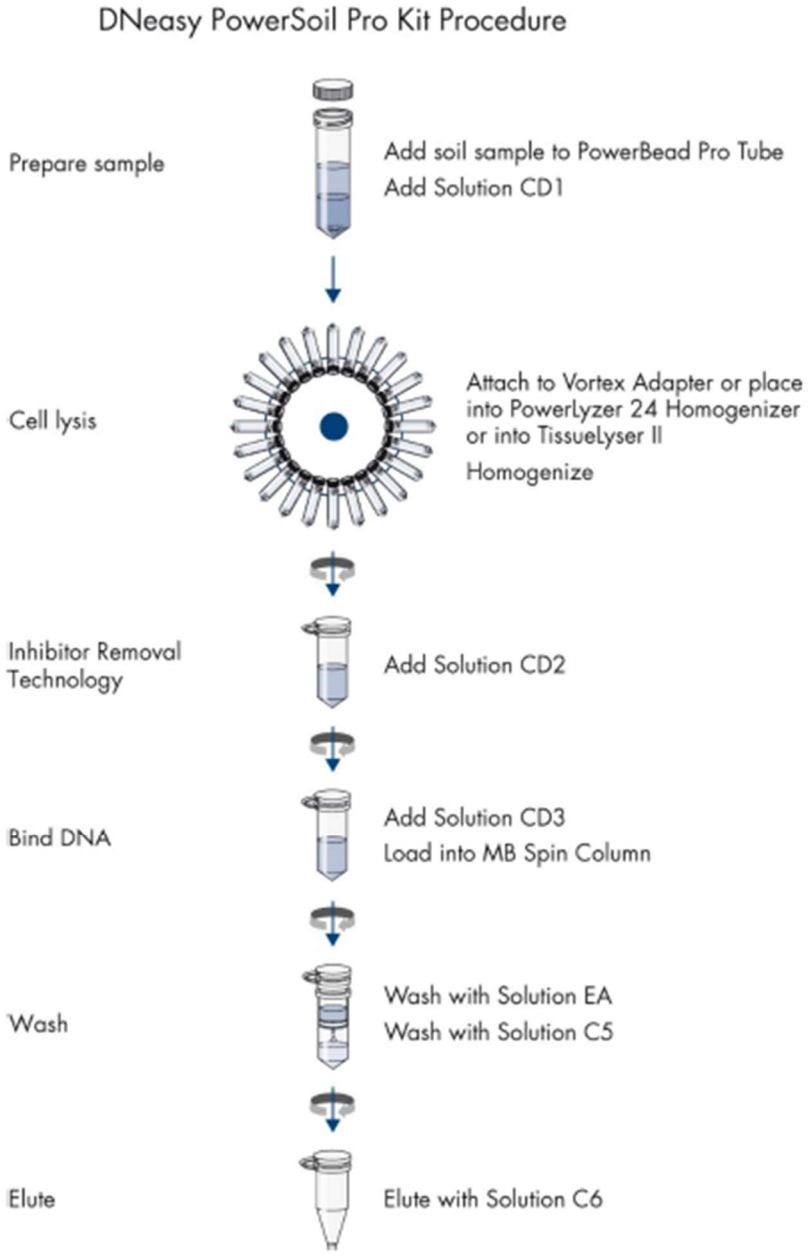

Figure 1: Synthetic DNA extraction protocol from soil with the DNeasy PowerSoil Pro kit.

The extracted DNA was quantified using a fluorometric method (Qubit 4 Fluorometer, Invitrogen), and its quality was assessed spectrophotometrically by evaluating the 260/230 and 260/280 absorbance ratios (NanoDrop 2000, Thermo Fisher Scientific), as well as by PCR amplification with the universal primers ITS1F–ITS4 (Gardes & Bruns, 1993; White et al., 1990). PCR products obtained with these primers were subsequently subjected to species-specific PCR amplification using the UncI–UncII primer pair designed by Mello et al. (2002), which selectively amplifies *T. aestivum*

DNA. This procedure was performed to confirm the presence or absence of *T. aestivum* DNA in the soil samples (Table 1).

Region	Direction	Primer Name	Primer Sequence (5'→ 3')	Riference	Specificity
ITS1	Forward	ITS1-F	CTTGGTCATTTAGAGGAAGTAA	Gardes & Bruns (1993)	Fungi
ITS2	Reverse	ITS4	TCCTCCGCTTATTGATATGC	White et al. (1990)	Universal
ITS1	Forward	UncI	TGGGCCGCCGAAAACTTG	Mello et al. (2002)	*Tuber aestivum*
ITS2	Reverse	UncII	CTGACGAGATGCCCCGGA	Mello et al. (2002)	*Tuber aestivum*

Table 1: Generic fungal primers and *Tuber aestivum*-specific primers used for PCR amplification of DNA isolated from different substrates.

The thermal cycling profiles for the two amplifications were as follows:

- **ITS1F/ITS4**: initial denaturation at 95 °C for 5 min; 35 cycles of denaturation at 94 °C for 45 s, annealing at 55 °C for 30 s, and extension at 72 °C for 1 min; followed by a final extension at 72 °C for 10 min.
- **UncI/UncII**: initial denaturation at 95 °C for 4 min; 27 cycles of denaturation at 95 °C for 1 min, annealing at 59 °C for 45 s, and extension at 72 °C for 45 s; followed by a final extension at 72 °C for 5 min.

PCR amplification products were verified by electrophoresis on 1.5% (w/v) agarose gels.

The DNA extracted from soil samples was submitted to Eurofins Genomics for "Microbiome profiling" analysis using Illumina MiSeq technology, with the aim of taxonomically characterizing the fungal communities present in the samples on a large scale. Sequencing targeted the ITS region of the ribosomal DNA. The raw data provided by the sequencing service were subsequently filtered to remove low-quality sequences, and the remaining reads were clustered into taxonomic units (species, genus, etc.). For each taxonomic unit, the relative abundance was calculated using the following formula:

$$Relative\ abundance\ per\ taxonomic\ unit\ (\%) = \left(\frac{N_{unit}}{N_{total}}\right) \times\ 100$$

The microbiome analysis pipeline consisted of three main stages, with several intermediate filtering steps:

- Demultiplexing

  All reads that passed the standard Illumina quality filter (PF reads) were demultiplexed according to their index sequences.

- Primer removal

  The forward and reverse primer sequences of the target region were identified and removed from the start of the raw forward and reverse reads. If primer sequences did not match perfectly (no mismatches allowed), the read pairs were discarded at this stage to retain only high-quality reads.
- Read assembly

  When the ends of forward and reverse reads overlapped, they were merged to generate a single longer read covering the entire target region. If the target region was longer than twice the read length, merging should not be possible; in such cases, any read pair that was nevertheless merged was considered an artifact and removed during subsequent filtering. If the target region was slightly shorter than twice the read length, merging could fail due to insufficient overlap at the read ends, typically allowing only a fraction of read pairs to be successfully merged. In all cases where some read pairs could not be merged, the high-quality forward read was retained and processed in subsequent steps.

Reads were merged when possible, and the high-quality forward read was used as an alternative. No read pairs were entirely discarded at this stage.

- Quality filtering

  Merged reads were filtered based on the expected length and known variations of the target region (see Table 2). Reads that were significantly shorter than the minimum expected length or significantly longer than the maximum expected length of the target region were discarded at this stage. Additionally, merged or retained reads containing ambiguous bases ("N") were removed.

Region code	Expected length	Merging efficiency
ITS1b	(highly variable)	high
ITS2a	ca. 350 bp	high

Table 2: Target regions, approximate expected lengths, and read assembly efficiency.

Taxonomic composition of each sample was assessed by querying NCBI (https://www.ncbi.nlm.nih.gov/nuccore), UNITE (https://unite.ut.ee/), and BOLD (https://boldsystems.org/) databases using the Blastn algorithm (Altschul et al., 1990).

Molecular analysis of ectomycorrhizae

Mycorrhizal root tips from *Cistus incanus* and *Carya illinoinensis* plants were subjected to molecular analysis to verify the presence of *Tuber aestivum* and to assess the potential transfer of its mycelium from the inoculated host plants (*Cistus incanus*) to the potential host plants already present at the plantation sites. Selected root tips, after careful cleaning, were processed to extract total DNA from both the host and the mycobiont using the DNeasy Plant Mini Kit (Qiagen), following the protocol illustrated in Figure 2.

Figure 2: DNA extraction workflow using the Qiagen DNeasy Plant Mini Kit.

The extracted DNA was qualitatively assessed by electrophoresis on 1% (w/v) agarose gels. Two microliters of extract from each sample were subsequently subjected to PCR amplification to confirm both the identity of the host tree and the presence of *Tuber aestivum*. For the former, DNA extracted from *Cistus incanus* and *Carya illinoinensis* leaves was used as a positive control, while for the latter, DNA extracted from *T. aestivum* ascoma was used as the positive control.

Host plant check was performed following Demesure et al. (1995), using barcoding primers specific to the plastid trnL region: trnC (5′-CGAAATCGGTAGACGCTACG-3′) and trnD (5′-GGGGATAGAGGGACTTGAAC-3′). The PCR profile for amplifying the trnC–trnD region consisted of an initial denaturation at 94 °C for 4 min, followed by 35 cycles of denaturation at 92 °C for 45 s, annealing at 55 °C for 45 s, and extension at 72 °C for 1 min, with a final extension at 72 °C for 10 min. Amplification products were checked by electrophoresis on 1.5% (w/v) agarose gels.

The presence of *T. aestivum* mycelium in ectomycorrhizae collected beneath *Cistus incanus* and *Carya illinoinensis* was assessed using the same DNA extracts described above and the species-specific primer pair UncI/UncII (Mello et al., 2002), following the amplification protocol previously reported.

Molecular analyses for the characterization of Sicilian Tuber aestivum populations

Ascomata of Sicilian *T. aestivum* from three sites (Sicani Mountains, Iblei Mountains, and Nebrodi Mountains) were analyzed to identify markers of geographical origin.

DNA was extracted from whole ascomata, sampling the internal gleba under sterile conditions and preserving it in 96% ethanol without denaturing agents. In the laboratory, samples were dried using a speed-vac, weighed, and portioned for subsequent extraction.

DNAs were extracted by the DNeasy Plant Mini Kit (Qiagen) according to the manufacturer's instructions, as previously described. Prior to chemical lysis, each sample was disrupted with a TissueLyser bead mill (Qiagen). DNA was eluted in ultrapure water, and its quantity and quality were checked by electrophoretic, fluorometric, and spectrophotometric assays.

Each sample was amplified by PCR with UncI–UncII primers (Mello et al., 2002) to confirm species identity. Samples were further screened with molecular markers to detect polymorphisms associated with geographical origin. Controls included DNA from the *T. aestivum* MycoBank typification specimen (Typification number: MBT 10001890) from Monza (MB) (Leonardi et al., 2021) and a sample from the Abruzzo Apennines.

ITS-RFLP (Restriction Fragment Length Polymorphism of the Internal Transcribed Spacer) analysis was performed to identify polymorphic molecular markers. Restriction enzymes were used to digest ribosomal ITS regions, and the resulting fragments were analyzed by agarose gel electrophoresis. Different restriction enzymes were tested individually and in combination. In deep, the endonuclease *AluI*, which recognizes the sequence AG^CT and cleaves symmetrically at the recognition site, and *HinfI*, which cleaves asymmetrically at the sequence G^ANTC, were used.
DNA fragments were separated by 2% (w/v) agarose gel electrophoresis.
The mitochondrial large ribosomal subunit (mtLSU) marker was amplified according to Molinier et al. (2013) using primers ML3 and ML4 (White et al., 1990). The PCR cycling conditions were: 94 °C for 3 min; 35 cycles of 94 °C for 45 s, 50 °C for 45 s, and 72 °C for 1 min; followed by a final extension at 72 °C for 10 min. After, the amplicons were digested with AluI and the resulting restriction fragments were separated by electrophoresis on 2% (w/v) agarose gels.
An additional check was performed by targeting the *MCM7* gene, a phylogenetic marker usually used in Ascomycota and Basidiomycota that encodes a core component of the DNA replication-initiating Mcm2-7 helicase complex. This marker is also widely used for phylogenetic studies in Ascomycota and Basidiomycota. Amplification was performed with primers Mcm7-709for and Mcm7-1348rev (Schmitt et al., 2009) under the following conditions: 94 °C for 10 min; 38 cycles of 94 °C for 45 s, 56 °C for 50 s, and 72 °C for 1 min; and a final extension at 72 °C for 5 min. The resulting amplicons were digested with *AluI* and *HinfI* at 37 °C for 3 h and the restriction fragments were resolved via electrophoresis on 2% (w/v) agarose gels.
The latest marker tested was the variable V6 domain of the mitochondrial small subunit (SSU) rRNA, following Gonzalez & Labarère (1998). PCR amplification was performed using primers V6U (5′-TTAGTCGGTCTCGGAGCA-3′) and V6R (5′-TGACGACAGCCATGCAAC-3′). Cycling conditions included an initial denaturation at 95 °C for 5 min, followed by 40 cycles of 95 °C for 30 s, 54 °C for 30 s, and 72 °C for 1 min, with a final extension at 72 °C for 7 min. PCR products were analyzed on 2% (w/v) agarose gels.

Results and discussion

Analysis of soil fungal communities before and after the establishment of plantations inoculated with Tuber aestivum

The pre-plantation analysis of soil fungal communities, conducted using Illumina MiSeq NGS technology, involved three soil samples collected from the following sites:

- Sample A3: forest soil from a plot with *Quercus pubescens*, Motta Camastra (ME); producer: Orlando Daniele; collected in July 2024.
- Sample A2: forest soil containing *Pinus* sp., *Quercus* sp., and *Carya illinoinensis*; site: Poggio Alcanterra, Francavilla di Sicilia (ME); producer: Leonardi; collected in July 2024.
- Sample A1: agricultural soil from Francavilla di Sicilia (ME); producer: Leonardi; initially collected in July 2024 and resampled in October 2024.

The soil-extracted DNA showed both high yield and good integrity, with purity ratios falling within good ranges (Figure 3). These results confirmed that the DNA quality met the requirements for subsequent microbiome profiling analysis.

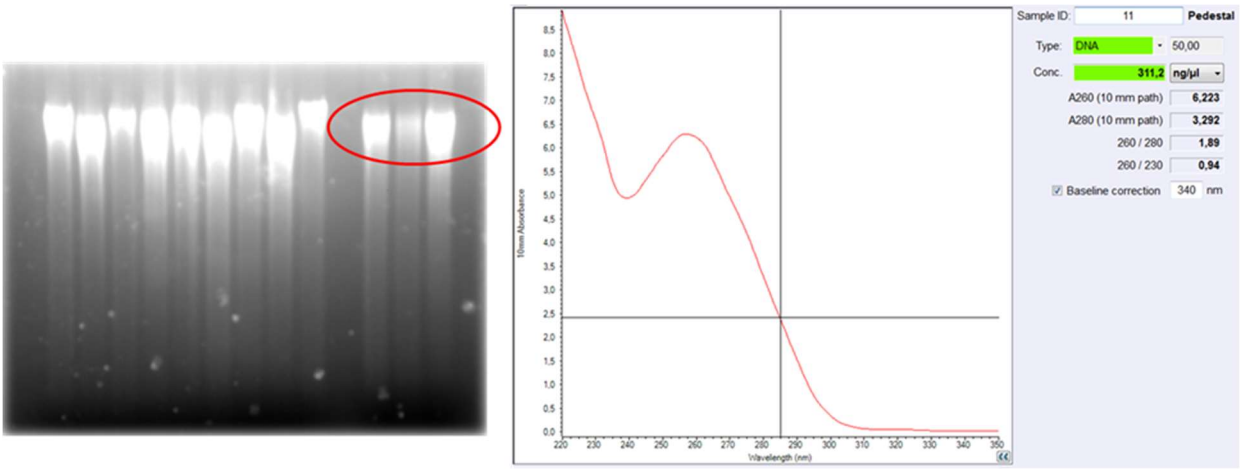

Figure 3: Agarose gel electrophoresis of soil DNA samples A1, A2, and A3 (highlighted in red) on the left, and spectrophotometric analysis of one representative sample on the right.

The statistical results of the microbiome analysis are summarized in Table 3, where: (1) indicates the number of initial sequences; (2) the percentage of sequences retained after preprocessing and chimera removal; (3) the percentage of sequences assigned to OTUs (Operational Taxonomic Units); (4) the percentage of sequences assigned to a specific taxon; and (5) the average sequence length after the initial filtering steps.

Sample	1)	2)	3)	4)	5)
A1	20 992	99.8%	71.4%	71.2%	226
A2	13 727	99.9%	63.4%	63.4%	243
A3	16 897	99.8%	66.2%	64.2%	234

Table 3: Summary of sequencing and taxonomic assignment statistics.

The following Table 4 provides an overview of the taxonomic units identified in each sample. The most specific taxonomic units are listed with their corresponding taxonomic rank and relative fraction (k…kingdom, p…phylum, c…class, o…order, f…family, g…genus, s…species). The lowest common taxonomic unit is reported in lowercase. These taxa represent the best database matches obtained from representative OTU sequences.

For each sample, the total number of reads assigned to OTUs is reported. Taxonomic units representing less than 0.1% of the total reads were gave under the category "Other." OTUs for which the representative sequence did not yield a significant match in the database remained unassigned, and the total reads of these unclassified OTUs are reported under "Unclassified."

Table 4 presents the results of the taxonomic identification and assignment for the analyzed samples.

Table 4: Taxonomic identification and assignment of the analyzed samples, showing the distribution of reads among taxonomic units and their relative abundances.

Sample Name (read counts)

Taxonomic Level	Taxonomic Unit	Fraction
A1.ITS1b (14 943 reads)		
s	**Myrothecium sp. 2 TMS-2011** (4 OTUs with 99-100% identity in 226-245bp to: Myrothecium sp. 2 TMS-2011)	12.8%
g	**Fusarium** (4 OTUs with 100% identity in 209-211bp to: 19 unclassified Fusarium strains, Fusarium andiyazi, Fusarium anthophilum, Fusarium beomiforme, Fusarium brachygibbosum, Fusarium cf. equiseti, Fusarium cf. incarnatum 30-a DPGS-2011, Fusarium cf. incarnatum hxa44, Fusarium circinatum, Fusarium clavum, Fusarium compactum, Fusarium concentricum, Fusarium dlaminii, Fusarium equiseti, Fusarium fujikuroi, Fusarium incarnatum, Fusarium lacertarum, Fusarium longipes, Fusarium nisikadoi, Fusarium oxysporum, Fusarium proliferatum, Fusarium pseudoanthophilum, Fusarium sambucinum, Fusarium scirpi, Fusarium sinensis, Fusarium solani, Fusarium verticillioides)	11.2%
s	**Clonostachys sp. SYP-F-7086** (2 OTUs with 99% identity in 222bp to: Clonostachys sp. SYP-F-7086)	6.2%
p	**Ascomycota** (7 OTUs with 100% identity in 200-262bp to: 2, 3, 5, 6, 7, 8, Alternaria, Aspergillus, Colletotrichum boninense, Darksidea sp., Didymella, Fusarium, Gloeotinia temulenta, Monodictys austrina, Neocosmospora rubicola, Ophiocordyceps sp., Paraconiothyrium fuckelii, Paraisaria heteropoda, Penicillium, Peyronellaea, Phoma, Purpureocillium lilacinum, Talaromyces, Trichoderma, Trichophyton rubrum, Xylaria psidii)	5.9%
f	**Stachybotryaceae** (5 OTUs with 100% identity in 220-253bp to: 12 unclassified Stachybotrys strains, 4 unclassified Myrothecium strains, Achroiostachys humicola, Albifimbria lateralis, Albifimbria terrestris, Albifimbria verrucaria, Albifimbria viridis, Memnoniella echinata, Myrothecium atroviride, Paramyrothecium roridum, Stachybotrys chartarum, Stachybotrys chlorohalonata, Stachybotrys elegans, Stachybotrys pallescens, Stachybotrys subreniformis, Stachybotrys xanthohalonata, Striatibotrys eucylindrospora, Striaticonidium brachysporum, Striaticonidium cinctum)	5.8%
g	**Monocillium** (1 OTU with 100% identity in 226bp to: Monocillium mucidum, Monocillium sp.)	5.0%
f	**Chaetomiaceae** (3 OTUs with 100% identity in 219-229bp to: 2 unclassified Humicola strains, 4 unclassified Chaetomium strains, Dichotomopilus erectus, Humicola nigrescens, Trichocladium uniseriatum)	4.4%
g	**Chaetomium** (5 OTUs with 99-100% identity in 234-236bp to: 18 unclassified Chaetomium strains, Chaetomium angustispirale, Chaetomium cirrhinum, Chaetomium coarctatum, Chaetomium cochliodes, Chaetomium cucumericola, Chaetomium elatum, Chaetomium globosum, Chaetomium grande, Chaetomium madrasense, Chaetomium megalocarpum, Chaetomium nozdrenkoae, Chaetomium olivaceum, Chaetomium pseudocochliodes, Chaetomium spiculipilium, Chaetomium spirochaete, Chaetomium subaffine, Chaetomium subglobosum, Chaetomium subspirale)	3.4%
f	**Plectosphaerellaceae** (2 OTUs with 100% identity in 203bp to: 2 unclassified Gibellulopsis strains, 2 unclassified Verticillium strains, Gibellulopsis nigrescens, Gibellulopsis serrae, Plectosphaerella sp. sedF4, Verticillium dahliae)	3.1%
k	**Eukaryota** (1 OTU with 100% identity in 209bp to: 3 unclassified Fusarium strains, Citrullus lanatus, Fusarium caucasicum, Fusarium cf. oxysporum, Fusarium oxysporum, Fusarium verticillioides, Humicola sp.)	2.4%
g	**Mortierella** (5 OTUs with 97-100% identity in 207-235bp to: 7 unclassified Mortierella strains, Mortierella alpina, Mortierella globalpina)	2.2%
o	**Hypocreales** (3 OTUs with 100% identity in 218-227bp to: 6 unclassified Myrothecium strains, Acremonium persicinum, Clonostachys sp., Cordyceps memorabilis, Cordyceps sp. HZ-19, Striaticonidium cinctum, Trichoderma stromaticum)	1.6%

s	**Chaetomium madrasense** (1 OTU with 97% identity in 221bp to: Chaetomium madrasense)	1.4%
g	**Aspergillus** (3 OTUs with 100% identity in 217-218bp to: 4 unclassified Aspergillus strains, Aspergillus calidoustus, Aspergillus germanicus, Aspergillus insuetus, Aspergillus keveii, Aspergillus minutus, Aspergillus parasiticus, Aspergillus pseudodeflectus, Aspergillus ustus)	1.4%
s	**Stachylidium bicolor** (1 OTU with 100% identity in 177bp to: Stachylidium bicolor)	1.3%
f	**Aspergillaceae** (2 OTUs with 100% identity in 204-247bp to: 4 unclassified Aspergillus strains, 4 unclassified Eurotium strains, Aspergillus amstelodami, Aspergillus awamori, Aspergillus chevalieri, Aspergillus cibarius, Aspergillus cristatus, Aspergillus foetidus, Aspergillus glaucus, Aspergillus heterocaryoticus, Aspergillus intermedius, Aspergillus niger, Aspergillus niveoglaucus, Aspergillus ruber, Aspergillus spiculosus, Aspergillus tubingensis, Aspergillus welwitschiae, Penicillium georgiense, aff. Aspergillus sp.)	1.2%
c	**Dothideomycetes** (2 OTUs with 100% identity in 201-208bp to: Dothichiza sp., Ectophoma pomi, Exosporium sp. 1 NV-2015, Lophiostoma corticola, Phoma sp.)	1.1%
f	**Nectriaceae** (1 OTU with 100% identity in 212bp to: 23 unclassified Fusarium strains, Fusarium cf. solani, Fusarium cf. solani B188, Fusarium falciforme, Fusarium oxysporum, Fusarium solani, Neocosmospora rubicola)	1.1%
g	**Solicoccozyma** (1 OTU with 100% identity in 226bp to: Solicoccozyma aeria, Solicoccozyma fuscescens)	1.0%
s	**Phialophora geniculata** (2 OTUs with 90-98% identity in 202-207bp to: Phialophora geniculata)	1.0%
s	**Coprinellus sassii** (1 OTU with 98% identity in 301bp to: Coprinellus sassii)	1.0%
f	**Sordariaceae** (1 OTU with 99% identity in 249bp to: 3 unclassified Sordaria strains, Neurospora sp., Sordaria tomentoalba)	1.0%
o	**Eurotiales** (2 OTUs with 99-100% identity in 239-240bp to: 3 unclassified Penicillium strains, 3 unclassified Talaromyces strains, Talaromyces calidicanius, Talaromyces flavus, Talaromyces funiculosus, Talaromyces pinophilus, Talaromyces verruculosus)	1.0%
s	**Actinomucor elegans** (2 OTUs with 100% identity in 314bp to: Actinomucor elegans)	1.0%
s	**Humicola brevis** (1 OTU with 99% identity in 211bp to: Humicola brevis)	0.9%
s	**Furcasterigmium furcatum** (1 OTU with 100% identity in 203bp to: Furcasterigmium furcatum)	0.8%
g	**Penicillium** (2 OTUs with 100% identity in 201-235bp to: 5 unclassified Penicillium strains, Penicillium citrinum, Penicillium griseofulvum)	0.7%
g	**Rhizopus** (1 OTU with 100% identity in 254bp to: Rhizopus delemar, Rhizopus oryzae, Rhizopus sp. ACCC 30795)	0.7%
g	**Trichoderma** (2 OTUs with 99-100% identity in 261-265bp to: 15 unclassified Trichoderma strains, Trichoderma afroharzianum, Trichoderma aureoviride, Trichoderma cf. harzianum, Trichoderma cf. harzianum BT-2012, Trichoderma cf. harzianum MO-2014, Trichoderma guizhouense, Trichoderma hamatum, Trichoderma harzianum, Trichoderma lixii, Trichoderma tawa, Trichoderma virens)	0.6%
s	**Pyrenochaeta nobilis** (1 OTU with 96% identity in 179bp to: Pyrenochaeta nobilis)	0.6%
s	**Schizothecium sp. F277858** (2 OTUs with 97% identity in 220bp to: Schizothecium sp. F277858)	0.6%
s	**Aspergillus lucknowensis** (1 OTU with 100% identity in 212bp to: Aspergillus lucknowensis)	0.6%
g	**Stachybotrys** (1 OTU with 100% identity in 224bp to: Stachybotrys limonispora, Stachybotrys microspora, Stachybotrys zeae)	0.6%
s	**Arcuadendron triangulare** (1 OTU with 85% identity in 263bp to: Arcuadendron triangulare)	0.6%
s	**Acremonium acutatum** (1 OTU with 100% identity in 224bp to: Acremonium acutatum)	0.6%
g	**Clonostachys** (2 OTUs with 100% identity in 218bp to: 12 unclassified Clonostachys strains, Clonostachys rosea)	0.5%
s	**Preussia sp. EAL2.5** (1 OTU with 97% identity in 203bp to: Preussia sp. EAL2.5)	0.5%
s	**Exophiala sp. 1 TMS-2011** (2 OTUs with 96-97% identity in 255bp to: Exophiala sp. 1 TMS-2011)	0.5%
c	**Sordariomycetes** (2 OTUs with 100% identity in 200-204bp to: 3 unclassified Plectosphaerella strains, Acrostalagmus luteoalbus, Acrostalagmus sp. JCM 28323, Colletotrichum pisi, Monographella sp., Nectria inventa, Plectosphaerella cucumerina, Plectosphaerella niemeijerarum, Plectosphaerella pauciseptata, Plectosphaerella plurivora, Verticillium sp. FPGLXJ08)	0.5%
s	**Stachybotrys limonispora** (1 OTU with 100% identity in 224bp to: Stachybotrys limonispora)	0.5%
g	**Cladosporium** (1 OTU with 100% identity in 217bp to: 4 unclassified Cladosporium strains, Cladosporium anthropophilum, Cladosporium cladosporioides, Cladosporium delicatulum, Cladosporium oxysporum, Cladosporium pseudocladosporioides, Cladosporium tenuissimum)	0.5%
f	**Ceratobasidiaceae** (2 OTUs with 99-100% identity in 265bp to: Ceratobasidium sp., Rhizoctonia sp. AG-Fb)	0.5%
s	**Macgarvieomyces borealis** (1 OTU with 81% identity in 193bp to: Macgarvieomyces borealis)	0.4%

s	**Humicola variabilis** (1 OTU with 100% identity in 228bp to: Humicola variabilis)	0.4%
s	**Monocillium indicum** (1 OTU with 100% identity in 240bp to: Monocillium indicum)	0.4%
s	**Corynascus sepedonium** (1 OTU with 100% identity in 226bp to: Corynascus sepedonium)	0.4%
s	**Preussia sp. (in** (2 OTUs with 97% identity in 243bp to: Preussia sp. (in)	0.4%
s	**Penicillium citrinum** (1 OTU with 80% identity in 325bp to: Penicillium citrinum)	0.4%
s	**Striaticonidium cinctum** (1 OTU with 99% identity in 223bp to: Striaticonidium cinctum)	0.4%
s	**Chaetomium seminudum** (2 OTUs with 98% identity in 232bp to: Chaetomium seminudum)	0.4%
s	**Fusarium penzigii** (1 OTU with 99% identity in 202bp to: Fusarium penzigii)	0.4%
s	**Acremonium sp. KUC21262** (1 OTU with 85% identity in 219bp to: Acremonium sp. KUC21262)	0.3%
s	**Mortierella exigua** (1 OTU with 99% identity in 194bp to: Mortierella exigua)	0.3%
s	**Cylindrocarpon sp. PB1-R7-A Lr** (1 OTU with 99% identity in 217bp to: Cylindrocarpon sp. PB1-R7-A Lr)	0.3%
g	**Pseudeurotium** (1 OTU with 100% identity in 223bp to: Pseudeurotium bakeri, Pseudeurotium sp. OTU018 AN-2016, Pseudeurotium zonatum)	0.3%
g	**Metarhizium** (1 OTU with 100% identity in 196bp to: 4 unclassified Metarhizium strains, Metarhizium anisopliae, Metarhizium brunneum, Metarhizium guizhouense, Metarhizium indigoticum, Metarhizium robertsii)	0.3%
s	**Myrothecium gramineum** (1 OTU with 100% identity in 224bp to: Myrothecium gramineum)	0.3%
s	**Sordaria araneosa** (1 OTU with 83% identity in 231bp to: Sordaria araneosa)	0.3%
f	**Pleosporaceae** (1 OTU with 100% identity in 223bp to: 3 unclassified Curvularia strains, 7 unclassified Bipolaris strains, Bipolaris maydis, Bipolaris tetramera, Curvularia australiensis, Curvularia beasleyi, Curvularia buchloes, Curvularia dactyloctenii, Curvularia hawaiiensis, Curvularia nodosa, Curvularia spicifera, Curvularia tsudae)	0.3%
s	**Cordana bisbyi** (1 OTU with 86% identity in 222bp to: Cordana bisbyi)	0.3%
s	**Acrophialophora jodhpurensis** (1 OTU with 100% identity in 224bp to: Acrophialophora jodhpurensis)	0.3%
s	**Cladorrhinum samala** (1 OTU with 100% identity in 229bp to: Cladorrhinum samala)	0.3%
s	**Kiflimonium curvulum** (1 OTU with 100% identity in 185bp to: Kiflimonium curvulum)	0.2%
s	**Podospora sp.** (1 OTU with 98% identity in 210bp to: Podospora sp.)	0.2%
s	**Cladorrhinum sp.** (1 OTU with 91% identity in 227bp to: Cladorrhinum sp.)	0.2%
s	**Volutella sp.** (1 OTU with 78% identity in 210bp to: Volutella sp.)	0.2%
s	**Chaetomium sp.** (1 OTU with 100% identity in 229bp to: Chaetomium sp.)	0.2%
s	**Fusarium acutisporum** (1 OTU with 98% identity in 214bp to: Fusarium acutisporum)	0.2%
s	**Fusicolla acetilerea** (1 OTU with 100% identity in 214bp to: Fusicolla acetilerea)	0.2%
s	**Glutinoagger fibulatus** (1 OTU with 80% identity in 326bp to: Glutinoagger fibulatus)	0.2%
s	**Nectria pyrosphaera** (1 OTU with 75% identity in 239bp to: Nectria pyrosphaera)	0.2%
s	**Sarcopodium sp. KN-2018** (1 OTU with 99% identity in 239bp to: Sarcopodium sp. KN-2018)	0.2%
o	**Sordariales** (1 OTU with 91% identity in 220bp to: Cercophora solaris, Mammaria echinobotryoides, Podospora sp. 1 RJ2014)	0.2%
s	**Arthrographis arxii** (1 OTU with 98% identity in 218bp to: Arthrographis arxii)	0.2%
s	**Subramaniula thielavioides** (1 OTU with 97% identity in 234bp to: Subramaniula thielavioides)	0.2%
s	**Trichocladium asperum** (1 OTU with 99% identity in 221bp to: Trichocladium asperum)	0.2%
s	**Acremonium sp. G4** (1 OTU with 100% identity in 229bp to: Acremonium sp. G4)	0.2%
s	**Muritestudina chiangraiensis** (1 OTU with 81% identity in 218bp to: Muritestudina chiangraiensis)	0.2%
g	**Talaromyces** (1 OTU with 100% identity in 244bp to: 2 unclassified Talaromyces strains, Talaromyces assiutensis, Talaromyces trachyspermus)	0.2%
s	**Clonostachys rossmaniae** (1 OTU with 100% identity in 219bp to: Clonostachys rossmaniae)	0.2%
g	**Alternaria** (1 OTU with 100% identity in 212bp to: Alternaria longissima, Alternaria sp. 1 TMS-2011)	0.1%
s	**Humicola fuscoatra** (1 OTU with 100% identity in 211bp to: Humicola fuscoatra)	0.1%

s	**Monodictys sp. 1 JAS-2013** (1 OTU with 94% identity in 194bp to: Monodictys sp. 1 JAS-2013)	0.1%
s	**Hydropisphaera erubescens** (1 OTU with 98% identity in 226bp to: Hydropisphaera erubescens)	0.1%
s	**Tetracladium furcatum** (1 OTU with 96% identity in 218bp to: Tetracladium furcatum)	0.1%
s	**Preussia subticinensis** (1 OTU with 100% identity in 191bp to: Preussia subticinensis)	0.1%
s	**Penicillium sp. ASR-191** (1 OTU with 99% identity in 242bp to: Penicillium sp. ASR-191)	0.1%
o	**Pleosporales** (1 OTU with 100% identity in 266bp to: 3 unclassified Leptosphaerulina strains, Pithomyces chartarum, Pseudopithomyces chartarum)	0.1%
o	**Tremellales** (1 OTU with 100% identity in 171bp to: 2 unclassified Cryptococcus strains, Papiliotrema flavescens, Papiliotrema terrestris, Tremella exigua)	0.1%
	Other (2 OTUs with 0.2%)	0.2%
	Unclassified (51 reads)	
	Filtered (0 reads)	

A2.ITS1b (8 708 reads)

s	**Helvellosebacina sp. 2 BHA-2017** (1 OTU with 94% identity in 234bp to: Helvellosebacina sp. 2 BHA-2017)	13.4%
s	**Tomentella sp.** (5 OTUs with 96-97% identity in 258-263bp to: Tomentella sp.)	7.0%
s	**Hymenogaster griseus** (1 OTU with 98% identity in 303bp to: Hymenogaster griseus)	6.9%
s	**Russula praetervisa** (1 OTU with 100% identity in 276bp to: Russula praetervisa)	6.0%
s	**Tomentella fuscocinerea** (3 OTUs with 93-97% identity in 261-264bp to: Tomentella fuscocinerea)	5.2%
s	**Russula chloroides** (3 OTUs with 97-100% identity in 247-250bp to: Russula chloroides)	4.1%
s	**Inocybe tiliae** (2 OTUs with 99% identity in 285bp to: Inocybe tiliae)	3.9%
c	**Dothideomycetes** (1 OTU with 100% identity in 201bp to: Dothichiza sp., Ectophoma pomi, Phoma sp.)	3.7%
s	**Membranomyces spurius** (2 OTUs with 96-97% identity in 293-298bp to: Membranomyces spurius)	3.5%
g	**Helvellosebacina** (1 OTU with 95% identity in 234bp to: 2 unclassified Helvellosebacina strains)	3.4%
k	**Eukaryota** (2 OTUs with 92-100% identity in 209-213bp to: 2 unclassified Capnodium strains, 3 unclassified Fusarium strains, Bactrocera tryoni, Chaetocapnodium placitae, Citrullus lanatus, Fusarium caucasicum, Fusarium cf. oxysporum, Fusarium oxysporum, Fusarium verticillioides, Humicola sp.)	3.1%
g	**Fusarium** (3 OTUs with 100% identity in 209-211bp to: 16 unclassified Fusarium strains, Fusarium beomiforme, Fusarium brachygibbosum, Fusarium cf. equiseti, Fusarium cf. incarnatum 30-a DPGS-2011, Fusarium cf. incarnatum hxa44, Fusarium clavum, Fusarium compactum, Fusarium equiseti, Fusarium incarnatum, Fusarium lacertarum, Fusarium longipes, Fusarium oxysporum, Fusarium sambucinum, Fusarium scirpi, Fusarium solani)	3.0%
p	**Ascomycota** (5 OTUs with 99-100% identity in 203-262bp to: 2 unclassified Acremonium strains, 2 unclassified Trichoderma strains, 3 unclassified Fusarium strains, 3 unclassified Humicola strains, Acremonium antarcticum, Aspergillus fumigatus, Botryosphaeria dothidea, Chaetomium sp. TR160, Chordomyces antarcticum, Furcasterigmium furcatum, Fusarium cf. solani, Fusarium oxysporum, Fusarium solani, Neocosmospora rubicola, Penicillium raphiae, Pseudallescheria angusta, Sagenomella oligospora, Trichoderma breve, Trichoderma hamatum, Trichoderma harzianum, Trichoderma inhamatum, Trichoderma lentiforme, Trichoderma lixii, Trichoderma simmonsii, Trichoderma viride)	2.9%
s	**Sebacina incrustans** (1 OTU with 99% identity in 232bp to: Sebacina incrustans)	2.7%
s	**Inocybe grammopodia** (2 OTUs with 99-100% identity in 324bp to: Inocybe grammopodia)	2.4%
g	**Rhizopus** (1 OTU with 100% identity in 254bp to: Rhizopus delemar, Rhizopus oryzae, Rhizopus sp. ACCC 30795)	2.2%
g	**Penicillium** (5 OTUs with 100% identity in 201-235bp to: 21 unclassified Penicillium strains, Penicillium aff. melinii, Penicillium arizonense, Penicillium canescens, Penicillium carminoviolaceum, Penicillium chalabudae, Penicillium citreonigrum, Penicillium citrinum, Penicillium griseofulvum, Penicillium janczewskii, Penicillium jensenii, Penicillium maclennaniae, Penicillium melinii, Penicillium murcianum, Penicillium namyslowskii, Penicillium philippinense, Penicillium radiatolobatum, Penicillium restrictum, Penicillium roseopurpureum, Penicillium sanguifluum, Penicillium terrenum, Penicillium vaccaeorum, Penicillium velutinum, Penicillium yarmokense)	2.0%

f	**Nectriaceae** (4 OTUs with 100% identity in 199-215bp to: 2 unclassified Ilyonectria strains, 23 unclassified Fusarium strains, Cylindrocarpon sp., Dactylonectria alcacerensis, Dactylonectria macrodidyma, Dactylonectria novozelandica, Dactylonectria sp., Dactylonectria torresensis, Dialonectria ullevolea, Fusarium acuminatum, Fusarium cf. solani, Fusarium cf. solani B188, Fusarium falciforme, Fusarium merismoides, Fusarium oxysporum, Fusarium solani, Fusicolla ossicola, Ilyonectria destructans, Nectria sp. SGLMf04, Neocosmospora rubicola, Thelonectria nodosa, Thelonectria veuillotiana)	2.0%
s	**Inosperma rhodiolum** (2 OTUs with 97-98% identity in 279bp to: Inosperma rhodiolum)	1.4%
g	**Mortierella** (2 OTUs with 98-100% identity in 207-235bp to: 5 unclassified Mortierella strains, Mortierella alpina, Mortierella globalpina)	1.2%
s	**Furcasterigmium furcatum** (1 OTU with 100% identity in 203bp to: Furcasterigmium furcatum)	1.1%
s	**Inocybe glabripes** (1 OTU with 93% identity in 315bp to: Inocybe glabripes)	1.0%
s	**Hebeloma sacchariolens** (1 OTU with 100% identity in 300bp to: Hebeloma sacchariolens)	0.9%
s	**Humicola variabilis** (1 OTU with 100% identity in 228bp to: Humicola variabilis)	0.9%
s	**Inocybe asterospora** (2 OTUs with 99% identity in 289bp to: Inocybe asterospora)	0.9%
g	**Exophiala** (1 OTU with 100% identity in 254bp to: Exophiala equina, Exophiala radicis, Exophiala sp.)	0.9%
s	**Penicillium thomii** (2 OTUs with 99-100% identity in 234bp to: Penicillium thomii)	0.8%
g	**Solicoccozyma** (1 OTU with 100% identity in 226bp to: Solicoccozyma aeria, Solicoccozyma fuscescens)	0.8%
f	**Chaetomiaceae** (2 OTUs with 100% identity in 227-230bp to: 3 unclassified Chaetomium strains, Humicola brevis, Humicola nigrescens, Trichocladium uniseriatum)	0.8%
s	**Trichophaea woolhopeia** (1 OTU with 100% identity in 201bp to: Trichophaea woolhopeia)	0.8%
g	**Aspergillus** (2 OTUs with 100% identity in 217-238bp to: 3 unclassified Aspergillus strains, Aspergillus aculeatus, Aspergillus cf. japonicus C15-68, Aspergillus floridensis, Aspergillus germanicus, Aspergillus insuetus, Aspergillus japonicus, Aspergillus keveii, Aspergillus minutus, Aspergillus parasiticus, Aspergillus ustus, Aspergillus uvarum, Aspergillus violaceofuscus)	0.7%
s	**Russula livescens** (2 OTUs with 99% identity in 276bp to: Russula livescens)	0.7%
s	**Tuber rapaeodorum** (1 OTU with 99% identity in 160bp to: Tuber rapaeodorum)	0.6%
s	**Helicomyces roseus** (1 OTU with 93% identity in 266bp to: Helicomyces roseus)	0.6%
s	**Sporothrix inflata** (1 OTU with 100% identity in 231bp to: Sporothrix inflata)	0.6%
s	**Fusarium penzigii** (1 OTU with 99% identity in 202bp to: Fusarium penzigii)	0.5%
s	**Inocybe sp. LM3619** (1 OTU with 99% identity in 297bp to: Inocybe sp. LM3619)	0.4%
s	**Phallus impudicus** (1 OTU with 88% identity in 221bp to: Phallus impudicus)	0.4%
f	**Aspergillaceae** (1 OTU with 100% identity in 247bp to: 3 unclassified Aspergillus strains, Aspergillus awamori, Aspergillus foetidus, Aspergillus niger, Aspergillus tubingensis, Aspergillus welwitschiae, Penicillium georgiense, aff. Aspergillus sp.)	0.4%
c	**Leotiomycetes** (1 OTU with 98% identity in 196bp to: 2 unclassified Mycoarthris strains, Golovinomyces sordidus, Mycoarthris corallina)	0.4%
s	**Tuber sp. T56 HM60233** (1 OTU with 95% identity in 272bp to: Tuber sp. T56_HM60233)	0.4%
s	**Mortierella exigua** (1 OTU with 99% identity in 194bp to: Mortierella exigua)	0.4%
s	**Fusarium sp. 5 SO-2015** (1 OTU with 100% identity in 211bp to: Fusarium sp. 5 SO-2015)	0.4%
o	**Eurotiales** (1 OTU with 99% identity in 240bp to: Penicillago kabunica, Penicillago moldavicum, Penicillium sp., Thermoascus verrucosus)	0.3%
s	**Penicillium striatisporum** (1 OTU with 99% identity in 235bp to: Penicillium striatisporum)	0.3%
s	**Clathrus ruber** (1 OTU with 100% identity in 199bp to: Clathrus ruber)	0.3%
s	**Talaromyces purpureogenus** (1 OTU with 100% identity in 244bp to: Talaromyces purpureogenus)	0.3%
s	**Pectenia cyanoloma** (1 OTU with 92% identity in 196bp to: Pectenia cyanoloma)	0.3%
s	**Trichoderma sp.** (1 OTU with 97% identity in 269bp to: Trichoderma sp.)	0.3%
g	**Stilbella** (1 OTU with 99% identity in 215bp to: 2 unclassified Stilbella strains)	0.3%
s	**Niesslia stellenboschiana** (1 OTU with 87% identity in 231bp to: Niesslia stellenboschiana)	0.3%
s	**Sebacina sp.** (1 OTU with 97% identity in 236bp to: Sebacina sp.)	0.3%

o	**Pleosporales** (1 OTU with 100% identity in 202bp to: 3 unclassified Ampelomyces strains, Allophoma tropica, Allophoma zantedeschiae, Ascochyta medicaginicola, Microsphaeropsis olivacea, Nothophoma quercina, Phoma sojicola, Phoma sp. MA 4621, Stagonosporopsis cucurbitacearum, Stagonosporopsis dorenboschii, Stagonosporopsis sp.)	0.3%
s	**Pithya sp.** (1 OTU with 97% identity in 225bp to: Pithya sp.)	0.2%
s	**Pochonia chlamydosporia** (1 OTU with 100% identity in 231bp to: Pochonia chlamydosporia)	0.2%
g	**Cladosporium** (1 OTU with 100% identity in 217bp to: 4 unclassified Cladosporium strains, Cladosporium anthropophilum, Cladosporium cladosporioides, Cladosporium delicatulum, Cladosporium oxysporum, Cladosporium pseudocladosporioides, Cladosporium tenuissimum)	0.2%
s	**Aporospora terricola** (1 OTU with 94% identity in 208bp to: Aporospora terricola)	0.2%
s	**Zopfiella erostrata** (1 OTU with 93% identity in 199bp to: Zopfiella erostrata)	0.2%
s	**Cistella granulosella** (1 OTU with 95% identity in 219bp to: Cistella granulosella)	0.2%
f	**Stachybotryaceae** (1 OTU with 100% identity in 217bp to: Stachybotrys chartarum, Striatibotrys rhabdospora, Striatibotrys yuccae)	0.2%
s	**Mortierella sp.** (1 OTU with 82% identity in 241bp to: Mortierella sp.)	0.2%
	Other (0 OTU with 0.0%)	0.0%
	Unclassified (0 reads)	
	Filtered (0 reads)	

A3.ITS1b (10 848 reads)

s	**Russula variicolor** (2 OTUs with 96-98% identity in 271-272bp to: Russula variicolor)	13.9%
g	**Penicillium** (13 OTUs with 90-100% identity in 234-242bp to: 36, Penicillium)	12.0%
f	**Pseudeurotiaceae** (3 OTUs with 100% identity in 234bp to: 12 unclassified Geomyces strains, 4 unclassified Pseudogymnoascus strains, Geomyces auratus, Pseudogymnoascus appendiculatus, Pseudogymnoascus pannorum)	7.2%
s	**Fusarium sp. 5 SO-2015** (1 OTU with 100% identity in 211bp to: Fusarium sp. 5 SO-2015)	6.8%
s	**Humicola homopilata** (3 OTUs with 99-100% identity in 231bp to: Humicola homopilata)	6.1%
f	**Chaetomiaceae** (2 OTUs with 100% identity in 223-230bp to: Chaetomium sp., Humicola brevis, Humicola sp., Trichocladium asperum, Trichocladium griseum, Trichocladium sp. 12NJ05)	3.5%
g	**Mortierella** (6 OTUs with 99-100% identity in 207-241bp to: 11 unclassified Mortierella strains, Mortierella aff. gamsii, Mortierella clonocystis, Mortierella epicladia, Mortierella gamsii, Mortierella minutissima)	3.0%
p	**Ascomycota** (2 OTUs with 100% identity in 220-262bp to: Keithomyces carneus, Paecilomyces sp. (in, Tetracladium sp., Trichosporiella cerebriformis)	2.7%
g	**Exophiala** (1 OTU with 100% identity in 254bp to: Exophiala equina, Exophiala radicis, Exophiala sp.)	2.2%
s	**Atractospora aquatica** (3 OTUs with 87-89% identity in 178-182bp to: Atractospora aquatica)	2.0%
g	**Fusarium** (2 OTUs with 100% identity in 210-212bp to: 9 unclassified Fusarium strains, Fusarium acuminatum, Fusarium arthrosporioides, Fusarium avenaceum, Fusarium californicum, Fusarium cf. avenaceum, Fusarium cf. solani, Fusarium cf. tricinctum, Fusarium flocciferum, Fusarium fujikuroi, Fusarium lateritium, Fusarium petersiae, Fusarium redolens, Fusarium reticulatum, Fusarium sambucinum, Fusarium sinensis, Fusarium solani, Fusarium subglutinans, Fusarium tricinctum)	1.8%
g	**Solicoccozyma** (2 OTUs with 100% identity in 226-229bp to: Solicoccozyma aeria, Solicoccozyma fuscescens, Solicoccozyma phenolica, Solicoccozyma terrea)	1.8%
s	**Pleuroascus nicholsonii** (1 OTU with 95% identity in 190bp to: Pleuroascus nicholsonii)	1.7%
g	**Aspergillus** (1 OTU with 100% identity in 240bp to: Aspergillus europaeus, Aspergillus fumigatus, Aspergillus wentii)	1.5%
s	**Humicola fuscoatra** (2 OTUs with 99-100% identity in 230bp to: Humicola fuscoatra)	1.5%
s	**Ascobolus sp.** (2 OTUs with 94% identity in 252bp to: Ascobolus sp.)	1.4%
f	**Trichosporonaceae** (2 OTUs with 100% identity in 179bp to: 7 unclassified Trichosporon strains, Apiotrichum dulcitum, Apiotrichum gracile, Apiotrichum porosum)	1.4%
c	**Sordariomycetes** (3 OTUs with 100% identity in 193-235bp to: Acrostalagmus luteoalbus, Acrostalagmus sp. JCM 28323, Chloridium sp., Metapochonia suchlasporia, Nectria inventa, Phialocephala humicola, Verticillium cephalosporum)	1.3%
s	**Humicola cuyabenoensis** (1 OTU with 98% identity in 193bp to: Humicola cuyabenoensis)	1.1%
g	**Preussia** (4 OTUs with 89-99% identity in 203-210bp to: 3 unclassified Preussia strains, Preussia aemulans, Preussia africana, Preussia funiculata, Preussia typharum)	1.0%
s	**Hortiboletus rubellus** (2 OTUs with 99-100% identity in 289bp to: Hortiboletus rubellus)	1.0%

s	**Phlebiella sp. 128 VM-2015** (2 OTUs with 98-99% identity in 233bp to: Phlebiella sp. 128 VM-2015)	0.9%
s	**Acremonium sp. KM1p** (1 OTU with 99% identity in 226bp to: Acremonium sp. KM1p)	0.8%
s	**Mycena maurella** (1 OTU with 84% identity in 294bp to: Mycena maurella)	0.8%
s	**Talaromyces purpureogenus** (1 OTU with 100% identity in 244bp to: Talaromyces purpureogenus)	0.8%
g	**Ilyonectria** (1 OTU with 100% identity in 195bp to: Ilyonectria communis, Ilyonectria crassa, Ilyonectria destructans, Ilyonectria mors-panacis, Ilyonectria panacis, Ilyonectria pseudodestructans, Ilyonectria sp.)	0.8%
k	**Eukaryota** (1 OTU with 100% identity in 209bp to: 3 unclassified Fusarium strains, Citrullus lanatus, Fusarium caucasicum, Fusarium cf. oxysporum, Fusarium oxysporum, Fusarium verticillioides, Humicola sp.)	0.7%
o	**Eurotiales** (2 OTUs with 99-100% identity in 240bp to: Penicillago kabunica, Penicillago moldavicum, Penicillium sp., Thermoascus verrucosus)	0.7%
g	**Sporothrix** (1 OTU with 99% identity in 242bp to: Sporothrix cf. inflata 2 PB-2018, Sporothrix inflata, Sporothrix sp. 16 RJ-2015)	0.7%
s	**Tricladium sp.** (3 OTUs with 98-99% identity in 213bp to: Tricladium sp.)	0.7%
g	**Chaetomium** (1 OTU with 100% identity in 236bp to: 15 unclassified Chaetomium strains, Chaetomium angustispirale, Chaetomium cirrhinum, Chaetomium coarctatum, Chaetomium cochliodes, Chaetomium cucumericola, Chaetomium elatum, Chaetomium globosum, Chaetomium madrasense, Chaetomium olivaceum, Chaetomium pseudocochliodes, Chaetomium spiculipilium, Chaetomium spirochaete, Chaetomium subaffine, Chaetomium subglobosum, Chaetomium subspirale)	0.7%
s	**Nectria sp. ICMP 13358** (1 OTU with 97% identity in 184bp to: Nectria sp. ICMP 13358)	0.6%
s	**Mortierella exigua** (1 OTU with 99% identity in 194bp to: Mortierella exigua)	0.6%
s	**Solicoccozyma terrea** (2 OTUs with 99-100% identity in 229bp to: Solicoccozyma terrea)	0.6%
s	**Oidiodendron sp.** (2 OTUs with 92-100% identity in 216bp to: Oidiodendron sp.)	0.6%
g	**Clonostachys** (1 OTU with 100% identity in 218bp to: 4 unclassified Clonostachys strains, Clonostachys rosea)	0.5%
s	**Podospora sp.** (1 OTU with 100% identity in 219bp to: Podospora sp.)	0.5%
s	**Oidiodendron setiferum** (1 OTU with 99% identity in 229bp to: Oidiodendron setiferum)	0.5%
g	**Trichoderma** (2 OTUs with 100% identity in 245-262bp to: 6 unclassified Trichoderma strains, Trichoderma atroviride, Trichoderma caribbaeum, Trichoderma cerinum, Trichoderma dingleyae, Trichoderma dorotheae, Trichoderma dorothopsis, Trichoderma gamsii, Trichoderma harzianum, Trichoderma koningii, Trichoderma koningiopsis, Trichoderma ovalisporum, Trichoderma tomentosum, Trichoderma viride, Trichoderma viridescens)	0.5%
f	**Nectriaceae** (1 OTU with 99% identity in 211bp to: 3 unclassified Fusarium strains, Fusarium solani, Fusarium solani-melongenae, Neocosmospora sp.)	0.5%
f	**Plectosphaerellaceae** (1 OTU with 100% identity in 203bp to: Gibellulopsis nigrescens, Plectosphaerella sp. sedF4, Verticillium dahliae, Verticillium sp. DU18)	0.5%
s	**Furcasterigmium furcatum** (1 OTU with 100% identity in 203bp to: Furcasterigmium furcatum)	0.5%
s	**Kurtzmanomyces tardus** (1 OTU with 97% identity in 201bp to: Kurtzmanomyces tardus)	0.5%
s	**Candelabrum spinulosum** (1 OTU with 99% identity in 226bp to: Candelabrum spinulosum)	0.4%
s	**Arachnopeziza aurelia** (2 OTUs with 82% identity in 253-257bp to: Arachnopeziza aurelia)	0.4%
g	**Tetracladium** (1 OTU with 100% identity in 222bp to: 3 unclassified Tetracladium strains, Tetracladium maxilliforme)	0.4%
g	**Paraphoma** (1 OTU with 100% identity in 230bp to: Paraphoma chrysanthemicola, Paraphoma sp.)	0.4%
s	**Hyaloscypha sp. TNS-F31287** (1 OTU with 100% identity in 226bp to: Hyaloscypha sp. TNS-F31287)	0.4%
o	**Diaporthales** (1 OTU with 100% identity in 232bp to: 2 unclassified Phomopsis strains, Diaporthe columnaris)	0.4%
s	**Paecilomyces purpureus** (1 OTU with 100% identity in 172bp to: Paecilomyces purpureus)	0.4%
s	**Xylohypha curta** (1 OTU with 98% identity in 254bp to: Xylohypha curta)	0.3%
f	**Aspergillaceae** (1 OTU with 100% identity in 236bp to: 2 unclassified Penicillium strains, Hamigera ingelheimensis, Penicillium cosmopolitanum, Penicillium godlewskii, Penicillium nothofagi, Penicillium westlingii)	0.3%
s	**Penicillium aff. ubiquetum** (1 OTU with 99% identity in 235bp to: Penicillium aff. ubiquetum)	0.3%
s	**Rhynchogastrema coronatum** (1 OTU with 98% identity in 171bp to: Rhynchogastrema coronatum)	0.3%
s	**Saitozyma podzolica** (2 OTUs with 99-100% identity in 169bp to: Saitozyma podzolica)	0.3%

s	**Coniochaeta lignicola** (1 OTU with 89% identity in 240bp to: Coniochaeta lignicola)	0.3%
s	**Marquandomyces Metarhizium marquandii** (1 OTU with 94% identity in 213bp to: Metarhizium marquandii)	0.3%
s	**Penicillium hoeksii** (1 OTU with 100% identity in 233bp to: Penicillium hoeksii)	0.3%
s	**Chloridium virescens** (1 OTU with 92% identity in 226bp to: Chloridium virescens)	0.3%
s	**Podospora appendiculata** (1 OTU with 90% identity in 228bp to: Podospora appendiculata)	0.3%
s	**Mortierella echinula** (1 OTU with 81% identity in 238bp to: Mortierella echinula)	0.3%
s	**Pleurophoma acaciae** (1 OTU with 88% identity in 247bp to: Pleurophoma acaciae)	0.3%
s	**Polyphilus sieberi** (2 OTUs with 96% identity in 220-221bp to: Polyphilus sieberi)	0.3%
s	**Geomyces sp. 12NJ08** (1 OTU with 100% identity in 238bp to: Geomyces sp. 12NJ08)	0.3%
g	**Volutella** (1 OTU with 98% identity in 229bp to: Volutella ciliata, Volutella rosea)	0.3%
s	**Podospora serotina** (1 OTU with 82% identity in 221bp to: Podospora serotina)	0.2%
s	**Penicillium sacculum** (1 OTU with 100% identity in 235bp to: Penicillium sacculum)	0.2%
s	**Clonostachys rossmaniae** (1 OTU with 99% identity in 219bp to: Clonostachys rossmaniae)	0.2%
o	**Pleosporales** (1 OTU with 86% identity in 205bp to: Didymella macrostoma, Microsphaeropsis olivacea, Microsphaeropsis proteae, Peyronellaea sp.)	0.2%
s	**Stromatinia narcissi** (1 OTU with 100% identity in 242bp to: Stromatinia narcissi)	0.2%
s	**Oidiodendron sp. T7604-5-1** (1 OTU with 100% identity in 229bp to: Oidiodendron sp. T7604-5-1)	0.2%
s	**Acaulium albonigrescens** (1 OTU with 90% identity in 260bp to: Acaulium albonigrescens)	0.2%
s	**Mortierella globulifera** (1 OTU with 100% identity in 229bp to: Mortierella globulifera)	0.2%
f	**Mycosphaerellaceae** (1 OTU with 100% identity in 207bp to: Dothistroma pini, Dothistroma septosporum, Mycosphaerella sp., Passalora arctostaphyli)	0.2%
s	**Oidiodendron sp. 07MA13** (1 OTU with 96% identity in 230bp to: Oidiodendron sp. 07MA13)	0.2%
s	**Glutinomyces vulgaris** (1 OTU with 94% identity in 231bp to: Glutinomyces vulgaris)	0.2%
s	**Gliomastix murorum** (1 OTU with 100% identity in 237bp to: Gliomastix murorum)	0.2%
s	**Cordana pauciseptata** (1 OTU with 73% identity in 227bp to: Cordana pauciseptata)	0.2%
s	**Remispora quadri-remis** (1 OTU with 84% identity in 257bp to: Remispora quadri-remis)	0.2%
s	**Coniochaeta verticillata** (1 OTU with 97% identity in 238bp to: Coniochaeta verticillata)	0.2%
f	**Sordariaceae** (1 OTU with 100% identity in 250bp to: Gelasinospora cratophora, Gelasinospora foveaconica, Gelasinospora goundaensis, Gelasinospora saitoi, Gelasinospora seminuda, Gelasinospora sp. VL222, Neurospora africana, Neurospora calospora, Neurospora cerealis, Neurospora dictyophora, Neurospora kobi, Neurospora retispora, Neurospora sp., Sordaria tenerifae)	0.2%
f	**Clavicipitaceae** (1 OTU with 100% identity in 233bp to: Metarhizium marquandii, Paecilomyces sp. GZU-BCECYN4-3)	0.1%
s	**Entrophospora sp. JJ61** (1 OTU with 75% identity in 340bp to: Entrophospora sp. JJ61)	0.1%
s	**Oidiodendron echinulatum** (1 OTU with 99% identity in 230bp to: Oidiodendron echinulatum)	0.1%
g	**Metarhizium** (1 OTU with 100% identity in 196bp to: 4 unclassified Metarhizium strains, Metarhizium anisopliae, Metarhizium brunneum, Metarhizium guizhouense, Metarhizium indigoticum, Metarhizium robertsii)	0.1%
	Other (0 OTU with 0.0%)	0.0%
	Unclassified (335 reads)	
	Filtered (0 reads)	

Table 4 shows that most of the taxonomic groups identified in the analysis belong to taxa commonly found in environments such as the sampling sites. However, particular attention must be given to the presence of mycorrhizal fungi, especially ectomycorrhizal species, and pathogens, which are potential competitors of the ectomycorrhizal genus *Tuber*. Therefore, their presence requires special consideration when planning the establishment of an artificial and/or assisted truffière.

Sample A3 from the Motta Camastra site showed notable abundance of the ectomycorrhizal basidiomycetes *Russula variicolor* (13.9%) and *Hortiboletus rubellus* (1.0%), both of which are commonly associated with truffle-interacting soils and host plants. Additionally, *Mycena* aff. *maurella* was detected. *Mycena* spp. are saprotrophic and don't compete with *Tuber* for root colonisation. Instead, they may enhance soil quality by decomposing organic matter.

The presence of a large number of *Mortierella* spp. was identified as a potentially beneficial interaction. Several studies have indicated that *Mortierella* spp. can promote the growth of *Tuber* species by enhancing nutrient availability and improving soil conditions. *Mortierella* has been reported to mobilize phosphorus, thereby increasing its accessibility for host plants and, indirectly, for *Tuber* mycelium. Other samples also contained a number of members of this genus, along with potentially harmful species such as *Fusarium* and *Trichoderma*. These genera can either compete with *Tuber* for host root colonization or secrete compounds that inhibit mycorrhiza formation. Particularly, some *Fusarium* species are able to produce toxic metabolites that have the capacity to suppress *Tuber* growth.

A number of fungi may create a positive environment for *Tuber* mycorrhization through cooperative interactions or by improving soil conditions, and several of these species were well represented, particularly in sample A2 from Francavilla Fontana. Specifically, the community included *Helvellosebacina*, *Tomentella*, *Hymenogaster griseus*, *Russula praetervisa*, *Tomentella fuscocinerea*, *Russula chloroides*, *Inocybe tiliae*, *Sebacina incrustans*, *Inocybe grammopodia*, *Inocybe glabripes*, *Hebeloma sacchariolens*, *Inocybe asterospora*, and *Russula livescens*. This plot thus exhibited the most structured soil fungal community from a forest ecology perspective. Mycelia of two *Tuber* species, *Tuber rapaeodorum* and *Tuber* sp. T56 HM60233 (both belonging to the Puberulum clade), were also detected.

The post-plantation analysis of soil fungal communities, conducted using Illumina MiSeq NGS technology, involved seven soil samples collected from the following sites:

- Samples after agroforestry treatment, designated ODA, ODB, and ODC; producer: Orlando Daniele.
- Samples after agroforestry treatment, designated LA, LB, LC, and LD; producer: Leonardi.

The DNA extracted from soil samples exhibited generally good yield and quality, with the exception of sample ODC, which likely reflected suboptimal sampling or inadequate preservation (Figure 4). Soil DNA extracts showed good yield and quality, except for sample ODC (Figure 4).

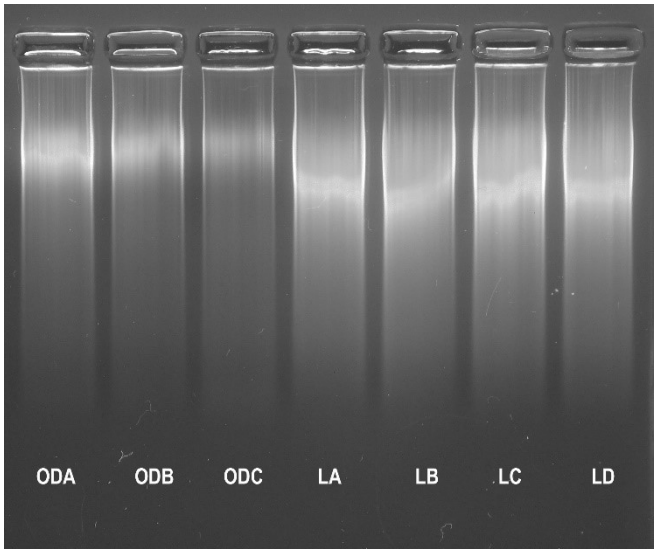

Figure 4: Quality and yield of DNA extracted from soils after agronomic preparation treatments.

The statistical results of the microbiome analysis are summarized in Table 5 below.

Total number of input sequences	449 521	100.0%
Remaining sequences after preprocessing and quality filtering	449 413	100.0%
Remaining sequences after chimera detection and filtering	448 999	99.9%
Total number of sequences assigned to OTUs	336 320	74.8%
Total number of sequences assigned to taxa	325 836	72.5%
Total number of OTUs	969	100.0%
Number of OTUs assigned to taxa	883	91.1%

Table 5: Summary of statistical results.

The number of OTUs, which is related to the dataset's diversity, is shown in Table 6.

Sample	1)	2)	3)	4)	5)
LA.ITS1b	78 409	99.7%	72.3%	71.4%	222
LB.ITS1b	78 137	99.9%	75.3%	74.2%	222
LC.ITS1b	78 439	99.9%	75.2%	74.2%	219
LD.ITS1b	78 351	99.9%	75.7%	74.6%	222
ODA.ITS1b	59 075	99.9%	73.2%	66.7%	234
ODB.ITS1b	77 107	99.9%	76.9%	72.4%	234
ODC.ITS1b	3	100.0%	0.0%	0.0%	243

Table 6: Sequence processing and OTU assessment statistics. Key metrics include: 1) Raw read count, 2) Post-quality control & chimera removal retention (%), 3) Sequences assigned to OTUs (%), 4) Taxonomically classified sequences (%), and 5) Mean read length after filtering.

Table 7 provides a summary overview of the taxonomic composition of the samples examined in this second sampling round.

Table 7: Summary overview of the taxonomic composition of the samples examined post-treatment.

Sample Name (read counts)

Taxonomic Level	Taxonomic Unit	Fraction
LA.ITS1b (55 963 reads)		
g	**Fusarium** (7 OTUs with 99-100% identity in 209-211bp to: 17 unclassified Fusarium strains, Fusarium beomiforme, Fusarium brachygibbosum, Fusarium cf. equiseti, Fusarium cf. incarnatum 30-a DPGS-2011, Fusarium cf. incarnatum hxa44, Fusarium clavum, Fusarium compactum, Fusarium delphinoides, Fusarium equiseti, Fusarium incarnatum, Fusarium lacertarum, Fusarium longipes, Fusarium oxysporum, Fusarium sambucinum, Fusarium scirpi, Fusarium solani)	9.5%
f	**Plectosphaerellaceae** (8 OTUs with 99-100% identity in 202-203bp to: 2 unclassified Gibellulopsis strains, 2 unclassified Verticillium strains, Gibellulopsis nigrescens, Gibellulopsis serrae, Plectosphaerella sp. sedF4, Verticillium dahliae)	8.1%
g	**Cladosporium** (6 OTUs with 99-100% identity in 215-222bp to: 13 unclassified Cladosporium strains, Cladosporium allicinum, Cladosporium anthropophilum, Cladosporium cf. cladosporioides EXF-5884, Cladosporium cf. ramotenellum, Cladosporium cladosporioides, Cladosporium cucumerinum, Cladosporium delicatulum, Cladosporium herbarum, Cladosporium lignicola, Cladosporium limoniforme, Cladosporium oxysporum, Cladosporium phaenocomae, Cladosporium pseudocladosporioides, Cladosporium puyae, Cladosporium ramotenellum, Cladosporium sphaerospermum, Cladosporium tenellum, Cladosporium tenuissimum)	8.0%
s	**Alternaria alternata** (4 OTUs with 99-100% identity in 231-232bp to: Alternaria alternata)	6.9%
g	**Mortierella** (8 OTUs with 97-100% identity in 207-253bp to: 14 unclassified Mortierella strains, Mortierella alpina, Mortierella clonocystis, Mortierella epicladia, Mortierella globalpina, Mortierella minutissima)	4.8%
p	**Ascomycota** (14 OTUs with 99-100% identity in 200-262bp to: 2, 3, 5, 6, 7, 8, Alternaria, Aspergillus, Botryosphaeria dothidea, Chaetomium sp. TR160, Cladophialophora bantiana, Cladosporium, Colletotrichum boninense, Cytospora sp., Darksidea sp., Didymella, Fusarium, Gloeotinia temulenta, Monodictys austrina, Neocosmospora rubicola, Ophiocordyceps sp., Paraconiothyrium fuckelii, Paraisaria heteropoda, Parengyodontium album, Penicillium, Peyronellaea, Phoma, Pseudallescheria angusta, Purpureocillium lilacinum, Sagenomella oligospora, Talaromyces, Trichoderma, Trichophyton rubrum, Xylaria psidii)	4.6%
f	**Chaetomiaceae** (11 OTUs with 98-100% identity in 219-250bp to: 2 unclassified Humicola strains, 6 unclassified Chaetomium strains, Acrophialophora jodhpurensis, Cladorrhinum sp. P1E6, Dichotomopilus erectus, Humicola nigrescens, Podospora bulbillosa, Trichocladium griseum, Trichocladium uniseriatum)	4.1%
c	**Sordariomycetes** (4 OTUs with 99-100% identity in 200bp to: 3 unclassified Plectosphaerella strains, Colletotrichum pisi, Monographella sp., Plectosphaerella cucumerina, Plectosphaerella niemeijerarum, Plectosphaerella pauciseptata, Plectosphaerella plurivora, Verticillium sp. FPGLXJ08)	4.0%
g	**Plectosphaerella** (2 OTUs with 99-100% identity in 200bp to: Plectosphaerella cucumerina, Plectosphaerella niemeijerarum, Plectosphaerella pauciseptata, Plectosphaerella plurivora, Plectosphaerella populi, Plectosphaerella sp.)	2.9%
k	**Eukaryota** (3 OTUs with 99-100% identity in 209-243bp to: 3 unclassified Fusarium strains, Alternaria sp., Aspergillus fiemonthi, Aspergillus flavus, Aspergillus fumigatus, Aspergillus nomiae, Aspergillus oryzae, Aspergillus sp., Aspergillus subolivaceus, Citrullus lanatus, Davidiella sp., Fusarium caucasicum, Fusarium cf. oxysporum, Fusarium oxysporum, Fusarium verticillioides, Humicola sp., Monoraphidium convolutum, Rhizopus oryzae)	2.7%
g	**Monocillium** (3 OTUs with 99-100% identity in 226bp to: Monocillium mucidum, Monocillium sp.)	2.4%

s	**Cordana bisbyi** (4 OTUs with 86-94% identity in 222-223bp to: Cordana bisbyi)	2.2%
g	**Chaetomium** (5 OTUs with 99-100% identity in 234-236bp to: 16 unclassified Chaetomium strains, Chaetomium angustispirale, Chaetomium cirrhinum, Chaetomium coarctatum, Chaetomium cochliodes, Chaetomium cucumericola, Chaetomium elatum, Chaetomium globosum, Chaetomium grande, Chaetomium madrasense, Chaetomium megalocarpum, Chaetomium nozdrenkoae, Chaetomium olivaceum, Chaetomium pseudocochliodes, Chaetomium spiculipilium, Chaetomium spirochaete, Chaetomium subaffine, Chaetomium subglobosum, Chaetomium subspirale)	2.1%
f	**Stachybotryaceae** (7 OTUs with 99-100% identity in 217-253bp to: 12 unclassified Stachybotrys strains, 4 unclassified Myrothecium strains, Achroiostachys humicola, Albifimbria lateralis, Albifimbria terrestris, Albifimbria verrucaria, Albifimbria viridis, Memnoniella echinata, Myrothecium atroviride, Paramyrothecium roridum, Stachybotrys chartarum, Stachybotrys chlorohalonata, Stachybotrys elegans, Stachybotrys pallescens, Stachybotrys subreniformis, Stachybotrys xanthohalonata, Striatibotrys eucylindrospora, Striatibotrys rhabdospora, Striatibotrys yuccae, Striaticonidium brachysporum, Striaticonidium cinctum)	2.0%
f	**Nectriaceae** (4 OTUs with 99-100% identity in 197-212bp to: 2 unclassified Ilyonectria strains, 23 unclassified Fusarium strains, Cylindrocarpon sp., Dactylonectria alcacerensis, Dactylonectria estremocensis, Dactylonectria hordeicola, Dactylonectria macrodidyma, Dactylonectria novozelandica, Dactylonectria sp., Dactylonectria torresensis, Fusarium acuminatum, Fusarium cf. solani, Fusarium cf. solani B188, Fusarium falciforme, Fusarium oxysporum, Fusarium solani, Ilyonectria destructans, Neocosmospora rubicola)	1.8%
s	**Ascobolus sp.** (4 OTUs with 89% identity in 259-261bp to: Ascobolus sp.)	1.8%
s	**Mortierella exigua** (1 OTU with 99% identity in 194bp to: Mortierella exigua)	1.2%
g	**Aspergillus** (7 OTUs with 100% identity in 217-242bp to: 5 unclassified Aspergillus strains, Aspergillus calidoustus, Aspergillus chrysellus, Aspergillus dimorphicus, Aspergillus flavipes, Aspergillus flavus, Aspergillus fumigatus, Aspergillus germanicus, Aspergillus insuetus, Aspergillus keveii, Aspergillus melleus, Aspergillus minutus, Aspergillus nomiae, Aspergillus ochraceus, Aspergillus oryzae, Aspergillus parasiticus, Aspergillus pseudodeflectus, Aspergillus pseudonomius, Aspergillus sepultus, Aspergillus sojae, Aspergillus terricola, Aspergillus toxicarius, Aspergillus transmontanensis, Aspergillus ustus, Aspergillus wentii)	1.2%
g	**Solicoccozyma** (1 OTU with 100% identity in 226bp to: Solicoccozyma aeria, Solicoccozyma fuscescens)	1.0%
s	**Phaeoramularia capsicicola** (1 OTU with 99% identity in 207bp to: Phaeoramularia capsicicola)	0.9%
s	**Humicola variabilis** (1 OTU with 100% identity in 228bp to: Humicola variabilis)	0.9%
s	**Chaetomium seminudum** (3 OTUs with 97-98% identity in 232bp to: Chaetomium seminudum)	0.9%
s	**Humicola brevis** (2 OTUs with 99% identity in 211bp to: Humicola brevis)	0.8%
s	**Sphaerobolus ingoldii** (2 OTUs with 74-75% identity in 335-336bp to: Sphaerobolus ingoldii)	0.7%
s	**Minimedusa polyspora** (4 OTUs with 97-100% identity in 266-279bp to: Minimedusa polyspora)	0.7%
g	**Trichoderma** (5 OTUs with 99-100% identity in 246-265bp to: 20 unclassified Trichoderma strains, Trichoderma afroharzianum, Trichoderma atroviride, Trichoderma aureoviride, Trichoderma cf. harzianum, Trichoderma cf. harzianum BT-2012, Trichoderma cf. harzianum MO-2014, Trichoderma gamsii, Trichoderma guizhouense, Trichoderma hamatum, Trichoderma harzianum, Trichoderma koningii, Trichoderma lixii, Trichoderma speciosum, Trichoderma tawa, Trichoderma virens)	0.7%
s	**Acremonium acutatum** (1 OTU with 100% identity in 224bp to: Acremonium acutatum)	0.7%
s	**Rhizoctonia sp. T-849** (2 OTUs with 99-100% identity in 258bp to: Rhizoctonia sp. T-849)	0.7%
s	**Stromatinia narcissi** (1 OTU with 99% identity in 242bp to: Stromatinia narcissi)	0.6%
g	**Stachybotrys** (1 OTU with 100% identity in 224bp to: Stachybotrys limonispora, Stachybotrys microspora, Stachybotrys zeae)	0.6%
s	**Cladorrhinum samala** (3 OTUs with 96-100% identity in 229-231bp to: Cladorrhinum samala)	0.6%
f	**Aspergillaceae** (2 OTUs with 100% identity in 204-247bp to: 4 unclassified Aspergillus strains, 4 unclassified Eurotium strains, Aspergillus amstelodami, Aspergillus awamori, Aspergillus chevalieri, Aspergillus cibarius, Aspergillus cristatus, Aspergillus foetidus, Aspergillus glaucus, Aspergillus heterocaryoticus, Aspergillus intermedius, Aspergillus niger, Aspergillus niveoglaucus, Aspergillus ruber, Aspergillus spiculosus, Aspergillus tubingensis, Aspergillus welwitschiae, Penicillium georgiense, aff. Aspergillus sp.)	0.6%
s	**Trichocladium asperum** (1 OTU with 99% identity in 221bp to: Trichocladium asperum)	0.6%
s	**Pyrenochaeta nobilis** (1 OTU with 96% identity in 179bp to: Pyrenochaeta nobilis)	0.5%
g	**Rhizopus** (1 OTU with 100% identity in 254bp to: Rhizopus delemar, Rhizopus oryzae, Rhizopus sp. ACCC 30795)	0.5%

s	**Cladorrhinum sp.** (2 OTUs with 91% identity in 227bp to: Cladorrhinum sp.)	0.5%
g	**Alternaria** (3 OTUs with 100% identity in 212-227bp to: 3 unclassified Ulocladium strains, 4 unclassified Alternaria strains, Alternaria atra, Alternaria chartarum, Alternaria consortialis, Alternaria longissima, Alternaria multiformis, Alternaria preussii, Alternaria sorghi, Alternaria tericola, [Ulocladium] sp.)	0.4%
s	**Fusicolla acetilerea** (1 OTU with 100% identity in 214bp to: Fusicolla acetilerea)	0.4%
s	**Hemimycena mairei** (2 OTUs with 93-94% identity in 290bp to: Hemimycena mairei)	0.4%
g	**Clonostachys** (3 OTUs with 100% identity in 218bp to: 18 unclassified Clonostachys strains, Clonostachys rosea, Clonostachys solani, aff. Clonostachys sp.)	0.4%
s	**Mortierella capitata** (2 OTUs with 95% identity in 281-282bp to: Mortierella capitata)	0.4%
s	**Chaetomium madrasense** (2 OTUs with 97% identity in 221bp to: Chaetomium madrasense)	0.4%
s	**Trichocladium Chaetomium acropullum** (1 OTU with 99% identity in 225bp to: Chaetomium acropullum)	0.4%
s	**Clonostachys rossmaniae** (1 OTU with 100% identity in 219bp to: Clonostachys rossmaniae)	0.4%
s	**Clonostachys sp. SYP-F-7086** (2 OTUs with 99% identity in 222bp to: Clonostachys sp. SYP-F-7086)	0.4%
s	**Cylindrocarpon sp. PB1-R7-A Lr** (2 OTUs with 99% identity in 217bp to: Cylindrocarpon sp. PB1-R7-A Lr)	0.4%
o	**Eurotiales** (1 OTU with 100% identity in 239bp to: 3 unclassified Penicillium strains, 3 unclassified Talaromyces strains, Talaromyces calidicanius, Talaromyces flavus, Talaromyces funiculosus, Talaromyces pinophilus, Talaromyces verruculosus)	0.4%
s	**Pyxidiophora arvernensis** (1 OTU with 73% identity in 270bp to: Pyxidiophora arvernensis)	0.4%
s	**Neottiosporina cylindrica** (1 OTU with 99% identity in 218bp to: Neottiosporina cylindrica)	0.4%
s	**Stachybotrys limonispora** (1 OTU with 100% identity in 224bp to: Stachybotrys limonispora)	0.3%
s	**Cylindrocarpon sp.** (3 OTUs with 99% identity in 220-223bp to: Cylindrocarpon sp.)	0.3%
o	**Hypocreales** (3 OTUs with 100% identity in 218-227bp to: 6 unclassified Myrothecium strains, Acremonium persicinum, Clonostachys sp., Cordyceps memorabilis, Cordyceps sp. HZ-19, Striaticonidium cinctum, Trichoderma stromaticum)	0.3%
g	**Penicillium** (2 OTUs with 100% identity in 235bp to: 3 unclassified Penicillium strains, Penicillium janthinellum)	0.3%
s	**Fusarium penzigii** (1 OTU with 99% identity in 202bp to: Fusarium penzigii)	0.3%
s	**Schizothecium sp. F277858** (2 OTUs with 97% identity in 220bp to: Schizothecium sp. F277858)	0.3%
s	**Acrophialophora jodhpurensis** (3 OTUs with 99-100% identity in 224bp to: Acrophialophora jodhpurensis)	0.3%
s	**Furcasterigmium furcatum** (1 OTU with 100% identity in 203bp to: Furcasterigmium furcatum)	0.3%
s	**Chlamydocillium cyanophilum** (1 OTU with 100% identity in 163bp to: Chlamydocillium cyanophilum)	0.3%
s	**Mortierella ambigua** (2 OTUs with 99-100% identity in 238bp to: Mortierella ambigua)	0.3%
f	**Sclerotiniaceae** (1 OTU with 100% identity in 208bp to: Botryotinia narcissicola, Botryotinia sp., Botrytis cinerea, Botrytis fabae, Botrytis paeoniae, Botrytis sp., Monilinia seaveri, Sclerotinia sclerotiorum)	0.3%
o	**Sordariales** (1 OTU with 91% identity in 220bp to: Cercophora solaris, Mammaria echinobotryoides, Podospora sp. 1 RJ2014)	0.3%
s	**Orbilia alba** (1 OTU with 83% identity in 255bp to: Orbilia alba)	0.2%
s	**Paulisebacina allantoidea** (2 OTUs with 73-74% identity in 232-233bp to: Paulisebacina allantoidea)	0.2%
s	**Rhizophlyctis rosea** (1 OTU with 88% identity in 285bp to: Rhizophlyctis rosea)	0.2%
s	**Monodictys sp. 1 JAS-2013** (1 OTU with 94% identity in 194bp to: Monodictys sp. 1 JAS-2013)	0.2%
s	**Pyrenochaetopsis decipiens** (1 OTU with 100% identity in 202bp to: Pyrenochaetopsis decipiens)	0.2%
s	**Stachylidium bicolor** (1 OTU with 100% identity in 177bp to: Stachylidium bicolor)	0.2%
s	**Cystofilobasidium macerans** (1 OTU with 100% identity in 207bp to: Cystofilobasidium macerans)	0.2%
s	**Ochroconis tshawytschae** (1 OTU with 100% identity in 398bp to: Ochroconis tshawytschae)	0.2%
g	**Talaromyces** (1 OTU with 100% identity in 244bp to: 2 unclassified Talaromyces strains, Talaromyces assiutensis, Talaromyces trachyspermus)	0.2%
s	**Tausonia pullulans** (1 OTU with 100% identity in 215bp to: Tausonia pullulans)	0.2%
s	**Marchandiobasidium sp.** (1 OTU with 71% identity in 253bp to: Marchandiobasidium sp.)	0.2%
c	**Dothideomycetes** (1 OTU with 100% identity in 201bp to: Dothichiza sp., Ectophoma pomi, Phoma sp.)	0.2%

s	**Volutella sp.** (1 OTU with 78% identity in 209bp to: Volutella sp.)	0.2%
s	**Preussia sp. (in** (2 OTUs with 97% identity in 243bp to: Preussia sp. (in)	0.2%
s	**Tetracladium furcatum** (1 OTU with 96% identity in 218bp to: Tetracladium furcatum)	0.2%
o	**Pleosporales** (2 OTUs with 100% identity in 202-266bp to: 3 unclassified Ampelomyces strains, 3 unclassified Leptosphaerulina strains, Allophoma tropica, Allophoma zantedeschiae, Ascochyta medicaginicola, Microsphaeropsis olivacea, Nothophoma quercina, Phoma sojicola, Phoma sp. MA 4621, Pithomyces chartarum, Pseudopithomyces chartarum, Stagonosporopsis cucurbitacearum, Stagonosporopsis dorenboschii, Stagonosporopsis sp.)	0.2%
s	**Trichocladium griseum** (1 OTU with 100% identity in 218bp to: Trichocladium griseum)	0.2%
s	**Sarcopodium sp. KN-2018** (1 OTU with 99% identity in 239bp to: Sarcopodium sp. KN-2018)	0.1%
s	**Striaticonidium cinctum** (1 OTU with 99% identity in 223bp to: Striaticonidium cinctum)	0.1%
s	**Clypeosphaeria sp. D4a2a2** (1 OTU with 81% identity in 200bp to: Clypeosphaeria sp. D4a2a2)	0.1%
s	**Exophiala sp. 1 TMS-2011** (2 OTUs with 96-97% identity in 255bp to: Exophiala sp. 1 TMS-2011)	0.1%
s	**Staphylotrichum coccosporum** (1 OTU with 99% identity in 238bp to: Staphylotrichum coccosporum)	0.1%
s	**Cladosporium tenuissimum** (1 OTU with 100% identity in 217bp to: Cladosporium tenuissimum)	0.1%
s	**Mariannaea dimorpha** (1 OTU with 100% identity in 219bp to: Mariannaea dimorpha)	0.1%
s	**Acremonium sp. KUC21262** (1 OTU with 87% identity in 220bp to: Acremonium sp. KUC21262)	0.1%
g	**Metarhizium** (1 OTU with 100% identity in 196bp to: 4 unclassified Metarhizium strains, Metarhizium anisopliae, Metarhizium brunneum, Metarhizium guizhouense, Metarhizium indigoticum, Metarhizium robertsii)	0.1%
s	**Tricellula sp. DV-2018a** (1 OTU with 82% identity in 232bp to: Tricellula sp. DV-2018a)	0.1%
s	**Preussia sp. EAL2.5** (1 OTU with 97% identity in 203bp to: Preussia sp. EAL2.5)	0.1%
s	**Chalara sp. TMS-2011** (1 OTU with 99% identity in 222bp to: Chalara sp. TMS-2011)	0.1%
s	**Crocicreas cyathoideum** (1 OTU with 95% identity in 224bp to: Crocicreas cyathoideum)	0.1%
s	**Subramaniula thielavioides** (1 OTU with 97% identity in 234bp to: Subramaniula thielavioides)	0.1%
s	**Filobasidium stepposum** (1 OTU with 100% identity in 214bp to: Filobasidium stepposum)	0.1%
s	**Globisporangium ultimum** (1 OTU with 100% identity in 283bp to: Globisporangium ultimum)	0.1%
o	**Tremellales** (1 OTU with 100% identity in 171bp to: 2 unclassified Cryptococcus strains, Papiliotrema flavescens, Papiliotrema terrestris, Tremella exigua)	0.1%
s	**Sordaria araneosa** (1 OTU with 83% identity in 231bp to: Sordaria araneosa)	0.1%
g	**Tetracladium** (1 OTU with 100% identity in 222bp to: 2 unclassified Tetracladium strains)	0.1%
s	**Pseudocatenomycopsis rothmanniae** (2 OTUs with 82-83% identity in 191-193bp to: Pseudocatenomycopsis rothmanniae)	0.1%
s	**Lulworthia cf. purpurea FCUL280207CF9** (1 OTU with 80% identity in 207bp to: Lulworthia cf. purpurea FCUL280207CF9)	0.1%
s	**Corynascus sepedonium** (1 OTU with 100% identity in 226bp to: Corynascus sepedonium)	0.1%
g	**Periconia** (1 OTU with 100% identity in 212bp to: Periconia cf. macrospinosa Fun502A, Periconia macrospinosa, Periconia sp.)	0.1%
f	**Pleosporaceae** (1 OTU with 100% identity in 223bp to: 3 unclassified Curvularia strains, 7 unclassified Bipolaris strains, Bipolaris maydis, Bipolaris tetramera, Curvularia australiensis, Curvularia beasleyi, Curvularia buchloes, Curvularia dactyloctenii, Curvularia hawaiiensis, Curvularia nodosa, Curvularia spicifera, Curvularia tsudae)	0.1%
g	**Colletotrichum** (1 OTU with 97% identity in 236bp to: Colletotrichum coccodes, Colletotrichum sp. ITCC 6079)	0.1%
s	**Torula ficus** (1 OTU with 97% identity in 224bp to: Torula ficus)	0.1%
s	**Staphylotrichum boninense** (1 OTU with 97% identity in 238bp to: Staphylotrichum boninense)	0.1%
	Other (32 OTUs with 2.2%)	2.2%
	Unclassified (746 reads)	
	Filtered (0 reads)	

LB.ITS1b (58 016 reads)

g	**Fusarium** (12 OTUs with 99-100% identity in 209-211bp to: 19 unclassified Fusarium strains, Fusarium andiyazi, Fusarium anthophilum, Fusarium beomiforme, Fusarium brachygibbosum, Fusarium cf. equiseti, Fusarium cf. incarnatum 30-a DPGS-2011, Fusarium cf. incarnatum hxa44, Fusarium circinatum, Fusarium clavum, Fusarium compactum, Fusarium concentricum, Fusarium dlaminii, Fusarium equiseti, Fusarium fujikuroi, Fusarium incarnatum, Fusarium lacertarum, Fusarium longipes, Fusarium nisikadoi, Fusarium oxysporum, Fusarium proliferatum, Fusarium pseudoanthophilum, Fusarium sambucinum, Fusarium scirpi, Fusarium sinensis, Fusarium solani, Fusarium verticillioides)	13.1%
f	**Plectosphaerellaceae** (5 OTUs with 99-100% identity in 203bp to: 2 unclassified Gibellulopsis strains, 2 unclassified Verticillium strains, Gibellulopsis nigrescens, Gibellulopsis serrae, Plectosphaerella sp. sedF4, Verticillium dahliae)	9.6%
f	**Chaetomiaceae** (13 OTUs with 81-100% identity in 219-248bp to: 2 unclassified Humicola strains, 6 unclassified Chaetomium strains, Acrophialophora jodhpurensis, Amesia nigricolor, Chaetomium convolutum, Chaetomium pachypodioides, Cladorrhinum sp. P1E6, Collariella bostrychodes, Collariella carteri, Collariella robusta, Dichotomopilus erectus, Humicola nigrescens, Podospora bulbillosa, Trichocladium asperum, Trichocladium griseum, Trichocladium sp. 12NJ05, Trichocladium uniseriatum)	5.3%
p	**Ascomycota** (17 OTUs with 96-100% identity in 200-262bp to: 2, 28, 3, 4, 5, 6, 7, 8, 9, Acremonium, Alternaria, Aspergillus, Botryosphaeria dothidea, Botrytis sp., Chaetomium sp. TR160, Chordomyces antarcticum, Collarina aurantiaca, Colletotrichum boninense, Darksidea sp., Didymella, Furcasterigmium furcatum, Fusarium, Gloeotinia temulenta, Monocillium griseo-ochraceum, Monodictys austrina, Neocosmospora rubicola, Ophiocordyceps sp., Paraconiothyrium fuckelii, Paraisaria heteropoda, Parengyodontium album, Penicillium, Peyronellaea, Phoma, Plectosphaerella melonis, Pseudallescheria angusta, Purpureocillium lilacinum, Sagenomella oligospora, Sarocladium strictum, Stemphylium, Talaromyces, Trichoderma, Trichophyton rubrum, Xylaria psidii)	4.7%
g	**Mortierella** (10 OTUs with 97-100% identity in 207-250bp to: 17 unclassified Mortierella strains, Mortierella alpina, Mortierella clonocystis, Mortierella elongata, Mortierella epicladia, Mortierella globalpina, Mortierella minutissima)	4.0%
c	**Sordariomycetes** (3 OTUs with 99-100% identity in 200bp to: 3 unclassified Plectosphaerella strains, Colletotrichum pisi, Monographella sp., Plectosphaerella cucumerina, Plectosphaerella niemeijerarum, Plectosphaerella paucisepta, Plectosphaerella plurivora, Verticillium sp. FPGLXJ08)	3.8%
s	**Waitea circinata** (4 OTUs with 70-74% identity in 314-324bp to: Waitea circinata)	3.0%
g	**Monocillium** (4 OTUs with 99-100% identity in 226bp to: Monocillium mucidum, Monocillium sp.)	2.9%
k	**Eukaryota** (3 OTUs with 99-100% identity in 209-243bp to: 3 unclassified Fusarium strains, Alternaria sp., Aspergillus fiemonthi, Aspergillus flavus, Aspergillus fumigatus, Aspergillus nomiae, Aspergillus oryzae, Aspergillus sp., Aspergillus subolivaceus, Citrullus lanatus, Davidiella sp., Fusarium caucasicum, Fusarium cf. oxysporum, Fusarium oxysporum, Fusarium verticillioides, Humicola sp., Monoraphidium convolutum, Rhizopus oryzae)	2.6%
s	**Exophiala sp. 1 TMS-2011** (6 OTUs with 96-97% identity in 255bp to: Exophiala sp. 1 TMS-2011)	2.3%
f	**Stachybotryaceae** (8 OTUs with 99-100% identity in 220-253bp to: 12 unclassified Stachybotrys strains, 5 unclassified Myrothecium strains, Achroiostachys humicola, Albifimbria lateralis, Albifimbria terrestris, Albifimbria verrucaria, Albifimbria viridis, Memnoniella echinata, Myrothecium atroviride, Paramyrothecium roridum, Paramyrothecium terrestris, Stachybotrys chartarum, Stachybotrys chlorohalonata, Stachybotrys elegans, Stachybotrys pallescens, Stachybotrys subreniformis, Stachybotrys xanthohalonata, Striatibotrys eucylindrospora, Striaticonidium brachysporum, Striaticonidium cinctum)	2.0%
s	**Modicella malleola** (1 OTU with 84% identity in 183bp to: Modicella malleola)	1.8%
s	**Alternaria alternata** (1 OTU with 100% identity in 232bp to: Alternaria alternata)	1.8%
g	**Chaetomium** (5 OTUs with 99-100% identity in 234-236bp to: 16 unclassified Chaetomium strains, Chaetomium angustispirale, Chaetomium cirrhinum, Chaetomium coarctatum, Chaetomium cochliodes, Chaetomium cucumericola, Chaetomium elatum, Chaetomium globosum, Chaetomium grande, Chaetomium madrasense, Chaetomium megalocarpum, Chaetomium nozdrenkoae, Chaetomium olivaceum, Chaetomium pseudocochliodes, Chaetomium spiculipilium, Chaetomium spirochaete, Chaetomium subaffine, Chaetomium subglobosum, Chaetomium subspirale)	1.8%
f	**Nectriaceae** (5 OTUs with 99-100% identity in 197-212bp to: 2 unclassified Ilyonectria strains, 26 unclassified Fusarium strains, Cylindrocarpon sp., Dactylonectria alcacerensis, Dactylonectria estremocensis, Dactylonectria hordeicola, Dactylonectria macrodidyma, Dactylonectria novozelandica, Dactylonectria sp., Dactylonectria torresensis, Fusarium acuminatum, Fusarium cf. solani, Fusarium cf. solani B188, Fusarium falciforme, Fusarium oxysporum, Fusarium solani, Fusarium solani-melongenae, Ilyonectria destructans, Neocosmospora rubicola, Neocosmospora sp.)	1.7%

g	**Cladosporium** (3 OTUs with 100% identity in 215-222bp to: 13 unclassified Cladosporium strains, Cladosporium anthropophilum, Cladosporium cf. ramotenellum, Cladosporium cladosporioides, Cladosporium cucumerinum, Cladosporium delicatulum, Cladosporium lignicola, Cladosporium oxysporum, Cladosporium phaenocomae, Cladosporium pseudocladosporioides, Cladosporium puyae, Cladosporium ramotenellum, Cladosporium sphaerospermum, Cladosporium tenuissimum)	1.6%
s	**Volutella sp.** (5 OTUs with 78-79% identity in 208-210bp to: Volutella sp.)	1.5%
s	**Cladorrhinum samala** (6 OTUs with 96-100% identity in 229-232bp to: Cladorrhinum samala)	1.1%
s	**Humicola brevis** (2 OTUs with 99% identity in 211bp to: Humicola brevis)	1.1%
s	**Mortierella exigua** (1 OTU with 99% identity in 194bp to: Mortierella exigua)	1.0%
g	**Penicillium** (4 OTUs with 100% identity in 201-237bp to: 8 unclassified Penicillium strains, Penicillium citrinum, Penicillium griseofulvum, Penicillium janthinellum, Penicillium sizovae, Penicillium steckii)	1.0%
g	**Trichoderma** (6 OTUs with 99-100% identity in 246-265bp to: 20 unclassified Trichoderma strains, Trichoderma afroharzianum, Trichoderma atroviride, Trichoderma aureoviride, Trichoderma cf. harzianum, Trichoderma cf. harzianum BT-2012, Trichoderma cf. harzianum MO-2014, Trichoderma gamsii, Trichoderma guizhouense, Trichoderma hamatum, Trichoderma harzianum, Trichoderma koningii, Trichoderma lixii, Trichoderma speciosum, Trichoderma tawa, Trichoderma virens)	1.0%
g	**Aspergillus** (7 OTUs with 100% identity in 217-242bp to: 5 unclassified Aspergillus strains, Aspergillus calidoustus, Aspergillus chrysellus, Aspergillus dimorphicus, Aspergillus europaeus, Aspergillus flavipes, Aspergillus fumigatus, Aspergillus germanicus, Aspergillus insuetus, Aspergillus keveii, Aspergillus melleus, Aspergillus minutus, Aspergillus nomiae, Aspergillus ochraceus, Aspergillus parasiticus, Aspergillus pseudodeflectus, Aspergillus pseudonomius, Aspergillus sepultus, Aspergillus ustus, Aspergillus wentii)	0.9%
g	**Solicoccozyma** (1 OTU with 100% identity in 226bp to: Solicoccozyma aeria, Solicoccozyma fuscescens)	0.9%
o	**Hypocreales** (4 OTUs with 99-100% identity in 218-227bp to: 6 unclassified Myrothecium strains, Acremonium persicinum, Clonostachys sp., Cordyceps memorabilis, Cordyceps sp. HZ-19, Striaticonidium cinctum, Trichoderma stromaticum)	0.8%
s	**Trichocladium asperum** (2 OTUs with 99% identity in 221bp to: Trichocladium asperum)	0.8%
s	**Humicola variabilis** (2 OTUs with 99-100% identity in 228bp to: Humicola variabilis)	0.8%
f	**Sordariaceae** (2 OTUs with 98-99% identity in 249bp to: 3 unclassified Sordaria strains, Neurospora sp., Sordaria tomentoalba)	0.7%
s	**Mortierella sp. CF15** (3 OTUs with 79-91% identity in 215-252bp to: Mortierella sp. CF15)	0.7%
s	**Pyrenochaeta nobilis** (1 OTU with 96% identity in 179bp to: Pyrenochaeta nobilis)	0.7%
s	**Pyrenochaetopsis indica** (1 OTU with 100% identity in 201bp to: Pyrenochaetopsis indica)	0.6%
f	**Aspergillaceae** (2 OTUs with 100% identity in 204-247bp to: 4 unclassified Aspergillus strains, 4 unclassified Eurotium strains, Aspergillus amstelodami, Aspergillus awamori, Aspergillus chevalieri, Aspergillus cibarius, Aspergillus cristatus, Aspergillus foetidus, Aspergillus glaucus, Aspergillus heterocaryoticus, Aspergillus intermedius, Aspergillus niger, Aspergillus niveoglaucus, Aspergillus ruber, Aspergillus spiculosus, Aspergillus tubingensis, Aspergillus welwitschiae, Penicillium georgiense, aff. Aspergillus sp.)	0.6%
g	**Podospora** (3 OTUs with 99-100% identity in 214-215bp to: Podospora brasiliensis, Podospora nannopodalis, Podospora platensis, Podospora setosa, Podospora tarvisina)	0.6%
s	**Acremonium acutatum** (2 OTUs with 99-100% identity in 224bp to: Acremonium acutatum)	0.6%
g	**Alternaria** (2 OTUs with 100% identity in 212-226bp to: 2 unclassified Ulocladium strains, 3 unclassified Alternaria strains, Alternaria atra, Alternaria chartarum, Alternaria consortialis, Alternaria longissima, Alternaria multiformis, Alternaria preussii, Alternaria sorghi, Alternaria tericola)	0.6%
g	**Clonostachys** (2 OTUs with 100% identity in 218bp to: 12 unclassified Clonostachys strains, Clonostachys rosea)	0.6%
o	**Eurotiales** (3 OTUs with 99-100% identity in 239-240bp to: 3 unclassified Penicillium strains, 3 unclassified Talaromyces strains, Talaromyces calidicanius, Talaromyces flavus, Talaromyces funiculosus, Talaromyces pinophilus, Talaromyces verruculosus)	0.5%
s	**Acremonium sp. G4** (1 OTU with 100% identity in 229bp to: Acremonium sp. G4)	0.5%
s	**Cladorrhinum sp.** (2 OTUs with 91% identity in 227bp to: Cladorrhinum sp.)	0.5%
s	**Striaticonidium cinctum** (2 OTUs with 99% identity in 223bp to: Striaticonidium cinctum)	0.5%
o	**Sordariales** (2 OTUs with 91-100% identity in 220-227bp to: 2 unclassified Paecilomyces strains, Acrophialophora levis, Cercophora solaris, Mammaria echinobotryoides, Podospora sp. 1 RJ2014, Taifanglania sp. YZ-2014d)	0.5%
g	**Myrmecridium** (2 OTUs with 99-100% identity in 225bp to: Myrmecridium schulzeri, Myrmecridium sp. TMS-2011)	0.5%

s	**Chaetomium seminudum** (2 OTUs with 98% identity in 232bp to: Chaetomium seminudum)	0.4%
s	**Cercophora coronata** (2 OTUs with 83-84% identity in 218-219bp to: Cercophora coronata)	0.4%
s	**Cordana bisbyi** (1 OTU with 94% identity in 223bp to: Cordana bisbyi)	0.4%
s	**Entoloma cf. undatum** (2 OTUs with 94% identity in 295bp to: Entoloma cf. undatum)	0.4%
s	**Clonostachys rossmaniae** (1 OTU with 100% identity in 219bp to: Clonostachys rossmaniae)	0.4%
s	**Furcasterigmium furcatum** (1 OTU with 100% identity in 203bp to: Furcasterigmium furcatum)	0.4%
g	**Preussia** (2 OTUs with 98-100% identity in 203-204bp to: 5 unclassified Preussia strains, Preussia aemulans, Preussia funiculata, Preussia typharum)	0.4%
g	**Stachybotrys** (2 OTUs with 99-100% identity in 224-226bp to: Stachybotrys limonispora, Stachybotrys microspora, Stachybotrys nephrospora, Stachybotrys reniformis, Stachybotrys zeae)	0.4%
s	**Stachybotrys limonispora** (1 OTU with 100% identity in 224bp to: Stachybotrys limonispora)	0.3%
s	**Subulicystidium perlongisporum** (3 OTUs with 94-95% identity in 255bp to: Subulicystidium perlongisporum)	0.3%
s	**Clonostachys sp. SYP-F-7086** (2 OTUs with 99% identity in 222bp to: Clonostachys sp. SYP-F-7086)	0.3%
s	**Chaetomium madrasense** (2 OTUs with 97% identity in 221bp to: Chaetomium madrasense)	0.3%
s	**Monodictys sp. 1 JAS-2013** (1 OTU with 94% identity in 194bp to: Monodictys sp. 1 JAS-2013)	0.3%
s	**Clypeosphaeria sp. D4a2a2** (1 OTU with 81% identity in 200bp to: Clypeosphaeria sp. D4a2a2)	0.3%
g	**Plectosphaerella** (1 OTU with 100% identity in 200bp to: Plectosphaerella cucumerina, Plectosphaerella niemeijerarum, Plectosphaerella pauciseptata, Plectosphaerella plurivora, Plectosphaerella populi, Plectosphaerella sp.)	0.3%
s	**Acrophialophora jodhpurensis** (3 OTUs with 99-100% identity in 224bp to: Acrophialophora jodhpurensis)	0.3%
s	**Pyrenochaetopsis decipiens** (1 OTU with 100% identity in 202bp to: Pyrenochaetopsis decipiens)	0.3%
s	**Pseudocatenomycopsis rothmanniae** (1 OTU with 83% identity in 191bp to: Pseudocatenomycopsis rothmanniae)	0.3%
c	**Dothideomycetes** (2 OTUs with 100% identity in 201-208bp to: Dothichiza sp., Ectophoma pomi, Exosporium sp. 1 NV-2015, Lophiostoma corticola, Phoma sp.)	0.3%
s	**Schizothecium sp. F277858** (3 OTUs with 97% identity in 220bp to: Schizothecium sp. F277858)	0.3%
s	**Phialophora geniculata** (3 OTUs with 90-98% identity in 202-207bp to: Phialophora geniculata)	0.3%
s	**Fusarium penzigii** (1 OTU with 99% identity in 202bp to: Fusarium penzigii)	0.3%
s	**Stachylidium bicolor** (1 OTU with 100% identity in 177bp to: Stachylidium bicolor)	0.2%
s	**Cylindrocarpon sp.** (3 OTUs with 99% identity in 220-223bp to: Cylindrocarpon sp.)	0.2%
o	**Tremellales** (1 OTU with 100% identity in 171bp to: 2 unclassified Cryptococcus strains, Papiliotrema flavescens, Papiliotrema terrestris, Tremella exigua)	0.2%
s	**Sistotrema hypogaeum** (1 OTU with 91% identity in 234bp to: Sistotrema hypogaeum)	0.2%
s	**Mortierella gamsii** (1 OTU with 100% identity in 208bp to: Mortierella gamsii)	0.2%
g	**Rhizopus** (1 OTU with 100% identity in 254bp to: Rhizopus delemar, Rhizopus oryzae, Rhizopus sp. ACCC 30795)	0.2%
s	**Atractiella sp.** (1 OTU with 100% identity in 212bp to: Atractiella sp.)	0.2%
s	**Exophiala cancerae** (1 OTU with 94% identity in 254bp to: Exophiala cancerae)	0.2%
s	**Cylindrocarpon sp. PB1-R7-A Lr** (2 OTUs with 99% identity in 217bp to: Cylindrocarpon sp. PB1-R7-A Lr)	0.2%
s	**Preussia sp. (in** (3 OTUs with 91-97% identity in 243bp to: Preussia sp. (in)	0.2%
s	**Stilbella sp.** (1 OTU with 99% identity in 215bp to: Stilbella sp.)	0.2%
s	**Sarcopodium sp. KN-2018** (1 OTU with 99% identity in 239bp to: Sarcopodium sp. KN-2018)	0.2%
s	**cf. Tubulicrinis sp. 8 LR-2015** (1 OTU with 70% identity in 278bp to: cf. Tubulicrinis sp. 8 LR-2015)	0.2%
s	**Coniochaeta [Lecythophora] canina** (2 OTUs with 88-100% identity in 238-249bp to: [Lecythophora] canina)	0.2%
s	**Arthrographis arxii** (1 OTU with 98% identity in 218bp to: Arthrographis arxii)	0.2%
g	**Thaumatomonas** (1 OTU with 96% identity in 325bp to: 2 unclassified Thaumatomonas strains)	0.2%
s	**Fusarium equiseti** (1 OTU with 100% identity in 209bp to: Fusarium equiseti)	0.2%

s	**Staphylotrichum boninense** (1 OTU with 97% identity in 238bp to: Staphylotrichum boninense)	0.2%
s	**Cercophora mirabilis** (2 OTUs with 88-94% identity in 198bp to: Cercophora mirabilis)	0.2%
o	**Pleosporales** (2 OTUs with 100% identity in 200-202bp to: 2 unclassified Pyrenochaetopsis strains, 3 unclassified Ampelomyces strains, Allophoma tropica, Allophoma zantedeschiae, Ascochyta medicaginicola, Dokmaia monthadangii, Dokmaia sp., Microsphaeropsis olivacea, Nothophoma quercina, Phoma sojicola, Phoma sp. MA 4621, Stagonosporopsis cucurbitacearum, Stagonosporopsis dorenboschii, Stagonosporopsis sp.)	0.2%
f	**Ceratobasidiaceae** (2 OTUs with 100% identity in 243-256bp to: 4 unclassified Ceratobasidium strains, Rhizoctonia bicornis, Rhizoctonia endophytica, Rhizoctonia solani, Rhizoctonia sp. AG-G)	0.2%
s	**Penicillium janthinellum** (1 OTU with 100% identity in 237bp to: Penicillium janthinellum)	0.2%
s	**Chrysosporium sp.** (1 OTU with 97% identity in 239bp to: Chrysosporium sp.)	0.2%
s	**Corynascus sepedonium** (1 OTU with 100% identity in 226bp to: Corynascus sepedonium)	0.2%
s	**Fusicolla acetilerea** (1 OTU with 100% identity in 214bp to: Fusicolla acetilerea)	0.2%
s	**Subramaniula thielavioides** (1 OTU with 97% identity in 234bp to: Subramaniula thielavioides)	0.2%
s	**Burgoa anomala** (1 OTU with 100% identity in 242bp to: Burgoa anomala)	0.1%
s	**Preussia sp. EAL2.5** (1 OTU with 97% identity in 203bp to: Preussia sp. EAL2.5)	0.1%
s	**Ochroconis tshawytschae** (1 OTU with 100% identity in 398bp to: Ochroconis tshawytschae)	0.1%
s	**Zopfiella erostrata** (1 OTU with 98% identity in 198bp to: Zopfiella erostrata)	0.1%
s	**Tausonia pullulans** (1 OTU with 100% identity in 215bp to: Tausonia pullulans)	0.1%
g	**Exophiala** (1 OTU with 100% identity in 257bp to: Exophiala pisciphila, Exophiala sp. 2 TS-2016)	0.1%
s	**Chlamydocillium cyanophilum** (1 OTU with 100% identity in 163bp to: Chlamydocillium cyanophilum)	0.1%
f	**Clavicipitaceae** (2 OTUs with 99-100% identity in 199-201bp to: 2 unclassified Paecilomyces strains, Metarhizium marquandii)	0.1%
s	**Niesslia sp.** (1 OTU with 94% identity in 220bp to: Niesslia sp.)	0.1%
s	**Zygopleurage zygospora** (1 OTU with 78% identity in 200bp to: Zygopleurage zygospora)	0.1%
s	**Trichoderma sp. F31** (1 OTU with 76% identity in 301bp to: Trichoderma sp. F31)	0.1%
s	**Sporothrix inflata** (1 OTU with 100% identity in 231bp to: Sporothrix inflata)	0.1%
s	**Tetracladium furcatum** (1 OTU with 96% identity in 218bp to: Tetracladium furcatum)	0.1%
f	**Sclerotiniaceae** (1 OTU with 100% identity in 208bp to: Botryotinia narcissicola, Botryotinia sp., Botrytis cinerea, Botrytis fabae, Botrytis paeoniae, Botrytis sp., Monilinia seaveri, Sclerotinia sclerotiorum)	0.1%
s	**Chalara sp. TMS-2011** (1 OTU with 99% identity in 222bp to: Chalara sp. TMS-2011)	0.1%
s	**Achroiostachys phyllophila** (1 OTU with 70% identity in 281bp to: Achroiostachys phyllophila)	0.1%
s	**Exophiala sp. ATT135** (1 OTU with 97% identity in 252bp to: Exophiala sp. ATT135)	0.1%
s	**Monodictys castaneae** (1 OTU with 97% identity in 203bp to: Monodictys castaneae)	0.1%
s	**Chloridium sp.** (1 OTU with 100% identity in 198bp to: Chloridium sp.)	0.1%
s	**Ochroconis minima** (1 OTU with 100% identity in 287bp to: Ochroconis minima)	0.1%
s	**Mortierella capitata** (1 OTU with 95% identity in 282bp to: Mortierella capitata)	0.1%
s	**Phaeosphaeria sp. MZC47m1** (1 OTU with 100% identity in 224bp to: Phaeosphaeria sp. MZC47m1)	0.1%
	Other (50 OTUs with 3.5%)	3.5%
	Unclassified (809 reads)	
	Filtered (0 reads)	
LC.ITS1b (58 174 reads)		
f	**Plectosphaerellaceae** (11 OTUs with 99-100% identity in 201-203bp to: 2 unclassified Gibellulopsis strains, 2 unclassified Verticillium strains, Gibellulopsis nigrescens, Gibellulopsis serrae, Plectosphaerella sp. sedF4, Verticillium dahliae)	14.6%

g	**Fusarium** (9 OTUs with 99-100% identity in 208-211bp to: 21 unclassified Fusarium strains, Fusarium andiyazi, Fusarium anthophilum, Fusarium beomiforme, Fusarium brachygibbosum, Fusarium cf. equiseti, Fusarium cf. incarnatum 30-a DPGS-2011, Fusarium cf. incarnatum hxa44, Fusarium circinatum, Fusarium clavum, Fusarium compactum, Fusarium concentricum, Fusarium dlaminii, Fusarium equiseti, Fusarium fujikuroi, Fusarium incarnatum, Fusarium lacertarum, Fusarium longipes, Fusarium nisikadoi, Fusarium oxysporum, Fusarium proliferatum, Fusarium pseudoanthophilum, Fusarium sambucinum, Fusarium scirpi, Fusarium sinensis, Fusarium solani, Fusarium verticillioides)	9.8%
p	**Ascomycota** (20 OTUs with 96-100% identity in 200-262bp to: 2, 3, 34, 4, 5, 6, 7, 8, 9, Acremonium, Alternaria, Aspergillus, Botryosphaeria dothidea, Botrytis sp., Chaetomium sp. TR160, Chordomyces antarcticum, Collarina aurantiaca, Colletotrichum boninense, Darksidea sp., Didymella, Furcasterigmium furcatum, Fusarium, Gloeotinia temulenta, Monocillium griseo-ochraceum, Monodictys austrina, Neocosmospora rubicola, Ophiocordyceps sp., Paraconiothyrium fuckelii, Paraisaria heteropoda, Parengyodontium album, Penicillium, Peyronellaea, Phoma, Plectosphaerella melonis, Pseudallescheria angusta, Purpureocillium lilacinum, Sagenomella oligospora, Sarocladium strictum, Stemphylium, Talaromyces, Tetracladium sp., Trichoderma, Trichophyton rubrum, Trichosporiella cerebriformis, Xylaria psidii)	5.8%
s	**Phoma sp.** (3 OTUs with 99-100% identity in 202bp to: Phoma sp.)	5.2%
g	**Mortierella** (8 OTUs with 97-100% identity in 207-235bp to: 15 unclassified Mortierella strains, Mortierella alpina, Mortierella clonocystis, Mortierella elongata, Mortierella epicladia, Mortierella globalpina, Mortierella minutissima)	4.5%
f	**Chaetomiaceae** (13 OTUs with 98-100% identity in 219-250bp to: 2 unclassified Humicola strains, 6 unclassified Chaetomium strains, Acrophialophora jodhpurensis, Cladorrhinum sp. P1E6, Dichotomopilus erectus, Humicola nigrescens, Podospora bulbillosa, Trichocladium asperum, Trichocladium griseum, Trichocladium sp. 12NJ05, Trichocladium uniseriatum)	4.2%
g	**Cladosporium** (3 OTUs with 100% identity in 215-222bp to: 13 unclassified Cladosporium strains, Cladosporium anthropophilum, Cladosporium cf. ramotenellum, Cladosporium cladosporioides, Cladosporium cucumerinum, Cladosporium delicatulum, Cladosporium lignicola, Cladosporium oxysporum, Cladosporium phaenocomae, Cladosporium pseudocladosporioides, Cladosporium puyae, Cladosporium ramotenellum, Cladosporium sphaerospermum, Cladosporium tenuissimum)	3.1%
c	**Sordariomycetes** (2 OTUs with 99-100% identity in 200bp to: 3 unclassified Plectosphaerella strains, Colletotrichum pisi, Monographella sp., Plectosphaerella cucumerina, Plectosphaerella niemeijerarum, Plectosphaerella pauciseptata, Plectosphaerella plurivora, Verticillium sp. FPGLXJ08)	3.0%
k	**Eukaryota** (3 OTUs with 99-100% identity in 209-223bp to: 3 unclassified Fusarium strains, Beauveria bassiana, Beauveria rudraprayagi, Citrullus lanatus, Fusarium caucasicum, Fusarium cf. oxysporum, Fusarium oxysporum, Fusarium verticillioides, Humicola sp., Leptinotarsa decemlineata)	2.6%
s	**Chlamydocillium cyanophilum** (2 OTUs with 100% identity in 163bp to: Chlamydocillium cyanophilum)	2.3%
f	**Stachybotryaceae** (6 OTUs with 99-100% identity in 220-253bp to: 12 unclassified Stachybotrys strains, 4 unclassified Myrothecium strains, Achroiostachys humicola, Albifimbria lateralis, Albifimbria terrestris, Albifimbria verrucaria, Albifimbria viridis, Memnoniella echinata, Myrothecium atroviride, Paramyrothecium roridum, Stachybotrys chartarum, Stachybotrys chlorohalonata, Stachybotrys elegans, Stachybotrys pallescens, Stachybotrys subreniformis, Stachybotrys xanthohalonata, Striatibotrys eucylindrospora, Striaticonidium brachysporum, Striaticonidium cinctum)	2.0%
s	**Alternaria alternata** (1 OTU with 100% identity in 232bp to: Alternaria alternata)	2.0%
f	**Nectriaceae** (6 OTUs with 99-100% identity in 197-212bp to: 2 unclassified Ilyonectria strains, 26 unclassified Fusarium strains, 3 unclassified Cylindrocarpon strains, Dactylonectria alcacerensis, Dactylonectria estremocensis, Dactylonectria hordeicola, Dactylonectria macrodidyma, Dactylonectria novozelandica, Dactylonectria sp., Dactylonectria torresensis, Fusarium acuminatum, Fusarium cf. solani, Fusarium cf. solani B188, Fusarium falciforme, Fusarium oxysporum, Fusarium solani, Fusarium solani-melongenae, Ilyonectria destructans, Ilyonectria europaea, Ilyonectria lusitanica, Neocosmospora rubicola, Neocosmospora sp.)	1.8%
g	**Monocillium** (2 OTUs with 99-100% identity in 226bp to: Monocillium mucidum, Monocillium sp.)	1.7%
g	**Chaetomium** (5 OTUs with 99-100% identity in 234-236bp to: 16 unclassified Chaetomium strains, Chaetomium angustispirale, Chaetomium cirrhinum, Chaetomium coarctatum, Chaetomium cochliodes, Chaetomium cucumericola, Chaetomium elatum, Chaetomium globosum, Chaetomium grande, Chaetomium madrasense, Chaetomium megalocarpum, Chaetomium nozdrenkoae, Chaetomium olivaceum, Chaetomium pseudocochliodes, Chaetomium spiculipilium, Chaetomium spirochaete, Chaetomium subaffine, Chaetomium subglobosum, Chaetomium subspirale)	1.6%
s	**Cordana bisbyi** (2 OTUs with 94% identity in 223bp to: Cordana bisbyi)	1.5%

g	**Plectosphaerella** (2 OTUs with 99-100% identity in 200bp to: Plectosphaerella cucumerina, Plectosphaerella niemeijerarum, Plectosphaerella pauciseptata, Plectosphaerella plurivora, Plectosphaerella populi, Plectosphaerella sp.)	1.4%
g	**Aspergillus** (7 OTUs with 100% identity in 217-244bp to: 5 unclassified Aspergillus strains, Aspergillus caelatus, Aspergillus calidoustus, Aspergillus chrysellus, Aspergillus dimorphicus, Aspergillus europaeus, Aspergillus flavipes, Aspergillus flavofurcatus, Aspergillus flavus, Aspergillus fumigatus, Aspergillus germanicus, Aspergillus insuetus, Aspergillus keveii, Aspergillus melleus, Aspergillus minutus, Aspergillus nomiae, Aspergillus ochraceus, Aspergillus parasiticus, Aspergillus pseudodeflectus, Aspergillus sepultus, Aspergillus tamarii, Aspergillus toxicarius, Aspergillus ustus, Aspergillus wentii)	1.2%
s	**Cladorrhinum samala** (4 OTUs with 96-100% identity in 229-232bp to: Cladorrhinum samala)	1.1%
s	**Mortierella exigua** (1 OTU with 99% identity in 194bp to: Mortierella exigua)	1.1%
g	**Trichoderma** (7 OTUs with 99-100% identity in 246-266bp to: 21 unclassified Trichoderma strains, Trichoderma afroharzianum, Trichoderma atroviride, Trichoderma aureoviride, Trichoderma brevicompactum, Trichoderma cf. harzianum, Trichoderma cf. harzianum BT-2012, Trichoderma cf. harzianum MO-2014, Trichoderma gamsii, Trichoderma guizhouense, Trichoderma hamatum, Trichoderma harzianum, Trichoderma koningii, Trichoderma lixii, Trichoderma simmonsii, Trichoderma speciosum, Trichoderma tawa, Trichoderma turrialbense, Trichoderma virens)	1.0%
s	**Acremonium acutatum** (2 OTUs with 99-100% identity in 224bp to: Acremonium acutatum)	0.9%
s	**Humicola brevis** (2 OTUs with 99% identity in 211bp to: Humicola brevis)	0.9%
o	**Hypocreales** (3 OTUs with 100% identity in 218-227bp to: 6 unclassified Myrothecium strains, Acremonium persicinum, Clonostachys sp., Cordyceps memorabilis, Cordyceps sp. HZ-19, Striaticonidium cinctum, Trichoderma stromaticum)	0.9%
g	**Solicoccozyma** (1 OTU with 100% identity in 226bp to: Solicoccozyma aeria, Solicoccozyma fuscescens)	0.8%
g	**Penicillium** (2 OTUs with 100% identity in 201-235bp to: 5 unclassified Penicillium strains, Penicillium citrinum, Penicillium griseofulvum)	0.8%
s	**Cladorrhinum sp.** (2 OTUs with 91% identity in 227bp to: Cladorrhinum sp.)	0.7%
f	**Aspergillaceae** (2 OTUs with 100% identity in 204-247bp to: 4 unclassified Aspergillus strains, 4 unclassified Eurotium strains, Aspergillus amstelodami, Aspergillus awamori, Aspergillus chevalieri, Aspergillus cibarius, Aspergillus cristatus, Aspergillus foetidus, Aspergillus glaucus, Aspergillus heterocaryoticus, Aspergillus intermedius, Aspergillus niger, Aspergillus niveoglaucus, Aspergillus ruber, Aspergillus spiculosus, Aspergillus tubingensis, Aspergillus welwitschiae, Penicillium georgiense, aff. Aspergillus sp.)	0.6%
s	**Exophiala sp. 1 TMS-2011** (3 OTUs with 96-97% identity in 255bp to: Exophiala sp. 1 TMS-2011)	0.6%
s	**Pseudocatenomycopsis rothmanniae** (3 OTUs with 82-83% identity in 191-193bp to: Pseudocatenomycopsis rothmanniae)	0.6%
s	**Clonostachys rossmaniae** (1 OTU with 100% identity in 219bp to: Clonostachys rossmaniae)	0.6%
s	**Penicillium sp. 5 MM-2011** (1 OTU with 96% identity in 241bp to: Penicillium sp. 5 MM-2011)	0.5%
g	**Alternaria** (3 OTUs with 100% identity in 212-227bp to: 3 unclassified Ulocladium strains, 4 unclassified Alternaria strains, Alternaria atra, Alternaria chartarum, Alternaria consortialis, Alternaria longissima, Alternaria multiformis, Alternaria preussii, Alternaria sorghi, Alternaria tericola, [Ulocladium] sp.)	0.5%
g	**Stachybotrys** (2 OTUs with 99-100% identity in 224-226bp to: Stachybotrys limonispora, Stachybotrys microspora, Stachybotrys nephrospora, Stachybotrys reniformis, Stachybotrys zeae)	0.5%
s	**Clonostachys sp. SYP-F-7086** (2 OTUs with 99% identity in 222bp to: Clonostachys sp. SYP-F-7086)	0.5%
s	**Humicola variabilis** (2 OTUs with 99-100% identity in 228bp to: Humicola variabilis)	0.5%
s	**Trichocladium griseum** (1 OTU with 100% identity in 218bp to: Trichocladium griseum)	0.5%
s	**Minimedusa polyspora** (2 OTUs with 99-100% identity in 266bp to: Minimedusa polyspora)	0.5%
s	**Schizothecium sp. F277858** (3 OTUs with 97% identity in 220bp to: Schizothecium sp. F277858)	0.5%
s	**Ascobolus sp.** (2 OTUs with 89-94% identity in 254-260bp to: Ascobolus sp.)	0.4%
g	**Clonostachys** (3 OTUs with 99-100% identity in 218-221bp to: 13 unclassified Clonostachys strains, Clonostachys cf. rossmaniae MSX 47401, Clonostachys rosea)	0.4%
s	**Chaetomium madrasense** (1 OTU with 97% identity in 221bp to: Chaetomium madrasense)	0.4%
s	**Pyrenochaeta nobilis** (1 OTU with 96% identity in 179bp to: Pyrenochaeta nobilis)	0.4%
s	**Furcasterigmium furcatum** (1 OTU with 100% identity in 203bp to: Furcasterigmium furcatum)	0.4%
s	**Preussia sp. (in** (3 OTUs with 91-97% identity in 243bp to: Preussia sp. (in)	0.4%

s	**Cercophora striata** (1 OTU with 95% identity in 232bp to: Cercophora striata)	0.4%
s	**Stachybotrys limonispora** (1 OTU with 100% identity in 224bp to: Stachybotrys limonispora)	0.3%
s	**Cylindrocarpon sp.** (3 OTUs with 99% identity in 220-223bp to: Cylindrocarpon sp.)	0.3%
s	**Chaetomium seminudum** (2 OTUs with 98% identity in 232bp to: Chaetomium seminudum)	0.3%
s	**Mortierella sp. CF15** (1 OTU with 90% identity in 217bp to: Mortierella sp. CF15)	0.3%
c	**Dothideomycetes** (2 OTUs with 100% identity in 201-208bp to: Dothichiza sp., Ectophoma pomi, Exosporium sp. 1 NV-2015, Lophiostoma corticola, Phoma sp.)	0.3%
f	**Sclerotiniaceae** (1 OTU with 100% identity in 208bp to: Botryotinia narcissicola, Botryotinia sp., Botrytis cinerea, Botrytis fabae, Botrytis paeoniae, Botrytis sp., Monilinia seaveri, Sclerotinia sclerotiorum)	0.3%
s	**Mortierella capitata** (2 OTUs with 95% identity in 281-282bp to: Mortierella capitata)	0.3%
s	**Chalara sp. TMS-2011** (1 OTU with 99% identity in 222bp to: Chalara sp. TMS-2011)	0.3%
s	**Mortierella gamsii** (1 OTU with 100% identity in 208bp to: Mortierella gamsii)	0.3%
s	**Acrophialophora jodhpurensis** (3 OTUs with 99-100% identity in 224bp to: Acrophialophora jodhpurensis)	0.3%
s	**Subramaniula thielavioides** (1 OTU with 97% identity in 234bp to: Subramaniula thielavioides)	0.3%
s	**Fusariella hughesii** (1 OTU with 98% identity in 224bp to: Fusariella hughesii)	0.3%
s	**Cercophora coronata** (2 OTUs with 83-84% identity in 218bp to: Cercophora coronata)	0.3%
g	**Rhizopus** (1 OTU with 100% identity in 254bp to: Rhizopus delemar, Rhizopus oryzae, Rhizopus sp. ACCC 30795)	0.3%
s	**Disciotis venosa** (1 OTU with 82% identity in 280bp to: Disciotis venosa)	0.3%
s	**Podospora sp.** (1 OTU with 99% identity in 209bp to: Podospora sp.)	0.3%
s	**Monodictys sp. 1 JAS-2013** (1 OTU with 94% identity in 194bp to: Monodictys sp. 1 JAS-2013)	0.2%
g	**Myrmecridium** (1 OTU with 100% identity in 225bp to: Myrmecridium schulzeri, Myrmecridium sp. TMS-2011)	0.2%
g	**Preussia** (2 OTUs with 98-100% identity in 203-204bp to: 5 unclassified Preussia strains, Preussia aemulans, Preussia funiculata, Preussia typharum)	0.2%
s	**Stachylidium bicolor** (1 OTU with 100% identity in 177bp to: Stachylidium bicolor)	0.2%
g	**Metarhizium** (1 OTU with 100% identity in 196bp to: 4 unclassified Metarhizium strains, Metarhizium anisopliae, Metarhizium brunneum, Metarhizium guizhouense, Metarhizium indigoticum, Metarhizium robertsii)	0.2%
f	**Sordariaceae** (1 OTU with 99% identity in 249bp to: 3 unclassified Sordaria strains, Neurospora sp., Sordaria tomentoalba)	0.2%
g	**Talaromyces** (1 OTU with 100% identity in 244bp to: 2 unclassified Talaromyces strains, Talaromyces assiutensis, Talaromyces trachyspermus)	0.2%
o	**Eurotiales** (2 OTUs with 99-100% identity in 239-240bp to: 3 unclassified Penicillium strains, 3 unclassified Talaromyces strains, Talaromyces calidicanius, Talaromyces flavus, Talaromyces funiculosus, Talaromyces pinophilus, Talaromyces verruculosus)	0.2%
s	**Chloridium sp.** (1 OTU with 100% identity in 198bp to: Chloridium sp.)	0.2%
s	**Pyrenochaetopsis decipiens** (1 OTU with 100% identity in 202bp to: Pyrenochaetopsis decipiens)	0.2%
s	**Lectera nordwiniana** (1 OTU with 98% identity in 205bp to: Lectera nordwiniana)	0.2%
s	**Acremonium sp. KUC21262** (2 OTUs with 86-87% identity in 219-220bp to: Acremonium sp. KUC21262)	0.2%
s	**Rhizophlyctis rosea** (2 OTUs with 87-88% identity in 285bp to: Rhizophlyctis rosea)	0.2%
s	**Acremonium sp. G4** (1 OTU with 100% identity in 229bp to: Acremonium sp. G4)	0.2%
s	**Cylindrocarpon sp. PB1-R7-A Lr** (2 OTUs with 99% identity in 217bp to: Cylindrocarpon sp. PB1-R7-A Lr)	0.2%
s	**Fusarium equiseti** (1 OTU with 100% identity in 209bp to: Fusarium equiseti)	0.2%
s	**Phialophora geniculata** (2 OTUs with 90-98% identity in 202-207bp to: Phialophora geniculata)	0.2%
s	**Corynascus sepedonium** (1 OTU with 100% identity in 226bp to: Corynascus sepedonium)	0.2%
s	**Trichocladium brosimi** (1 OTU with 92% identity in 156bp to: Trichocladium brosimi)	0.2%
f	**Ceratobasidiaceae** (1 OTU with 100% identity in 243bp to: 2 unclassified Ceratobasidium strains, Rhizoctonia bicornis, Rhizoctonia sp. AG-G)	0.2%
s	**Pilobolus longipes** (1 OTU with 100% identity in 293bp to: Pilobolus longipes)	0.2%

s	**Alternaria japonica** (1 OTU with 100% identity in 258bp to: Alternaria japonica)	0.2%
s	**Neopyrenochaeta inflorescentiae** (1 OTU with 100% identity in 222bp to: Neopyrenochaeta inflorescentiae)	0.2%
s	**Preussia sp. EAL2.5** (1 OTU with 97% identity in 203bp to: Preussia sp. EAL2.5)	0.2%
s	**Ochroconis tshawytschae** (1 OTU with 100% identity in 398bp to: Ochroconis tshawytschae)	0.2%
s	**Fusarium penzigii** (1 OTU with 99% identity in 202bp to: Fusarium penzigii)	0.2%
s	**Mortierella ambigua** (2 OTUs with 96-100% identity in 230-238bp to: Mortierella ambigua)	0.2%
s	**Staphylotrichum boninense** (1 OTU with 97% identity in 238bp to: Staphylotrichum boninense)	0.1%
g	**Colletotrichum** (1 OTU with 100% identity in 236bp to: Colletotrichum coccodes, Colletotrichum sp. ITCC 6079)	0.1%
s	**Arthrographis arxii** (1 OTU with 98% identity in 218bp to: Arthrographis arxii)	0.1%
s	**Fusarium acutisporum** (1 OTU with 98% identity in 214bp to: Fusarium acutisporum)	0.1%
s	**Mariannaea dimorpha** (1 OTU with 100% identity in 219bp to: Mariannaea dimorpha)	0.1%
s	**Torula ficus** (1 OTU with 97% identity in 224bp to: Torula ficus)	0.1%
s	**Stilbella sp.** (1 OTU with 99% identity in 215bp to: Stilbella sp.)	0.1%
o	**Tremellales** (1 OTU with 100% identity in 171bp to: 2 unclassified Cryptococcus strains, Papiliotrema flavescens, Papiliotrema terrestris, Tremella exigua)	0.1%
s	**Staphylotrichum coccosporum** (2 OTUs with 99% identity in 238bp to: Staphylotrichum coccosporum)	0.1%
s	**Clypeosphaeria sp. D4a2a2** (2 OTUs with 81-82% identity in 200bp to: Clypeosphaeria sp. D4a2a2)	0.1%
s	**Fusicolla acetilerea** (1 OTU with 100% identity in 214bp to: Fusicolla acetilerea)	0.1%
o	**Pleosporales** (1 OTU with 100% identity in 202bp to: 3 unclassified Ampelomyces strains, Allophoma tropica, Allophoma zantedeschiae, Ascochyta medicaginicola, Microsphaeropsis olivacea, Nothophoma quercina, Phoma sojicola, Phoma sp. MA 4621, Stagonosporopsis cucurbitacearum, Stagonosporopsis dorenboschii, Stagonosporopsis sp.)	0.1%
s	**Oedocephalum sp. AEH3 2** (1 OTU with 84% identity in 282bp to: Oedocephalum sp. AEH3_2)	0.1%
s	**Cercophora sp. TMS-2011** (1 OTU with 79% identity in 204bp to: Cercophora sp. TMS-2011)	0.1%
s	**Sordaria araneosa** (1 OTU with 83% identity in 231bp to: Sordaria araneosa)	0.1%
	Other (40 OTUs with 2.7%)	2.7%
	Unclassified (792 reads)	
	Filtered (0 reads)	

LD.ITS1b (58 445 reads)

f	**Plectosphaerellaceae** (8 OTUs with 99-100% identity in 203bp to: 2 unclassified Gibellulopsis strains, 2 unclassified Verticillium strains, Gibellulopsis nigrescens, Gibellulopsis serrae, Plectosphaerella sp. sedF4, Verticillium dahliae)	9.3%
g	**Cladosporium** (9 OTUs with 99-100% identity in 215-222bp to: 13 unclassified Cladosporium strains, Cladosporium anthropophilum, Cladosporium cf. ramotenellum, Cladosporium cladosporioides, Cladosporium cucumerinum, Cladosporium delicatulum, Cladosporium lignicola, Cladosporium oxysporum, Cladosporium phaenocomae, Cladosporium pseudocladosporioides, Cladosporium puyae, Cladosporium ramotenellum, Cladosporium sphaerospermum, Cladosporium tenuissimum)	9.2%
s	**Cordana bisbyi** (9 OTUs with 86-94% identity in 222-223bp to: Cordana bisbyi)	7.9%
g	**Fusarium** (7 OTUs with 99-100% identity in 209-211bp to: 19 unclassified Fusarium strains, Fusarium andiyazi, Fusarium anthophilum, Fusarium beomiforme, Fusarium brachygibbosum, Fusarium cf. equiseti, Fusarium cf. incarnatum 30-a DPGS-2011, Fusarium cf. incarnatum hxa44, Fusarium circinatum, Fusarium clavum, Fusarium compactum, Fusarium concentricum, Fusarium dlaminii, Fusarium equiseti, Fusarium fujikuroi, Fusarium incarnatum, Fusarium lacertarum, Fusarium longipes, Fusarium nisikadoi, Fusarium oxysporum, Fusarium proliferatum, Fusarium pseudoanthophilum, Fusarium sambucinum, Fusarium scirpi, Fusarium sinensis, Fusarium solani, Fusarium verticillioides)	7.0%
g	**Mortierella** (9 OTUs with 97-100% identity in 207-250bp to: 17 unclassified Mortierella strains, Mortierella alpina, Mortierella clonocystis, Mortierella elongata, Mortierella epicladia, Mortierella globalpina, Mortierella minutissima)	5.3%

c	**Sordariomycetes** (5 OTUs with 99-100% identity in 200-263bp to: 3 unclassified Plectosphaerella strains, 3 unclassified Trichoderma strains, Colletotrichum pisi, Monographella sp., Plectosphaerella cucumerina, Plectosphaerella niemeijerarum, Plectosphaerella pauciseptata, Plectosphaerella plurivora, Trichoderma aff. harzianum MO-2014, Trichoderma afroharzianum, Trichoderma aureoviride, Trichoderma brevicompactum, Trichoderma fomitopsis, Trichoderma hamatum, Trichoderma harzianum, Trichoderma inhamatum, Trichoderma intricatum, Trichoderma lixii, Verticillium sacchari, Verticillium sp. FPGLXJ08)	5.0%
p	**Ascomycota** (17 OTUs with 96-100% identity in 200-262bp to: 2, 28, 3, 4, 5, 6, 7, 8, 9, Acremonium, Alternaria, Aspergillus, Botryosphaeria dothidea, Botrytis sp., Chaetomium sp. TR160, Chordomyces antarcticum, Cladophialophora bantiana, Cladosporium, Colletotrichum boninense, Darksidea sp., Didymella, Furcasterigmium furcatum, Fusarium, Gloeotinia temulenta, Monodictys austrina, Neocosmospora rubicola, Ophiocordyceps sp., Paraconiothyrium fuckelii, Paraisaria heteropoda, Penicillium, Peyronellaea, Phoma, Plectosphaerella melonis, Pseudallescheria angusta, Purpureocillium lilacinum, Sagenomella oligospora, Sarocladium strictum, Stemphylium, Talaromyces, Trichoderma, Trichophyton rubrum, Xylaria psidii)	4.6%
s	**Alternaria alternata** (2 OTUs with 99-100% identity in 232bp to: Alternaria alternata)	3.9%
f	**Chaetomiaceae** (11 OTUs with 98-100% identity in 219-250bp to: 2 unclassified Humicola strains, 6 unclassified Chaetomium strains, Acrophialophora jodhpurensis, Cladorrhinum sp. P1E6, Dichotomopilus erectus, Humicola nigrescens, Podospora bulbillosa, Trichocladium asperum, Trichocladium griseum, Trichocladium sp. 12NJ05, Trichocladium uniseriatum)	3.3%
f	**Stachybotryaceae** (10 OTUs with 99-100% identity in 217-253bp to: 12 unclassified Stachybotrys strains, 5 unclassified Myrothecium strains, Achroiostachys humicola, Albifimbria lateralis, Albifimbria terrestris, Albifimbria verrucaria, Albifimbria viridis, Gregatothecium humicola, Memnoniella echinata, Myrothecium atroviride, Myrothecium gramineum, Myrothecium lachastrae, Neomyrothecium humicola, Paramyrothecium humicola, Paramyrothecium nigrum, Paramyrothecium roridum, Paramyrothecium viridisporum, Stachybotrys chartarum, Stachybotrys chlorohalonata, Stachybotrys elegans, Stachybotrys pallescens, Stachybotrys subreniformis, Stachybotrys xanthohalonata, Striatibotrys eucylindrospora, Striatibotrys rhabdospora, Striatibotrys yuccae, Striaticonidium brachysporum, Striaticonidium cinctum, Xenomyrothecium tongaense)	2.5%
g	**Trichoderma** (9 OTUs with 99-100% identity in 261-266bp to: 18 unclassified Trichoderma strains, Trichoderma afroharzianum, Trichoderma aureoviride, Trichoderma brevicompactum, Trichoderma cf. harzianum, Trichoderma cf. harzianum BT-2012, Trichoderma cf. harzianum MO-2014, Trichoderma guizhouense, Trichoderma hamatum, Trichoderma harzianum, Trichoderma lixii, Trichoderma simmonsii, Trichoderma tawa, Trichoderma turrialbense, Trichoderma virens)	2.2%
g	**Monocillium** (3 OTUs with 99-100% identity in 226bp to: Monocillium mucidum, Monocillium sp.)	2.1%
k	**Eukaryota** (4 OTUs with 99-100% identity in 209-243bp to: 3, 6, Alternaria sp., Aspergillus, Citrullus lanatus, Cladophialophora minourae, Cladosporium, Fusarium, Humicola sp., Monoraphidium convolutum, Piromyces sp., Rhizopus oryzae, Yuchengia narymica, aff. Cladosporium sp.)	2.0%
g	**Plectosphaerella** (2 OTUs with 99-100% identity in 200bp to: Plectosphaerella cucumerina, Plectosphaerella niemeijerarum, Plectosphaerella pauciseptata, Plectosphaerella plurivora, Plectosphaerella populi, Plectosphaerella sp.)	1.7%
f	**Nectriaceae** (5 OTUs with 99-100% identity in 197-214bp to: 2 unclassified Ilyonectria strains, 2 unclassified Nectria strains, 23 unclassified Fusarium strains, Cosmospora coccinea, Cylindrocarpon sp., Dactylonectria alcacerensis, Dactylonectria estremocensis, Dactylonectria hordeicola, Dactylonectria macrodidyma, Dactylonectria novozelandica, Dactylonectria sp., Dactylonectria torresensis, Fusarium acuminatum, Fusarium cf. solani, Fusarium cf. solani B188, Fusarium falciforme, Fusarium oxysporum, Fusarium solani, Fusicolla aquaeductuum, Ilyonectria destructans, Neocosmospora rubicola)	1.7%
g	**Chaetomium** (4 OTUs with 99-100% identity in 234bp to: Chaetomium globosum, Chaetomium grande, Chaetomium megalocarpum, Chaetomium nozdrenkoae, Chaetomium sp. 12 JAS-2013)	1.5%
g	**Aspergillus** (10 OTUs with 100% identity in 217-244bp to: 6, Aspergillus)	1.4%
s	**Ascobolus sp.** (1 OTU with 94% identity in 255bp to: Ascobolus sp.)	1.2%
s	**Chlamydocillium cyanophilum** (1 OTU with 100% identity in 163bp to: Chlamydocillium cyanophilum)	1.0%
g	**Solicoccozyma** (1 OTU with 100% identity in 226bp to: Solicoccozyma aeria, Solicoccozyma fuscescens)	0.9%
s	**Chloridium sp.** (2 OTUs with 100% identity in 198bp to: Chloridium sp.)	0.9%
s	**Cladorrhinum samala** (4 OTUs with 96-100% identity in 229-232bp to: Cladorrhinum samala)	0.9%
s	**Humicola brevis** (1 OTU with 99% identity in 211bp to: Humicola brevis)	0.9%
s	**Mortierella exigua** (1 OTU with 99% identity in 194bp to: Mortierella exigua)	0.9%
s	**Minimedusa polyspora** (3 OTUs with 98-100% identity in 266-279bp to: Minimedusa polyspora)	0.8%

s	**Pseudocatenomycopsis rothmanniae** (2 OTUs with 83% identity in 191bp to: Pseudocatenomycopsis rothmanniae)	0.8%
s	**Niesslia sp.** (2 OTUs with 94% identity in 220bp to: Niesslia sp.)	0.6%
f	**Sclerotiniaceae** (3 OTUs with 100% identity in 208bp to: 2 unclassified Botryotinia strains, Botryotinia narcissicola, Botrytis cinerea, Botrytis fabae, Botrytis paeoniae, Botrytis sp., Monilinia seaveri, Sclerotinia sclerotiorum)	0.6%
s	**Acremonium acutatum** (2 OTUs with 99-100% identity in 224bp to: Acremonium acutatum)	0.6%
f	**Didymellaceae** (1 OTU with 100% identity in 201bp to: 3 unclassified Phoma strains, Nothophoma gossypiicola, aff. Phoma sp.)	0.6%
s	**Preussia sp. EAL2.5** (1 OTU with 97% identity in 203bp to: Preussia sp. EAL2.5)	0.5%
c	**Dothideomycetes** (2 OTUs with 100% identity in 201-208bp to: Dothichiza sp., Ectophoma pomi, Exosporium sp. 1 NV-2015, Lophiostoma corticola, Phoma sp.)	0.5%
s	**Humicola variabilis** (1 OTU with 100% identity in 228bp to: Humicola variabilis)	0.5%
g	**Stachybotrys** (2 OTUs with 99-100% identity in 224bp to: Stachybotrys limonispora, Stachybotrys microspora, Stachybotrys zeae)	0.4%
f	**Aspergillaceae** (2 OTUs with 100% identity in 204-247bp to: 4 unclassified Aspergillus strains, 4 unclassified Eurotium strains, Aspergillus amstelodami, Aspergillus awamori, Aspergillus chevalieri, Aspergillus cibarius, Aspergillus cristatus, Aspergillus foetidus, Aspergillus glaucus, Aspergillus heterocaryoticus, Aspergillus intermedius, Aspergillus niger, Aspergillus niveoglaucus, Aspergillus ruber, Aspergillus spiculosus, Aspergillus tubingensis, Aspergillus welwitschiae, Penicillium georgiense, aff. Aspergillus sp.)	0.4%
s	**Burgoa anomala** (1 OTU with 100% identity in 242bp to: Burgoa anomala)	0.4%
s	**Zopfiella erostrata** (2 OTUs with 93-98% identity in 198-199bp to: Zopfiella erostrata)	0.4%
s	**Schizothecium sp. F277858** (3 OTUs with 97% identity in 220bp to: Schizothecium sp. F277858)	0.4%
s	**Cladorrhinum sp.** (2 OTUs with 91% identity in 227bp to: Cladorrhinum sp.)	0.4%
s	**Monodictys sp. 1 JAS-2013** (2 OTUs with 94-95% identity in 193-194bp to: Monodictys sp. 1 JAS-2013)	0.3%
o	**Hypocreales** (3 OTUs with 100% identity in 218-227bp to: 6 unclassified Myrothecium strains, Acremonium persicinum, Clonostachys sp., Cordyceps memorabilis, Cordyceps sp. HZ-19, Striaticonidium cinctum, Trichoderma stromaticum)	0.3%
g	**Rhizopus** (1 OTU with 100% identity in 254bp to: Rhizopus delemar, Rhizopus oryzae, Rhizopus sp. ACCC 30795)	0.3%
o	**Sordariales** (1 OTU with 91% identity in 220bp to: Cercophora solaris, Mammaria echinobotryoides, Podospora sp. 1 RJ2014)	0.3%
s	**Hyphodermella corrugata** (1 OTU with 82% identity in 258bp to: Hyphodermella corrugata)	0.3%
s	**Stachybotrys limonispora** (1 OTU with 100% identity in 224bp to: Stachybotrys limonispora)	0.3%
s	**Podospora bulbillosa** (1 OTU with 100% identity in 246bp to: Podospora bulbillosa)	0.3%
g	**Stemphylium** (1 OTU with 100% identity in 236bp to: Stemphylium eturmiunum, Stemphylium sp.)	0.3%
f	**Sordariaceae** (1 OTU with 99% identity in 249bp to: 3 unclassified Sordaria strains, Neurospora sp., Sordaria tomentoalba)	0.3%
s	**Chaetomium madrasense** (1 OTU with 97% identity in 221bp to: Chaetomium madrasense)	0.3%
g	**Penicillium** (1 OTU with 100% identity in 235bp to: 3 unclassified Penicillium strains)	0.3%
s	**Clonostachys sp. SYP-F-7086** (2 OTUs with 99% identity in 222bp to: Clonostachys sp. SYP-F-7086)	0.3%
s	**Mortierella capitata** (2 OTUs with 95% identity in 281-282bp to: Mortierella capitata)	0.3%
s	**Furcasterigmium furcatum** (1 OTU with 100% identity in 203bp to: Furcasterigmium furcatum)	0.3%
s	**Rhizophlyctis rosea** (1 OTU with 88% identity in 285bp to: Rhizophlyctis rosea)	0.3%
g	**Alternaria** (3 OTUs with 100% identity in 212-227bp to: 3 unclassified Ulocladium strains, 4 unclassified Alternaria strains, Alternaria atra, Alternaria chartarum, Alternaria consortialis, Alternaria longissima, Alternaria multiformis, Alternaria preussii, Alternaria sorghi, Alternaria terricola, [Ulocladium] sp.)	0.2%
s	**Acrophialophora jodhpurensis** (1 OTU with 100% identity in 224bp to: Acrophialophora jodhpurensis)	0.2%
s	**Alternaria japonica** (1 OTU with 100% identity in 258bp to: Alternaria japonica)	0.2%
s	**Chaetomium seminudum** (2 OTUs with 98% identity in 232bp to: Chaetomium seminudum)	0.2%
s	**Entoloma cf. undatum** (2 OTUs with 94% identity in 295bp to: Entoloma cf. undatum)	0.2%
s	**Torula ficus** (1 OTU with 97% identity in 224bp to: Torula ficus)	0.2%
s	**Trichoderma tomentosum** (1 OTU with 100% identity in 263bp to: Trichoderma tomentosum)	0.2%

s	**Cylindrocarpon sp.** (2 OTUs with 99% identity in 220-223bp to: Cylindrocarpon sp.)	0.2%
o	**Eurotiales** (1 OTU with 100% identity in 239bp to: 3 unclassified Penicillium strains, 3 unclassified Talaromyces strains, Talaromyces calidicanius, Talaromyces flavus, Talaromyces funiculosus, Talaromyces pinophilus, Talaromyces verruculosus)	0.2%
s	**Tetracladium sp.** (1 OTU with 94% identity in 231bp to: Tetracladium sp.)	0.2%
o	**Pleosporales** (1 OTU with 100% identity in 202bp to: 3 unclassified Ampelomyces strains, Allophoma tropica, Allophoma zantedeschiae, Ascochyta medicaginicola, Microsphaeropsis olivacea, Nothophoma quercina, Phoma sojicola, Phoma sp. MA 4621, Stagonosporopsis cucurbitacearum, Stagonosporopsis dorenboschii, Stagonosporopsis sp.)	0.2%
s	**Cystofilobasidium macerans** (1 OTU with 100% identity in 207bp to: Cystofilobasidium macerans)	0.2%
g	**Diaporthe** (1 OTU with 100% identity in 236bp to: Diaporthe ambigua, Diaporthe scabra)	0.2%
s	**Exophiala sp. 1 TMS-2011** (2 OTUs with 96-97% identity in 255bp to: Exophiala sp. 1 TMS-2011)	0.2%
s	**Subulicystidium perlongisporum** (3 OTUs with 94-95% identity in 255bp to: Subulicystidium perlongisporum)	0.2%
g	**Talaromyces** (1 OTU with 100% identity in 244bp to: 2 unclassified Talaromyces strains, Talaromyces assiutensis, Talaromyces trachyspermus)	0.2%
s	**Trichocladium griseum** (1 OTU with 100% identity in 218bp to: Trichocladium griseum)	0.2%
s	**Trichoderma harzianum** (1 OTU with 100% identity in 262bp to: Trichoderma harzianum)	0.2%
s	**Periconia macrospinosa** (1 OTU with 100% identity in 212bp to: Periconia macrospinosa)	0.2%
s	**Chalara sp. TMS-2011** (1 OTU with 99% identity in 222bp to: Chalara sp. TMS-2011)	0.2%
s	**Cylindrocarpon sp. PB1-R7-A Lr** (2 OTUs with 99% identity in 217bp to: Cylindrocarpon sp. PB1-R7-A Lr)	0.2%
s	**Cladosporium tenuissimum** (1 OTU with 100% identity in 217bp to: Cladosporium tenuissimum)	0.2%
g	**Clonostachys** (1 OTU with 100% identity in 218bp to: 10 unclassified Clonostachys strains, Clonostachys rosea)	0.2%
s	**Clonostachys rossmaniae** (1 OTU with 100% identity in 219bp to: Clonostachys rossmaniae)	0.2%
s	**Lectera nordwiniana** (1 OTU with 98% identity in 205bp to: Lectera nordwiniana)	0.1%
s	**Kiflimonium curvulum** (1 OTU with 87% identity in 197bp to: Kiflimonium curvulum)	0.1%
s	**Torula pluriseptata** (1 OTU with 99% identity in 221bp to: Torula pluriseptata)	0.1%
s	**Fusarium equiseti** (1 OTU with 100% identity in 209bp to: Fusarium equiseti)	0.1%
g	**Mucor** (1 OTU with 100% identity in 270bp to: 2 unclassified Mucor strains, Mucor fragilis)	0.1%
s	**Trichocladium asperum** (1 OTU with 99% identity in 221bp to: Trichocladium asperum)	0.1%
g	**Colletotrichum** (1 OTU with 100% identity in 236bp to: Colletotrichum coccodes, Colletotrichum sp. ITCC 6079)	0.1%
s	**Pyrenochaetopsis decipiens** (1 OTU with 100% identity in 202bp to: Pyrenochaetopsis decipiens)	0.1%
s	**Remispora quadri-remis** (1 OTU with 83% identity in 257bp to: Remispora quadri-remis)	0.1%
s	**Preussia sp. (in** (2 OTUs with 97% identity in 243bp to: Preussia sp. (in)	0.1%
s	**Striaticonidium cinctum** (1 OTU with 99% identity in 223bp to: Striaticonidium cinctum)	0.1%
s	**Filobasidium oeirense** (1 OTU with 100% identity in 214bp to: Filobasidium oeirense)	0.1%
s	**Pyrenochaeta nobilis** (1 OTU with 96% identity in 179bp to: Pyrenochaeta nobilis)	0.1%
s	**Fusarium penzigii** (1 OTU with 99% identity in 202bp to: Fusarium penzigii)	0.1%
s	**Dokmaia sp. 2 TMS-2011** (1 OTU with 98% identity in 200bp to: Dokmaia sp. 2 TMS-2011)	0.1%
s	**Tetracladium furcatum** (1 OTU with 96% identity in 218bp to: Tetracladium furcatum)	0.1%
s	**Cercophora sp. TMS-2011** (1 OTU with 79% identity in 204bp to: Cercophora sp. TMS-2011)	0.1%
s	**cf. Tubulicrinis sp. 8 LR-2015** (1 OTU with 70% identity in 278bp to: cf. Tubulicrinis sp. 8 LR-2015)	0.1%
g	**Metarhizium** (1 OTU with 100% identity in 196bp to: 4 unclassified Metarhizium strains, Metarhizium anisopliae, Metarhizium brunneum, Metarhizium guizhouense, Metarhizium indigoticum, Metarhizium robertsii)	0.1%
s	**Rosasphaeria moravica** (1 OTU with 78% identity in 214bp to: Rosasphaeria moravica)	0.1%
s	**Corynascus sepedonium** (1 OTU with 100% identity in 226bp to: Corynascus sepedonium)	0.1%

s	**Subramaniula thielavioides** (1 OTU with 97% identity in 234bp to: Subramaniula thielavioides)	0.1%
	Other (46 OTUs with 3.2%)	3.2%
	Unclassified (871 reads)	
	Filtered (0 reads)	

ODA.ITS1b (39 379 reads)

p	**Ascomycota** (18 OTUs with 91-100% identity in 202-262bp to: 11, 2, 3, 4, 5, 7, Acremonium sp. YT04, Allantophomopsis lycopodina, Alternaria, Aotearoamyces nothofagi, Ascochyta phacae, Aureobasidium, Auxarthron zuffianum, Chaetomium globosum, Cladosporium cladosporioides, Colletotrichum boninense, Dendrophoma, Epicoccum, Fusarium equiseti, Gliomastix murorum, Halenospora, Helicodendron giganteum, Helicorhoidion sp. DV-2018a, Kabatiella microsticta, Keithomyces carneus, Lambertella tubulosa, Metschnikowia sp. (in, Neocucurbitaria cava, Ophiocordyceps sp., Papulaspora sp. MTFD02, Paraisaria heteropoda, Phacidium mollerianum, Phialophorophoma litoralis, Pseudallescheria angusta, Pseudogymnoascus roseus, Purpureocillium lilacinum, Sagenomella oligospora, Strasseria geniculata, Trichophyton rubrum, Truncatella, Zalerion sp. Pb1-R5-B Lr)	8.9%
g	**Mortierella** (13 OTUs with 99-100% identity in 207-241bp to: 24 unclassified Mortierella strains, Mortierella aff. gamsii, Mortierella clonocystis, Mortierella dichotoma, Mortierella elongata, Mortierella epicladia, Mortierella gamsii, Mortierella minutissima, Mortierella parvispora)	8.8%
f	**Chaetomiaceae** (8 OTUs with 97-100% identity in 223-225bp to: 2 unclassified Trichocladium strains, 5 unclassified Humicola strains, Acrophialophora sp., Corynascus verrucosus, Trichocladium asperum, Trichocladium griseum)	6.6%
o	**Agaricales** (8 OTUs with 99-100% identity in 309bp to: Coprinopsis gonophylla, Coprinus sp. r072)	5.1%
s	**Furcasterigmium furcatum** (5 OTUs with 99-100% identity in 202-203bp to: Furcasterigmium furcatum)	4.7%
g	**Ilyonectria** (4 OTUs with 99-100% identity in 195bp to: Ilyonectria communis, Ilyonectria crassa, Ilyonectria cyclaminicola, Ilyonectria destructans, Ilyonectria mors-panacis, Ilyonectria panacis, Ilyonectria pseudodestructans, Ilyonectria sp.)	3.2%
s	**Fibulochlamys chilensis** (6 OTUs with 97-100% identity in 292-293bp to: Fibulochlamys chilensis)	2.8%
f	**Trichosporonaceae** (4 OTUs with 99-100% identity in 179-180bp to: 8 unclassified Trichosporon strains, Apiotrichum dulcitum, Apiotrichum gracile, Apiotrichum porosum, Cutaneotrichosporon moniliiforme, Cutaneotrichosporon sp.)	2.7%
s	**Cryptosporiopsis sp.** (1 OTU with 98% identity in 230bp to: Cryptosporiopsis sp.)	2.6%
g	**Clonostachys** (3 OTUs with 99-100% identity in 217-218bp to: 4 unclassified Clonostachys strains, Clonostachys candelabrum, Clonostachys rosea)	2.4%
s	**Podospora serotina** (2 OTUs with 82-83% identity in 221bp to: Podospora serotina)	2.4%
g	**Plectosphaerella** (2 OTUs with 99-100% identity in 200bp to: Plectosphaerella cucumerina, Plectosphaerella niemeijerarum, Plectosphaerella pauciseptata, Plectosphaerella plurivora, Plectosphaerella populi, Plectosphaerella sp.)	2.3%
s	**Penicillium arenicola** (4 OTUs with 95% identity in 244bp to: Penicillium arenicola)	2.3%
s	**Nigrograna mackinnonii** (4 OTUs with 89-90% identity in 272bp to: Nigrograna mackinnonii)	2.2%
s	**Sporothrix sp. T7508-1-3** (5 OTUs with 97-98% identity in 231bp to: Sporothrix sp. T7508-1-3)	2.1%
s	**Sphaerosporella sp.** (2 OTUs with 96-97% identity in 223bp to: Sphaerosporella sp.)	2.1%
s	**Microscypha sp.** (8 OTUs with 77-79% identity in 244-266bp to: Microscypha sp.)	1.7%
f	**Pseudeurotiaceae** (4 OTUs with 100% identity in 234bp to: 15 unclassified Geomyces strains, 5 unclassified Pseudogymnoascus strains, Geomyces auratus, Pseudogymnoascus appendiculatus, Pseudogymnoascus pannorum)	1.6%
s	**Peziza varia** (1 OTU with 100% identity in 253bp to: Peziza varia)	1.3%
c	**Sordariomycetes** (5 OTUs with 98-100% identity in 200-235bp to: 3 unclassified Plectosphaerella strains, Acrostalagmus luteoalbus, Acrostalagmus sp. JCM 28323, Colletotrichum pisi, Metapochonia suchlasporia, Monographella sp., Nectria inventa, Plectosphaerella cucumerina, Plectosphaerella niemeijerarum, Plectosphaerella pauciseptata, Plectosphaerella plurivora, Verticillium cephalosporum, Verticillium sp. FPGLXJ08)	1.2%
s	**Mortierella sp.** (2 OTUs with 99-100% identity in 206bp to: Mortierella sp.)	1.2%
s	**Leptodontidium sp. aurim655** (3 OTUs with 99-100% identity in 247bp to: Leptodontidium sp. aurim655)	1.1%
s	**Zopfiella sp.** (2 OTUs with 80-81% identity in 214bp to: Zopfiella sp.)	1.1%
s	**Humicola homopilata** (2 OTUs with 99-100% identity in 231bp to: Humicola homopilata)	1.0%
s	**Acrobeloides cf. nanus WB-2017** (4 OTUs with 98% identity in 351bp to: Acrobeloides cf. nanus WB-2017)	0.9%

s	**Acremonium sp. KM1p** (2 OTUs with 99% identity in 226bp to: Acremonium sp. KM1p)	0.8%
s	**Tetracladium furcatum** (1 OTU with 100% identity in 222bp to: Tetracladium furcatum)	0.8%
g	**Solicoccozyma** (2 OTUs with 100% identity in 226-229bp to: Solicoccozyma aeria, Solicoccozyma fuscescens, Solicoccozyma phenolica, Solicoccozyma terrea)	0.8%
g	**Penicillium** (8 OTUs with 99-100% identity in 234-237bp to: 30, Penicillium)	0.8%
o	**Eurotiales** (2 OTUs with 99-100% identity in 240bp to: Penicillago kabunica, Penicillago moldavicum, Penicillium sp., Thermoascus verrucosus)	0.8%
s	**Lyophyllum decastes** (1 OTU with 96% identity in 293bp to: Lyophyllum decastes)	0.7%
g	**Cladosporium** (2 OTUs with 100% identity in 216-217bp to: 5 unclassified Cladosporium strains, Cladosporium anthropophilum, Cladosporium cf. herbarum, Cladosporium cladosporioides, Cladosporium delicatulum, Cladosporium herbarum, Cladosporium oxysporum, Cladosporium pseudocladosporioides, Cladosporium rhusicola, Cladosporium sinuosum, Cladosporium tenellum, Cladosporium tenuissimum)	0.7%
s	**Flagellospora sp. VG 31-4** (2 OTUs with 91% identity in 224-225bp to: Flagellospora sp. VG 31-4)	0.7%
o	**Pleosporales** (4 OTUs with 100% identity in 199-266bp to: 2 unclassified Phoma strains, 3 unclassified Ampelomyces strains, 3 unclassified Leptosphaerulina strains, Allophoma tropica, Allophoma zantedeschiae, Ascochyta medicaginicola, Coniothyrium dispersellum, Coniothyrium euonymi-japonicae, Coniothyrium genistae, Coniothyrium glomerulatum, Coniothyrium lignorum, Coniothyrium populinum, Coniothyrium sp. TS-2016, Didymella macrostoma, Microsphaeropsis olivacea, Microsphaeropsis sp., Microsphaeropsis spartii-juncei, Neopyrenochaeta acicola, Nothophoma quercina, Phoma herbarum, Phoma sojicola, Pithomyces chartarum, Pseudopithomyces chartarum, Stagonosporopsis cucurbitacearum, Stagonosporopsis dorenboschii, Stagonosporopsis sp.)	0.6%
g	**Sporothrix** (3 OTUs with 98-99% identity in 242bp to: Sporothrix cf. inflata 2 PB-2018, Sporothrix inflata, Sporothrix sp. 16 RJ-2015)	0.6%
s	**Microthecium sepedonioides** (1 OTU with 97% identity in 207bp to: Microthecium sepedonioides)	0.5%
s	**Pezoloma sp. NBRC 103659** (1 OTU with 94% identity in 224bp to: Pezoloma sp. NBRC 103659)	0.5%
s	**Inosperma cookei** (2 OTUs with 98% identity in 289-290bp to: Inosperma cookei)	0.5%
s	**Trichoderma polysporum** (1 OTU with 100% identity in 267bp to: Trichoderma polysporum)	0.5%
s	**Podospora vesticola** (1 OTU with 93% identity in 234bp to: Podospora vesticola)	0.5%
s	**Hormiactis candida** (2 OTUs with 97-98% identity in 166bp to: Hormiactis candida)	0.4%
f	**Nectriaceae** (3 OTUs with 100% identity in 197-216bp to: Cosmospora butyri, Dactylonectria estremocensis, Dialonectria ullevolea, Fusarium merismoides, Fusicolla ossicola, Ilyonectria sp. 2 AC-2011, Pseudocosmospora vilior)	0.4%
s	**Mortierella horticola** (1 OTU with 100% identity in 194bp to: Mortierella horticola)	0.4%
s	**Ciliolarina ligniseda** (1 OTU with 99% identity in 220bp to: Ciliolarina ligniseda)	0.4%
g	**Trichoderma** (1 OTU with 100% identity in 245bp to: 6 unclassified Trichoderma strains, Trichoderma atroviride, Trichoderma caribbaeum, Trichoderma dingleyae, Trichoderma dorotheae, Trichoderma dorothopsis, Trichoderma gamsii, Trichoderma harzianum, Trichoderma koningii, Trichoderma koningiopsis, Trichoderma ovalisporum, Trichoderma viride, Trichoderma viridescens)	0.4%
s	**Pragmopora cf. pini** (2 OTUs with 74% identity in 256bp to: Pragmopora cf. pini)	0.3%
g	**Lipomyces** (1 OTU with 99% identity in 279bp to: Lipomyces starkeyi, Lipomyces tetrasporus)	0.3%
s	**Ramophialophora humicola** (2 OTUs with 93-100% identity in 195-204bp to: Ramophialophora humicola)	0.3%
s	**Penicillium sacculum** (2 OTUs with 99-100% identity in 235bp to: Penicillium sacculum)	0.3%
f	**Didymellaceae** (1 OTU with 100% identity in 201bp to: Juxtiphoma eupyrena, Phoma herbarum)	0.3%
s	**Hyaloscypha finlandica** (1 OTU with 99% identity in 275bp to: Hyaloscypha finlandica)	0.3%
s	**Ochrocladosporium sp.** (1 OTU with 99% identity in 205bp to: Ochrocladosporium sp.)	0.3%
s	**Clonostachys rossmaniae** (1 OTU with 99% identity in 219bp to: Clonostachys rossmaniae)	0.3%
g	**Fusarium** (1 OTU with 100% identity in 212bp to: 4 unclassified Fusarium strains, Fusarium acuminatum, Fusarium arthrosporioides, Fusarium avenaceum, Fusarium californicum, Fusarium cf. avenaceum, Fusarium cf. solani, Fusarium cf. tricinctum, Fusarium flocciferum, Fusarium lateritium, Fusarium petersiae, Fusarium redolens, Fusarium reticulatum, Fusarium sambucinum, Fusarium sinensis, Fusarium solani, Fusarium tricinctum)	0.3%
s	**Pseudoarthrographis phlogis** (3 OTUs with 87-88% identity in 241bp to: Pseudoarthrographis phlogis)	0.3%

g	**Chaetomium** (2 OTUs with 99-100% identity in 226-236bp to: 15 unclassified Chaetomium strains, Chaetomium angustispirale, Chaetomium cirrhinum, Chaetomium coarctatum, Chaetomium cochliodes, Chaetomium cucumericola, Chaetomium elatum, Chaetomium globosum, Chaetomium hispanicum, Chaetomium madrasense, Chaetomium olivaceum, Chaetomium pseudocochliodes, Chaetomium spiculipilium, Chaetomium spirochaete, Chaetomium subaffine, Chaetomium subglobosum, Chaetomium subspirale, Chaetomium subspirilliferum)	0.3%
s	**Humicola cuyabenoensis** (1 OTU with 98% identity in 193bp to: Humicola cuyabenoensis)	0.3%
s	**Aotearoamyces nothofagi** (1 OTU with 91% identity in 223bp to: Aotearoamyces nothofagi)	0.3%
o	**Diaporthales** (1 OTU with 100% identity in 232bp to: 2 unclassified Phomopsis strains, Diaporthe columnaris)	0.3%
s	**Thermoascus crustaceus** (3 OTUs with 95-100% identity in 242bp to: Thermoascus crustaceus)	0.3%
p	**Mucoromycota** (1 OTU with 100% identity in 233bp to: 9 unclassified Mortierella strains, Umbelopsis dimorpha, Umbelopsis nana, Umbelopsis sp.)	0.3%
s	**Sagenomella griseoviridis** (1 OTU with 100% identity in 279bp to: Sagenomella griseoviridis)	0.3%
f	**Plectosphaerellaceae** (1 OTU with 100% identity in 203bp to: Gibellulopsis nigrescens, Plectosphaerella sp. sedF4, Verticillium dahliae, Verticillium sp. DU18)	0.2%
s	**Thaumatomonas zhukovi** (1 OTU with 99% identity in 314bp to: Thaumatomonas zhukovi)	0.2%
s	**Peziza moseri** (1 OTU with 99% identity in 261bp to: Peziza moseri)	0.2%
s	**Inocybe acutofulva** (1 OTU with 100% identity in 285bp to: Inocybe acutofulva)	0.2%
s	**Lipomyces starkeyi** (1 OTU with 99% identity in 161bp to: Lipomyces starkeyi)	0.2%
s	**Xenodidymella sp. A SK-2018** (1 OTU with 97% identity in 199bp to: Xenodidymella sp. A SK-2018)	0.2%
s	**Atractospora reticulata** (1 OTU with 88% identity in 193bp to: Atractospora reticulata)	0.2%
o	**Helotiales** (2 OTUs with 100% identity in 220-295bp to: 2 unclassified Cadophora strains, Cadophora orchidicola, Ciliolarina ligniseda, Infundichalara microchona, Leptodontidium sp.)	0.2%
s	**Trichocladium asperum** (1 OTU with 100% identity in 221bp to: Trichocladium asperum)	0.2%
s	**Trichosporon sp. 05NY01** (1 OTU with 100% identity in 178bp to: Trichosporon sp. 05NY01)	0.2%
g	**Exophiala** (1 OTU with 100% identity in 254bp to: Exophiala equina, Exophiala radicis, Exophiala sp.)	0.2%
c	**Leotiomycetes** (1 OTU with 94% identity in 230bp to: Claussenomyces kirschsteinianus, Cryptosporiopsis sp., Phialocephala virens)	0.2%
s	**Claussenomyces cf. hydnicola H.B. 9975** (1 OTU with 77% identity in 196bp to: Claussenomyces cf. hydnicola H.B. 9975)	0.2%
s	**Aspergillus fumigatus** (1 OTU with 100% identity in 249bp to: Aspergillus fumigatus)	0.2%
s	**Saitozyma podzolica** (2 OTUs with 99-100% identity in 169bp to: Saitozyma podzolica)	0.2%
g	**Alternaria** (2 OTUs with 100% identity in 226-227bp to: 3 unclassified Alternaria strains, 3 unclassified Ulocladium strains, Alternaria atra, Alternaria chartarum, Alternaria consortialis, Alternaria multiformis, Alternaria preussii, Alternaria sorghi, Alternaria terricola, [Ulocladium] sp.)	0.2%
s	**Schizothecium inaequale** (1 OTU with 81% identity in 229bp to: Schizothecium inaequale)	0.2%
g	**Beauveria** (1 OTU with 99% identity in 223bp to: Beauveria asiatica, Beauveria bassiana, Beauveria brongniartii, Beauveria medogensis, Beauveria sp. NWHC 24825-01-01-03)	0.2%
s	**Cladophialophora chaetospira** (1 OTU with 100% identity in 253bp to: Cladophialophora chaetospira)	0.2%
s	**Cryptococcus sp. YKS 2004** (1 OTU with 100% identity in 168bp to: Cryptococcus sp. YKS 2004)	0.2%
s	**Cladophialophora sp. KO-groupO 2014** (1 OTU with 95% identity in 253bp to: Cladophialophora sp. KO-groupO 2014)	0.2%
s	**Rasamsonia argillacea** (1 OTU with 79% identity in 252bp to: Rasamsonia argillacea)	0.2%
s	**Trichoderma tomentosum** (1 OTU with 100% identity in 263bp to: Trichoderma tomentosum)	0.2%
s	**Humicola fuscoatra** (1 OTU with 99% identity in 230bp to: Humicola fuscoatra)	0.2%
s	**Calocera cornea** (2 OTUs with 88-89% identity in 163bp to: Calocera cornea)	0.2%
s	**Heteromita sp. HFCC 923** (1 OTU with 79% identity in 233bp to: Heteromita sp. HFCC 923)	0.2%
s	**Gliomastix murorum** (1 OTU with 100% identity in 237bp to: Gliomastix murorum)	0.2%
s	**Schizothecium sp. E33** (2 OTUs with 95-96% identity in 226bp to: Schizothecium sp. E33)	0.2%
s	**Harposporium helicoides** (1 OTU with 82% identity in 279bp to: Harposporium helicoides)	0.2%

c	**Dothideomycetes** (1 OTU with 98% identity in 208bp to: Exosporium sp. 1 NV-2015, Lophiostoma corticola)	0.2%
s	**Cephalotrichum microsporum** (1 OTU with 100% identity in 235bp to: Cephalotrichum microsporum)	0.2%
f	**Hyaloscyphaceae** (1 OTU with 79% identity in 268bp to: Microscypha sp., Pezizella chrysostigma)	0.2%
s	**Cytospora sp.** (1 OTU with 100% identity in 264bp to: Cytospora sp.)	0.1%
s	**Mortierella simplex** (1 OTU with 95% identity in 241bp to: Mortierella simplex)	0.1%
s	**Thaumatomonas sp. CCAP 1903/2** (1 OTU with 99% identity in 331bp to: Thaumatomonas sp. CCAP 1903/2)	0.1%
s	**Oidiodendron flavum** (1 OTU with 99% identity in 228bp to: Oidiodendron flavum)	0.1%
g	**Cephalotrichum** (1 OTU with 100% identity in 235bp to: Cephalotrichum nanum, Cephalotrichum stemonitis)	0.1%
s	**Talaromyces sp. FKI-6713** (1 OTU with 96% identity in 245bp to: Talaromyces sp. FKI-6713)	0.1%
s	**Inosperma maculatum** (1 OTU with 98% identity in 286bp to: Inosperma maculatum)	0.1%
k	**Eukaryota** (2 OTUs with 100% identity in 209-218bp to: 3 unclassified Fusarium strains, 4 unclassified Clonostachys strains, Auricularia polytricha, Citrullus lanatus, Clonostachys rhizophaga, Clonostachys rosea, Fusarium caucasicum, Fusarium cf. oxysporum, Fusarium oxysporum, Fusarium verticillioides, Humicola sp.)	0.1%
s	**Sagenomella striatispora** (2 OTUs with 99-100% identity in 248bp to: Sagenomella striatispora)	0.1%
s	**Thermothelomyces guttulatus** (1 OTU with 100% identity in 219bp to: Thermothelomyces guttulatus)	0.1%
s	**Geomyces sp. 12NJ08** (1 OTU with 100% identity in 238bp to: Geomyces sp. 12NJ08)	0.1%
s	**Mortierella sp. S-24** (1 OTU with 99% identity in 202bp to: Mortierella sp. S-24)	0.1%
s	**Atractospora aquatica** (2 OTUs with 88-89% identity in 180-182bp to: Atractospora aquatica)	0.1%
s	**Humicola sp.** (1 OTU with 98% identity in 228bp to: Humicola sp.)	0.1%
s	**Tricholoma matsutake** (1 OTU with 99% identity in 229bp to: Tricholoma matsutake)	0.1%
	Other (41 OTUs with 3.0%)	3.0%
	Unclassified (3 849 reads)	
	Filtered (0 reads)	

ODB.ITS1b (55 859 reads)

p	**Ascomycota** (26 OTUs with 99-100% identity in 226-262bp to: 2 unclassified Alternaria strains, 2 unclassified Pseudogymnoascus strains, 9 unclassified Geomyces strains, Acremonium sp. YT04, Alternaria alstroemeriae, Alternaria alternata, Alternaria angustiovoidea, Alternaria arborescens, Alternaria fasciculata, Alternaria infectoria, Alternaria longipes, Alternaria solani, Alternaria tenuissima, Auxarthron zuffianum, Colletotrichum boninense, Geomyces vinaceus, Gliomastix murorum, Halenospora sp., Halenospora varia, Helicodendron giganteum, Helicorhoidion sp. DV-2018a, Keithomyces carneus, Lambertella tubulosa, Paecilomyces sp. (in, Papulaspora sp. MTFD02, Pseudogymnoascus destructans, Pseudogymnoascus roseus, Zalerion sp. Pb1-R5-B Lr)	22.9%
s	**Inosperma cookei** (32 OTUs with 97-98% identity in 284-291bp to: Inosperma cookei)	20.7%
g	**Pseudeurotium** (11 OTUs with 95% identity in 221-223bp to: Pseudeurotium bakeri, Pseudeurotium sp. OTU018 AN-2016, Pseudeurotium zonatum)	11.9%
g	**Mortierella** (9 OTUs with 99-100% identity in 207-241bp to: 17 unclassified Mortierella strains, Mortierella aff. gamsii, Mortierella clonocystis, Mortierella elongata, Mortierella epicladia, Mortierella gamsii, Mortierella minutissima)	6.7%
g	**Ilyonectria** (5 OTUs with 99-100% identity in 195-197bp to: 2 unclassified Ilyonectria strains, Ilyonectria communis, Ilyonectria crassa, Ilyonectria cyclaminicola, Ilyonectria destructans, Ilyonectria mors-panacis, Ilyonectria panacis, Ilyonectria pseudodestructans, Ilyonectria robusta)	2.9%
s	**Mortierella simplex** (2 OTUs with 95% identity in 241bp to: Mortierella simplex)	2.2%
f	**Chaetomiaceae** (7 OTUs with 95-100% identity in 223-225bp to: 2 unclassified Trichocladium strains, 5 unclassified Humicola strains, Acrophialophora sp., Corynascus verrucosus, Podospora didyma, Trichocladium asperum, Trichocladium griseum, Zopfiella tabulata)	2.0%
s	**Cryptosporiopsis sp.** (2 OTUs with 97-98% identity in 230bp to: Cryptosporiopsis sp.)	1.9%
f	**Pseudeurotiaceae** (5 OTUs with 99-100% identity in 234-256bp to: 17 unclassified Geomyces strains, 6 unclassified Pseudogymnoascus strains, Geomyces auratus, Pseudogymnoascus appendiculatus, Pseudogymnoascus pannorum, Pseudogymnoascus roseus)	1.5%
s	**Ascobolus sp.** (1 OTU with 94% identity in 252bp to: Ascobolus sp.)	1.4%
s	**Lophium zalerioides** (3 OTUs with 97-98% identity in 232-234bp to: Lophium zalerioides)	1.1%

s	**Mortierella horticola** (1 OTU with 100% identity in 194bp to: Mortierella horticola)	1.0%
s	**Trichocladium asperum** (2 OTUs with 99-100% identity in 221bp to: Trichocladium asperum)	1.0%
o	**Helotiales** (2 OTUs with 100% identity in 220-295bp to: 2 unclassified Cadophora strains, Cadophora orchidicola, Chalara sp. 400, Leptodontidium sp., Xenopolyscytalum pinea)	1.0%
s	**Mortierella sp. S-25** (2 OTUs with 96-97% identity in 211-215bp to: Mortierella sp. S-25)	0.9%
s	**Furcasterigmium furcatum** (2 OTUs with 99-100% identity in 203bp to: Furcasterigmium furcatum)	0.9%
s	**Cercophora sparsa** (2 OTUs with 95-96% identity in 199bp to: Cercophora sparsa)	0.7%
s	**Pragmopora cf. pini** (1 OTU with 74% identity in 256bp to: Pragmopora cf. pini)	0.7%
c	**Sordariomycetes** (4 OTUs with 98-100% identity in 200-235bp to: 3 unclassified Plectosphaerella strains, Acrostalagmus luteoalbus, Acrostalagmus sp. JCM 28323, Colletotrichum pisi, Metapochonia suchlasporia, Monographella sp., Nectria inventa, Plectosphaerella cucumerina, Plectosphaerella niemeijerarum, Plectosphaerella pauciseptata, Plectosphaerella plurivora, Verticillium cephalosporum, Verticillium sp. FPGLXJ08)	0.6%
f	**Trichosporonaceae** (2 OTUs with 100% identity in 179bp to: 7 unclassified Trichosporon strains, Apiotrichum dulcitum, Apiotrichum gracile, Apiotrichum porosum)	0.6%
s	**Sphaerosporella sp.** (1 OTU with 96% identity in 223bp to: Sphaerosporella sp.)	0.6%
s	**Saitozyma podzolica** (3 OTUs with 99-100% identity in 169bp to: Saitozyma podzolica)	0.5%
o	**Eurotiales** (1 OTU with 100% identity in 240bp to: Penicillago kabunica, Penicillago moldavicum, Thermoascus verrucosus)	0.5%
s	**Tetracladium furcatum** (1 OTU with 100% identity in 222bp to: Tetracladium furcatum)	0.4%
g	**Cephalotrichum** (1 OTU with 100% identity in 235bp to: Cephalotrichum nanum, Cephalotrichum stemonitis)	0.4%
s	**Burgoa anomala** (1 OTU with 100% identity in 242bp to: Burgoa anomala)	0.4%
g	**Clonostachys** (1 OTU with 100% identity in 218bp to: 4 unclassified Clonostachys strains, Clonostachys rosea)	0.3%
s	**Neonectria sp.** (1 OTU with 97% identity in 197bp to: Neonectria sp.)	0.3%
g	**Fusarium** (1 OTU with 100% identity in 212bp to: 4 unclassified Fusarium strains, Fusarium acuminatum, Fusarium arthrosporioides, Fusarium avenaceum, Fusarium californicum, Fusarium cf. avenaceum, Fusarium cf. solani, Fusarium cf. tricinctum, Fusarium flocciferum, Fusarium lateritium, Fusarium petersiae, Fusarium redolens, Fusarium reticulatum, Fusarium sambucinum, Fusarium sinensis, Fusarium solani, Fusarium tricinctum)	0.3%
s	**Xenodidymella sp. A SK-2018** (1 OTU with 97% identity in 199bp to: Xenodidymella sp. A SK-2018)	0.3%
s	**Thielavia basicola** (1 OTU with 85% identity in 214bp to: Thielavia basicola)	0.3%
s	**Tyrannosorus hystrioides** (1 OTU with 100% identity in 220bp to: Tyrannosorus hystrioides)	0.3%
p	**Mucoromycota** (1 OTU with 100% identity in 233bp to: 9 unclassified Mortierella strains, Umbelopsis dimorpha, Umbelopsis nana, Umbelopsis sp.)	0.3%
s	**Hormiactis candida** (2 OTUs with 97-98% identity in 166bp to: Hormiactis candida)	0.3%
s	**Acrobeloides cf. nanus WB-2017** (2 OTUs with 98% identity in 351bp to: Acrobeloides cf. nanus WB-2017)	0.3%
s	**Mytilinidion mytilinellum** (2 OTUs with 71% identity in 298bp to: Mytilinidion mytilinellum)	0.3%
g	**Solicoccozyma** (2 OTUs with 100% identity in 226-229bp to: Solicoccozyma aeria, Solicoccozyma fuscescens, Solicoccozyma phenolica, Solicoccozyma terrea)	0.3%
s	**Cladorrhinum foecundissimum** (1 OTU with 100% identity in 218bp to: Cladorrhinum foecundissimum)	0.3%
g	**Plectosphaerella** (1 OTU with 100% identity in 200bp to: Plectosphaerella cucumerina, Plectosphaerella niemeijerarum, Plectosphaerella pauciseptata, Plectosphaerella plurivora, Plectosphaerella populi, Plectosphaerella sp.)	0.3%
s	**Sporothrix sp. T7508-1-3** (1 OTU with 98% identity in 231bp to: Sporothrix sp. T7508-1-3)	0.3%
s	**Schizothecium glutinans** (2 OTUs with 95% identity in 234bp to: Schizothecium glutinans)	0.3%
g	**Volutella** (1 OTU with 98% identity in 229bp to: Volutella ciliata, Volutella rosea)	0.2%
g	**Cladosporium** (1 OTU with 100% identity in 217bp to: 4 unclassified Cladosporium strains, Cladosporium anthropophilum, Cladosporium cladosporioides, Cladosporium delicatulum, Cladosporium oxysporum, Cladosporium pseudocladosporioides, Cladosporium tenuissimum)	0.2%
s	**Chalara sp. TMS-2011** (1 OTU with 95% identity in 223bp to: Chalara sp. TMS-2011)	0.2%
s	**Echria gigantospora** (1 OTU with 91% identity in 200bp to: Echria gigantospora)	0.2%

o	**Agaricales** (1 OTU with 100% identity in 309bp to: Coprinopsis gonophylla, Coprinus sp. r072)	0.2%
s	**Apodus deciduus** (2 OTUs with 99% identity in 212bp to: Apodus deciduus)	0.2%
s	**Lipomyces starkeyi** (1 OTU with 99% identity in 161bp to: Lipomyces starkeyi)	0.2%
s	**Entrophospora sp. JJ61** (2 OTUs with 76% identity in 330bp to: Entrophospora sp. JJ61)	0.2%
s	**Humicola homopilata** (1 OTU with 100% identity in 231bp to: Humicola homopilata)	0.2%
f	**Nectriaceae** (3 OTUs with 100% identity in 196-215bp to: Cylindrocarpon sp. IBL 03149, Dactylonectria pauciseptata, Dialonectria ullevolea, Fusarium merismoides, Fusicolla ossicola, Nectria sp. (in, Neonectria lugdunensis, Neonectria shennongjiana, Neonectria sp., Thelonectria lucida)	0.2%
g	**Schizothecium** (1 OTU with 94% identity in 222bp to: Schizothecium inaequale, Schizothecium sp.)	0.2%
s	**Neocucurbitaria juglandicola** (1 OTU with 100% identity in 202bp to: Neocucurbitaria juglandicola)	0.2%
s	**Collophorina africana** (1 OTU with 74% identity in 257bp to: Collophorina africana)	0.2%
s	**Thaumatomonas zhukovi** (1 OTU with 99% identity in 314bp to: Thaumatomonas zhukovi)	0.2%
k	**Eukaryota** (2 OTUs with 100% identity in 213-216bp to: 3 unclassified Davidiella strains, 6 unclassified Cladosporium strains, Cladophialophora minourae, Cladosporium aerium, Cladosporium allicinum, Cladosporium allii, Cladosporium angustiherbarum, Cladosporium antarcticum, Cladosporium cf. herbarum, Cladosporium cladosporioides, Cladosporium cucumerinum, Cladosporium floccosum, Cladosporium herbarum, Cladosporium macrocarpum, Cladosporium ossifragi, Cladosporium parasubtilissimum, Cladosporium sinuosum, Cladosporium subinflatum, Cladosporium variabile, Cladosporium wyomingense, Neobulgaria koningiana, Piromyces sp., Psychrophila antarctica, Yuchengia narymica, aff. Cladosporium sp.)	0.2%
s	**Mortierella sp.** (1 OTU with 100% identity in 206bp to: Mortierella sp.)	0.2%
s	**Helicoubisia coronata** (2 OTUs with 87-88% identity in 209bp to: Helicoubisia coronata)	0.2%
g	**Lipomyces** (1 OTU with 99% identity in 279bp to: Lipomyces starkeyi, Lipomyces tetrasporus)	0.2%
s	**Humicola fuscoatra** (1 OTU with 99% identity in 230bp to: Humicola fuscoatra)	0.2%
s	**Remispora quadri-remis** (1 OTU with 84% identity in 257bp to: Remispora quadri-remis)	0.2%
s	**Humicola sp.** (1 OTU with 98% identity in 228bp to: Humicola sp.)	0.2%
s	**Leptodontidium sp. aurim655** (1 OTU with 100% identity in 247bp to: Leptodontidium sp. aurim655)	0.2%
s	**Podospora sp.** (1 OTU with 98% identity in 217bp to: Podospora sp.)	0.2%
g	**Penicillium** (2 OTUs with 99-100% identity in 236-238bp to: 8 unclassified Penicillium strains, Penicillium cremeogriseum, Penicillium lagena, Penicillium oregonense, Penicillium parviverrucosum, Penicillium simplicissimum)	0.2%
o	**Diaporthales** (1 OTU with 100% identity in 232bp to: 2 unclassified Phomopsis strains, Diaporthe columnaris)	0.2%
s	**Mortierella sp. S-24** (1 OTU with 99% identity in 202bp to: Mortierella sp. S-24)	0.2%
s	**Lyomyces crustosus** (1 OTU with 100% identity in 284bp to: Lyomyces crustosus)	0.2%
s	**Peziza varia** (1 OTU with 100% identity in 253bp to: Peziza varia)	0.2%
s	**Trichoderma tomentosum** (1 OTU with 100% identity in 263bp to: Trichoderma tomentosum)	0.1%
s	**Serendipita herbamans** (1 OTU with 95% identity in 243bp to: Serendipita herbamans)	0.1%
f	**Hyaloscyphaceae** (1 OTU with 79% identity in 268bp to: Microscypha sp., Pezizella chrysostigma)	0.1%
c	**Leotiomycetes** (1 OTU with 94% identity in 230bp to: Claussenomyces kirschsteinianus, Cryptosporiopsis sp., Phialocephala virens)	0.1%
s	**Kraurogymnocarpa trochleospora** (1 OTU with 72% identity in 296bp to: Kraurogymnocarpa trochleospora)	0.1%
s	**Humicola cuyabenoensis** (1 OTU with 98% identity in 193bp to: Humicola cuyabenoensis)	0.1%
s	**Ramophialophora humicola** (1 OTU with 93% identity in 195bp to: Ramophialophora humicola)	0.1%
s	**Cenococcum sp.** (1 OTU with 89% identity in 223bp to: Cenococcum sp.)	0.1%
s	**Atractospora reticulata** (1 OTU with 88% identity in 193bp to: Atractospora reticulata)	0.1%
s	**Glutinomyces vulgaris** (2 OTUs with 94% identity in 231bp to: Glutinomyces vulgaris)	0.1%
s	**Gliomastix murorum** (1 OTU with 100% identity in 237bp to: Gliomastix murorum)	0.1%
s	**Russula praetervisa** (1 OTU with 100% identity in 276bp to: Russula praetervisa)	0.1%

s	**Cladophialophora sp. L359** (1 OTU with 100% identity in 232bp to: Cladophialophora sp. L359)	0.1%
s	**Penicillium arenicola** (1 OTU with 95% identity in 244bp to: Penicillium arenicola)	0.1%
s	**Clonostachys rossmaniae** (1 OTU with 99% identity in 219bp to: Clonostachys rossmaniae)	0.1%
s	**Peziza moseri** (1 OTU with 99% identity in 261bp to: Peziza moseri)	0.1%
	Other (37 OTUs with 2.6%)	2.6%
	Unclassified (3 417 reads)	
	Filtered (0 reads)	

As in the previous phase, microbiome profiling was carried out using an advanced pipeline, which included the removal of chimeric sequences, OTU clustering via Minimum Entropy Decomposition, and taxonomic assignment through comparison with reference databases. The overall quality of the dataset was high, with more than 99% of sequences retained after filtering and approximately 75% successfully assigned to OTUs and to known taxa.
In the first group of soil samples (ODA, ODB, and ODC), clear differences in fungal community composition were detected. Sample ODA was mainly dominated by *Mortierella* (8.8%) and members of the family Chaetomiaceae (6.6%), together with a substantial proportion of Ascomycota (8.9%). The presence of Agaricales (5.1%) and *Furcasterigmium* (4.7%) further indicates the contribution of saprotrophic and environmentally associated fungi, suggesting a soil community shaped by both nutrient cycling and environmental interactions.

Sample ODB, on the other hand, showed a very distinct profile, with a strong prevalence of Ascomycota (22.9%) and the basidiomycete *Inosperma cookei* (20.7%), in addition to *Pseudeurotium* (11.9%) and *Mortierella* (6.7%). This composition reflects a rich and diverse fungal community, characterized by both symbiotic and saprotrophic taxa, and points to a higher ecological complexity compared to ODA.

Sample ODC produced only three sequences, which could not be reliably assigned to OTUs or taxa. This outcome is most likely attributable to technical troubles, such as insufficient DNA recovery or the presence of inhibitory substances during extraction, rather than reflecting a genuine absence of fungal diversity in the sample.
Samples LA–LD showed a relatively homogeneous fungal community, dominated by *Fusarium* (7–13%), Plectosphaerellaceae (up to 14.6% in LC), *Cladosporium* (max 9.2% in LD), and *Alternaria alternata* (2–6.9%). *Mortierella*, *Trichoderma*, Chaetomium, and *Aspergillus* were also detected at variable levels.
Overall, the ODA–ODB group exhibited greater diversity and a more heterogeneous composition, characterized by the presence of numerous environmental and saprotrophic fungi. In contrast, the LA–LD group was dominated by taxa typically associated with agricultural soils or plant substrates, including several genera with well-known impacts on plant health.
From an applied perspective, the ODA–ODB soils appear more promising for truffle cultivation, as they support higher fungal biodiversity, show a lower incidence of agricultural pathogens, and display a community structure more compatible with forest soils. Conversely, the LA–LD samples, while displaying substantial microbial activity, may require additional corrective interventions aimed at improving soil quality and mitigating microbial competition from pathogenic taxa.

However, it is important to note that the mycelium of *Tuber aestivum* was completely absent from all analysed samples. This absence may be due to inappropriate sampling procedures, such as collecting too far from mycorrhized plants or at an insufficient soil depth. The absence of expert laboratory personnel - owing to unexpected circumstances - likely contributed adversely to this outcome.

Inter-host mycelial transfer

An additional objective of this study was to assess the potential host-to-host transfer of *Tuber aestivum* mycelium, from nursery-inoculated seedlings to naturally occurring host plants within the plantation sites. For this purpose, root tips were collected from both groups of plants and subjected to an initial morphological screening. Selected samples were then analyzed by molecular tools to confirm the presence of *Tuber aestivum* within the ectomycorrhizae and to determine the specific identity of the host plant. The quality of the collected root tips was generally poor, with dead mycorrhizae accounting for up to 100% of samples in some cases. This outcome may be due to several factors, including plant stress, improper sampling (again linked to the lack of a trained technician) and inadequate sample preservation. Nevertheless, a subset of samples, such as those shown in Figure 5, were processed for further analysis.

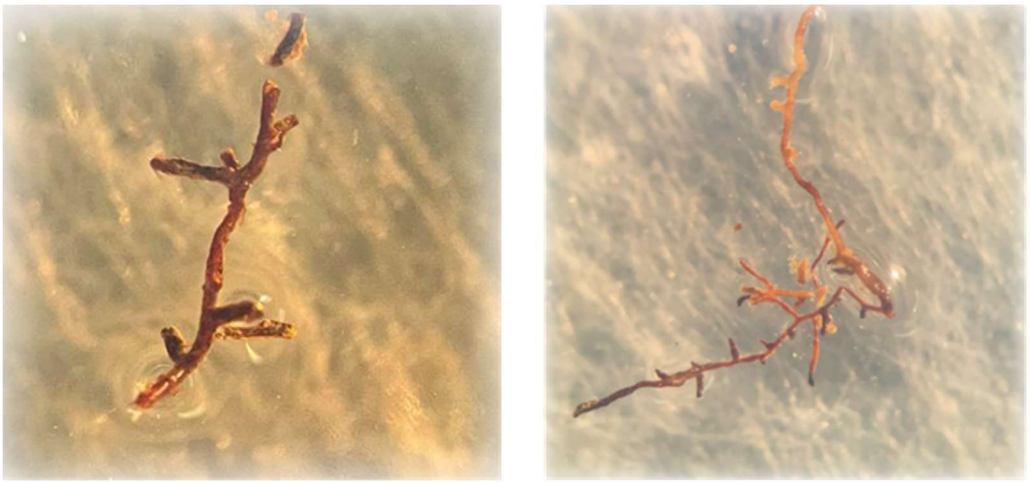

Figure 5: Representative ectomycorrhizal root tips collected for analysis: left, *Cistus incanus*; right, *Carya illinoinensis*.

The extracted DNA was subsequently subjected to PCR amplification using host-specific barcode primers targeting the plastid trnC–trnD region. Electrophoretic analysis confirmed that the samples corresponded to the expected host plants, *Cistus incanus* and *Carya illinoinensis* (Figure 6).

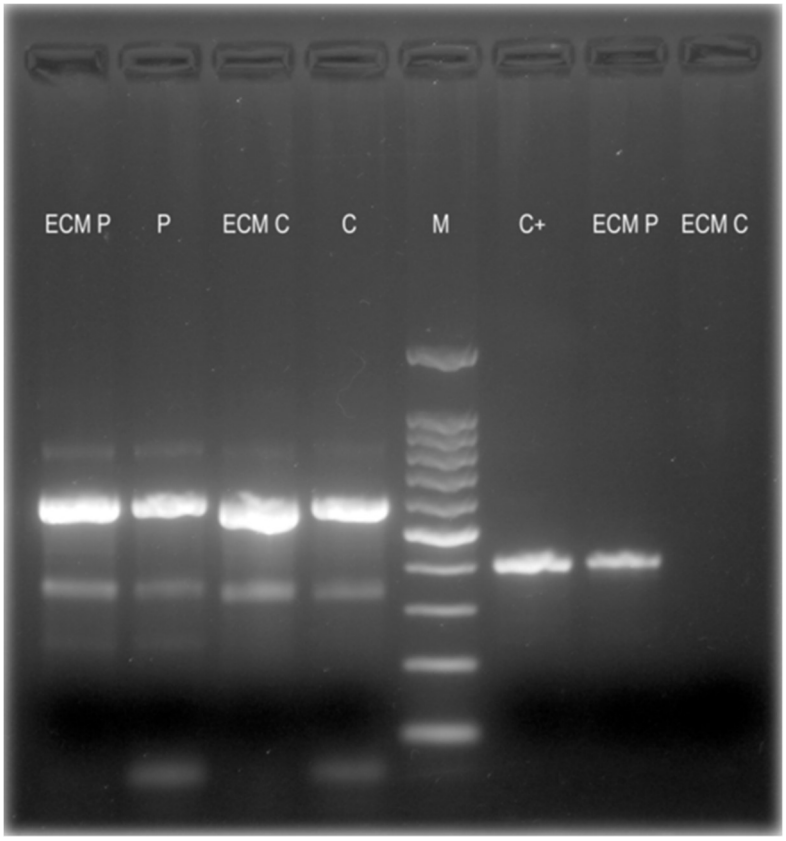

Figure 6: Left, relative to the ladder marker (M): verification of the host plant using barcode primers targeting the plastid trnL region; right: detection of *Tuber aestivum* in the mycorrhizae using species-specific ITS primers. C+ = positive control (DNA from *Tuber aestivum* ascoma).

The presence of *Tuber aestivum* was confirmed in *Carya illinoinensis* roots using species-specific UncI/UncII primers (ITS region), while its absence in *Cistus incanus* samples likely reflects limited sample quality. Overall, the results suggest that truffles were successfully established in pre-existing pecan plants following the planting of inoculated *Cistus incanus*.

Characterisation of the indigenous Sicilian truffle

A key aim of the project was to identify molecular markers for the geographical characterisation of Sicilian summer truffles in order to distinguish them from those of other origins.

For this purpose, DNA from samples collected from natural truffle grounds at three sites across the island was analyzed using PCR and RFLP methodologies.

Total genomic DNA extraction was generally successful, confirming the effectiveness of the adopted protocol (see Figures 7 and 8). However, only a few samples exhibited low yields: S5 from the Monti Sicani, and i2 and i5 from the Monti Iblei. This may reflect differences in tissue quality, or the presence of inhibitory compounds.

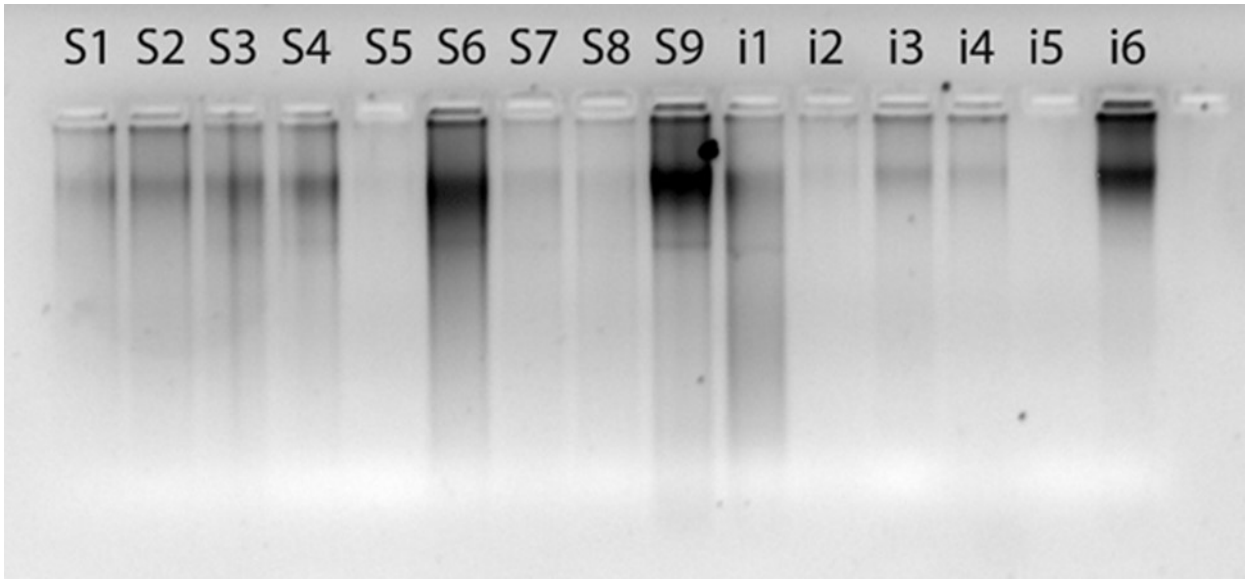

Figure 7: Total genomic DNA extraction from Sicilian *Tuber aestivum* samples. S = Monti Sicani; i = Monti Iblei.

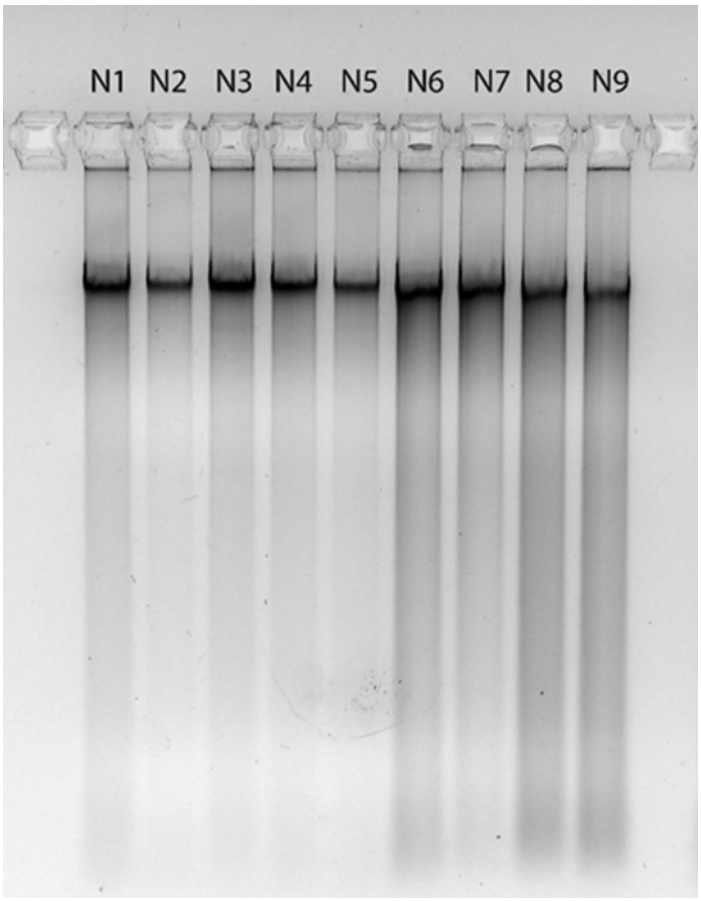

Figure 8: Total genomic DNA extraction from Sicilian *Tuber aestivum* samples, Monti Nebrodi.

Sample identity was confirmed using species-specific primers for *Tuber aestivum*. As a member of the Aestivum clade, this truffle forms a species complex in which morphological traits alone can be insufficient for differentiation due to overlap with closely related sister species.
The results are showed in Figures 9 and 10.

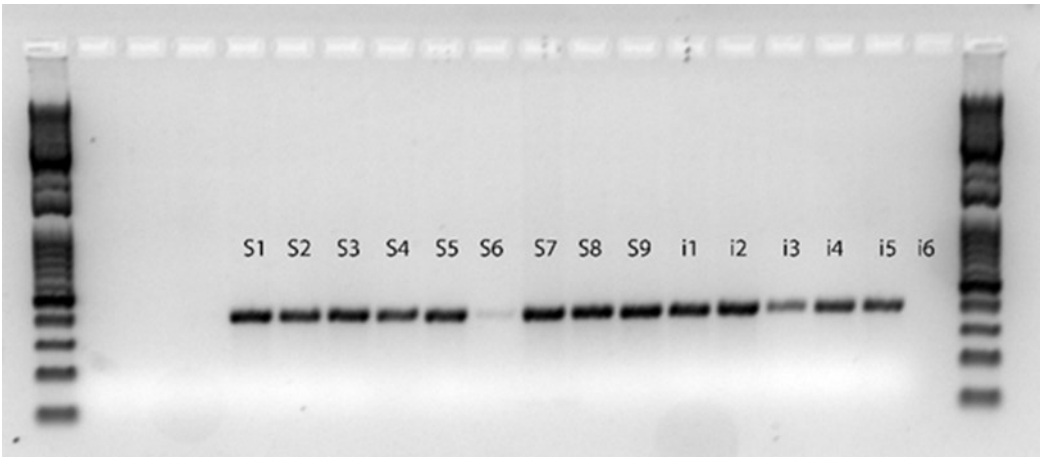

Figure 9: PCR amplification using species-specific UncI/II primers for *Tuber aestivum* from Sicily. S = Monti Sicani; i = Monti Iblei.

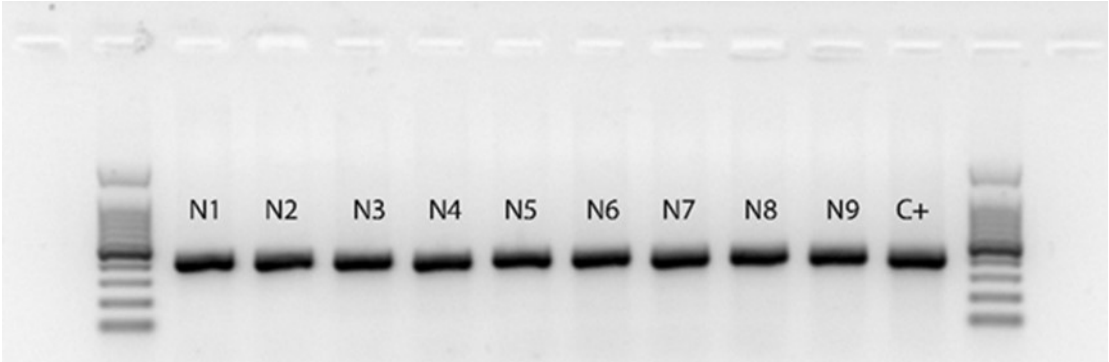

Figure 9: PCR amplification using species-specific UncI/II primers for *Tuber aestivum* from Sicily, Monti Nebrodi.

The image shows that sample i6 was identified as belonging to a different species.

Based on previous studies aimed at identifying distinct populations within the species *T. aestivum*, particularly those by Molinier et al. (2013), we performed an analysis of the mitochondrial ribosomal large subunit (mtLSU) using the primer pair ML3 and ML4.

The amplification products with these primers were subsequently subjected to restriction analysis, using the endonuclease enzyme AluI in a first test, in order to produce a fragment map capable of unmasking possible polymorphisms (Figure 11).

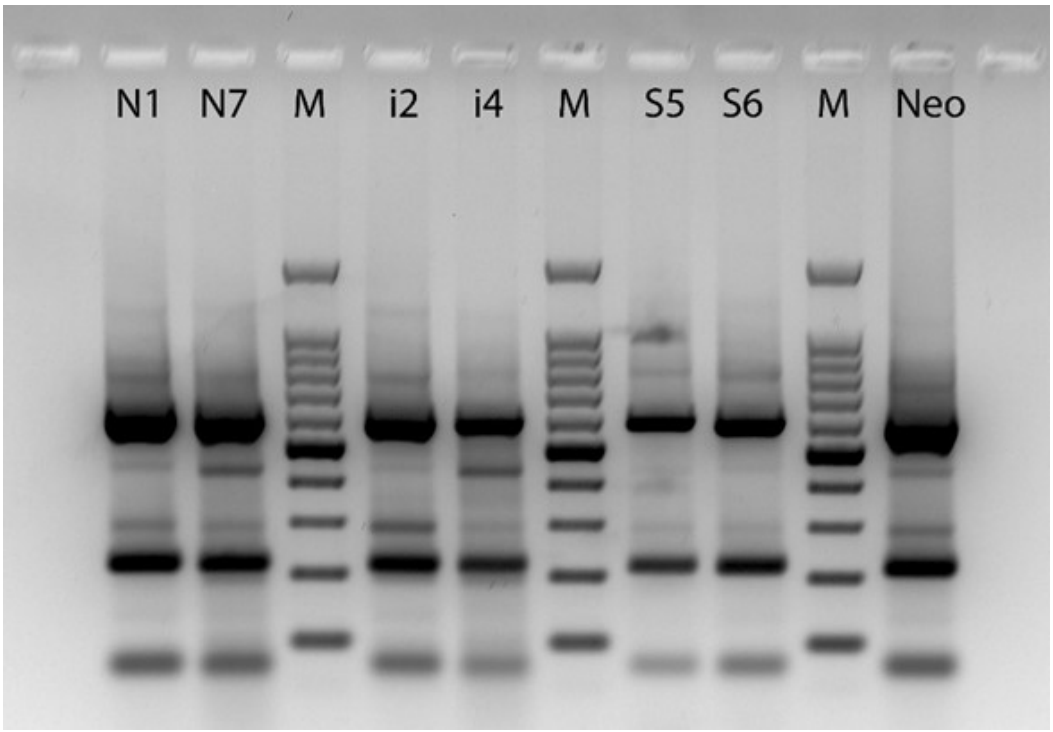

Figure 11: RFLP (Random Fragment Length Polymorphism) AluI - PCR ML3/4 *sensu* Molinier et al. 2013.

No significant differences were detected in this assay across all samples from the various collection sites, including in comparison with the positive control MBT 10001890. To validate these findings further, the MCM7 gene, a marker commonly used in phylogenetic studies of Ascomycota and Basidiomycota, was amplified by PCR using the primer pair Mcm7-709for and Mcm7-1348rev (Schmitt et al., 2009; see Figure 12). Subsequent restriction analysis was performed using the AluI and HinfI enzymes to digest the PCR products at 37 °C for three hours (Figure 13). These results support the consistency of the genetic profiles across the sampled populations.

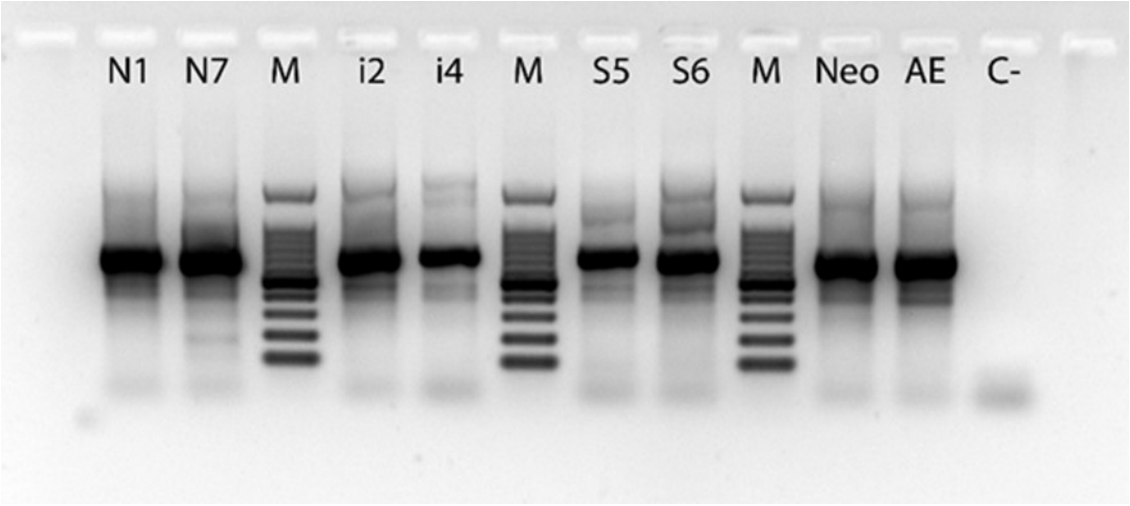

Figure 12: PCR amplification of MCM7 gene; Primers Mcm7-709for/-1348rev.

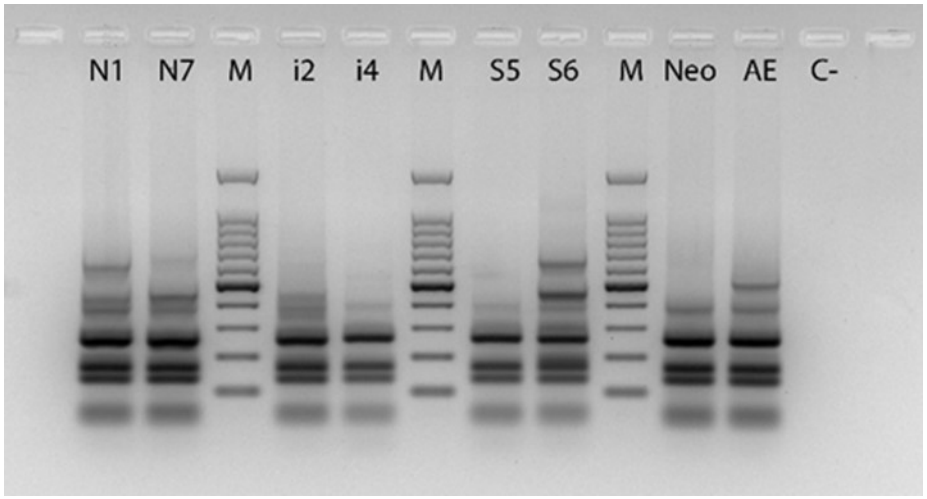

Figura 13: RFLP AluI/HinfI PCR Mcm7-709for/-1348rev *sensu* Eberhardt (Schmitt et al. 2009).

Once again, the pattern produced by the restriction map (Figure 13) did not indicate a suitable marker for the purposes of the research.

The final marker tested was the V6 variable domain of the mitochondrial small subunit (SSU) ribosomal RNA, as described by González and Labarère (1998). Subsequent RFLP analysis using the AluI/HinfI nuclease pair, even in this final attempt, did not produce the desired result (Figure 14).

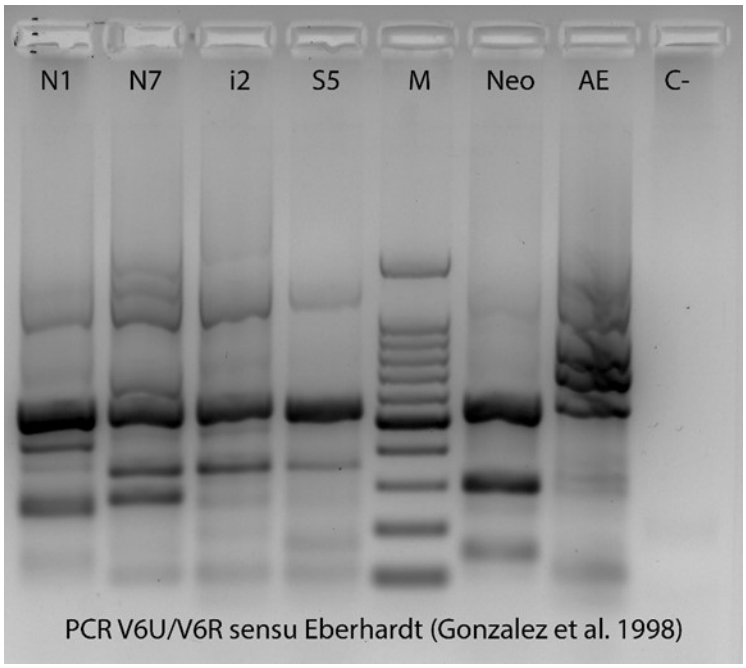

Figure 14: RFLP AluI/HinfI PCR V6U/V6R *sensu* Eberhardt (Gonzalez et al. 1998).

Numerous attempts have been made over the years to genetically characterise truffles of the genus *Tuber*, particularly those belonging to the species *Tuber aestivum* (Paolocci et al., 1995; Mello et al., 2002; Molinier et al., 2016a). However, these attempts have proved inconclusive, especially when the aim was to distinguish local populations grown in restricted geographical areas. These failures are due to complex reasons rooted in both the biology of the species and the technical limitations of the molecular methodologies employed to date.

Tuber aestivum is an extremely genetically variable species, with a population structure that exhibits no distinct boundaries or reproductive isolation between regional groups. This high genetic plasticity, combined with the ability to adapt to very different ecological contexts, makes it challenging to identify molecular markers that can distinguish between local populations. Furthermore, spore dispersal and gene flow between distant areas contribute to continuous genetic mixing, resulting in the inability to define stable molecular identities.

The symbiotic nature of the truffle adds further complexity. It grows in association with the roots of host plants and in environments rich in microorganisms. This biological context makes it difficult to extract pure and representative fungal DNA, often resulting in contaminated or unreliable molecular data (Benucci & Bonito, 2016). Even the most advanced sequencing techniques (Molinier et al., 2016b; Murat et al., 2018; Riccioni et al., 2019) have not entirely overcome these challenges, particularly in localised applications.

However, the genetic characterization of local *Tuber aestivum* populations is not merely a scientific pursuit; it also carries significant economic and commercial implications. Specifically, defining distinctive genetic profiles could enable the establishment of quality certifications, such as Protected Designations of Origin (PDOs) or Protected Geographical Indications (PGIs). These certifications are fundamental tools for valorizing local products and safeguarding them against fraud. In a market increasingly driven by traceability and authenticity, the ability to verify a truffle's geographic origin through molecular evidence would provide producers with a considerable competitive advantage. This, in turn, would strengthen the local supply chain, support rural economies, and promote the region's agri-food heritage.

In this context, the review by Creydt and Fischer (2024) on this issue offers several important conclusions. Despite technological advances, the authors note that determining the geographical origin of truffles remains a significant challenge and is not yet fully resolved. The development of reliable databases is hampered by difficulties in obtaining authentic and representative samples, as well as by the reluctance of harvesters to disclose their collection sites. Furthermore, although different species can be distinguished with high accuracy, discriminating between geographical origins requires a multidimensional approach that integrates genomics, isotopolomics, metabolomics, and microbiological analyses.

Unfortunately, the absence of a georeferenced molecular database and the scarcity of studies conducted with rigor on a local scale have so far prevented the achievement of this goal. Furthermore, the taxonomic controversy with *T. uncinatum* - sometimes considered a distinct species, sometimes an ecotype adapted to cooler climates - has led to an overlap of data and interpretations (Paolocci et al., 2004; Mello et al., 2002; Molinier et al., 2013; Molinier et al., 2016a).

In conclusion, the effective molecular characterisation of local *Tuber aestivum* populations requires a change in approach. Rather than relying on generalist or isolated methods, research should adopt an integrated, multidisciplinary strategy combining genomics, ecology, morphology and geographic information. These comprehensive strategies are crucial for overcoming current technical and analytical challenges, and for translating scientific insights into practical tools that can enhance the territorial and commercial value of truffle-producing regions.

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Appendix

ECOPOINT GREEN SOLUTIONS

LAB N° 0696 L

Rapporto di prova n°: **24LA08936**

Spettabile :
Università di L'Aquila
Via Vetoio, 40
67100 L'Aquila (AQ)

Dati del campione

Identificazione campione:	(#) **Terreno agricolo PSR-S1-2**
Provenienza:	(#) **Suolo siciliano Motta Camastra (ME)**
Produttore:	(#) **Orlando Daniele**

Dati di campionamento

Data prelievo:	(#) **19/07/2024**		
Data arrivo campione:	**05/11/2024**		
Data inizio analisi:	**05/11/2024**	Data fine analisi:	**06/12/2024**
Data RdP:	**06/12/2024**		
Prelevatore:	(#) **Committente**		

Il campionamento è stato effettuato da Committente pertanto la Ecopoint srl declina ogni responsabilità sulla modalità di campionamento adottata e sulle informazioni fornite in fase di accettazione. Le prove sono eseguite sul campione così come ricevuto.

Risultati prove

Prova *Metodo*	U.M.	Risultato
Granulometria per setacciatura ad umido e sedimentazione (Tessitura)		
(*) Sabbia (2,0-0,05 mm) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	308
(*) Limo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	530
(*) Argilla *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	162
ANALISI CHIMICO-FISICA		
(*) Scheletro *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.1 + II.3*	%	54,1
(*) Grado di reazione (pH) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	6,5
(*) Grado di reazione (pH) in KCl *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	5,5
(*) Sostanza organica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	%	6,5

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e-mail: info@ecopointsrl.it
Internet: www.ecopointsrl.it

segue Rapporto di prova n°: **24LA08936**

Prova *Metodo*	U.M.	Risultato
(*) Conducibilità elettrica (su estratto acquoso 2:1) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo IV.1*	dS/m	0,189
(*) Capacità di scambio cationico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2*	meq/100g	35,2
(*) Calcio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	24,4
(*) Magnesio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	5,4
(*) Potassio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	mg/kg	930
(*) Sodio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	0,4
(*) Saturazione basica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2 + XIII.5*	%	92,7
(*) Azoto totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIV.2 + XIV.3*	g/kg	4,0
(*) Carbonio organico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	g/kg	37,6
(*) Rapporto C/N *Calcolo*	-	9,39
(*) Fosforo assimilabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XV.3*	mg/kg	16
(*) Rapporto Ca/Mg *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	7,4
(*) Rapporto Mg/K *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	0,4
(*) Calcare totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.1*	g/kg	< 10
(*) Calcio carbonato attivo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.2*	g/kg	< 5
Rame *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	10,0
Ferro *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	8884

Legenda:
U.M. (unità di misura);

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Internet: www.ecopointsrl.it

segue Rapporto di prova n°: **24LA08936**

Note tecniche:
Note tecniche UNI EN 13656:2021:
- Metodo di separazione: Filtrazione
- Metodo di digestione: Microonde
- Pesata campione: 0.5123 g
- Volume mineralizzato: 50 ml
- Pretrattamento: Essiccazione e frantumazione meccanica

Note:
(*) = I metodi/prove così contrassegnati, non sono accreditati da Accredia

(#) = Dati forniti da cliente/terzi.

- I risultati contenuti nel presente Rapporto di Prova si riferiscono esclusivamente al campione sottoposto ad analisi.
- Qualora la modalità di campionamento non risulti accreditata (*), l'incertezza estesa è calcolata con livello di fidurcia al 95% e utilizzando un fattore di copertura k=2. In caso contrario, con modalità di campionamento accreditata, l'incertezza estesa è calcolata con livello di fiducia al 95%, utilizzando un fattore di copertura K=2, includendo sia l'attività di campionamento sia quella di prova.
- Nella dichiarazione di Conformità, il Laboratorio adotta come regola decisionale il confronto diretto del risultato con il limite applicato senza tenere conto dell'incertezza di misura.
- Nel caso di metodi che prevedono fasi di preparazione del campione (come estrazione, mineralizzazione, preconcentrazione o purificazione), ove non espressamente indicato, il recupero è da intendersi compreso all'interno dei limiti di accettabilità specifici previsti dal metodo di prova o dalla normativa vigente. Ove non espressamente indicato, il recupero non è stato utilizzato nei calcoli.
- Le sommatorie di più composti, ove non espressamente indicato, sono state calcolate con il criterio lower bound; il limite di quantificazione della somma si riferisce al composto meno sensibile.

Il Responsabile di Laboratorio

Dott. Stefano Gallina
Ordine dei Chimici Lazio Umbria Abruzzo Molise
Iscrizione n° 3517

Il Direttore Tecnico

Ing. Edmondo Metildi
Ordine degli Ingegneri della provincia dell'Aquila
Sezione A - n° 2739

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Sede legale e operativa: Via Cavour, 435
67051 Avezzano (AQ)
P.IVA: 01556840666

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Rapporto di prova n°: **24LA08937**

Spettabile :
Università di L'Aquila
Via Vetoio, 40
67100 L'Aquila (AQ)

Dati del campione

Identificazione campione:	(#) **Terreno agricolo PSR-S1-3**
Provenienza:	(#) **Suolo siciliano Francavilla di Sicilia (ME)**
Produttore:	(#) **Leonardi**

Dati di campionamento

Data prelievo:	(#) **18/07/2024**		
Data arrivo campione:	**05/11/2024**		
Data inizio analisi:	**05/11/2024**	Data fine analisi:	**06/12/2024**
Data RdP:	**06/12/2024**		
Prelevatore:	(#) **Committente**		

Il campionamento è stato effettuato da Committente pertanto la Ecopoint srl declina ogni responsabilità sulla modalità di campionamento adottata e sulle informazioni fornite in fase di accettazione. Le prove sono eseguite sul campione così come ricevuto.

Risultati prove

Prova *Metodo*	U.M.	Risultato
Granulometria per setacciatura ad umido e sedimentazione (Tessitura)		
(*) Sabbia (2,0-0,05 mm) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	213
(*) Limo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	599
(*) Argilla *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	188
ANALISI CHIMICO-FISICA		
(*) Scheletro *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.1 + II.3*	%	51,8
(*) Grado di reazione (pH) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	7,4
(*) Grado di reazione (pH) in KCl *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	6,5
(*) Sostanza organica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	%	8,8

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segue Rapporto di prova n°: **24LA08937**

Prova *Metodo*	U.M.	Risultato
(*) Conducibilità elettrica (su estratto acquoso 2:1) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo IV.1*	dS/m	0,278
(*) Capacità di scambio cationico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2*	meq/100g	37,4
(*) Calcio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	22,1
(*) Magnesio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	10,9
(*) Potassio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	mg/kg	800
(*) Sodio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	0,9
(*) Saturazione basica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2 + XIII.5*	%	96,0
(*) Azoto totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIV.2 + XIV.3*	g/kg	5,3
(*) Carbonio organico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	g/kg	50,8
(*) Rapporto C/N *Calcolo*	-	9,66
(*) Fosforo assimilabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XV.3*	mg/kg	16
(*) Rapporto Ca/Mg *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	3,3
(*) Rapporto Mg/K *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	0,8
(*) Calcare totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.1*	g/kg	< 10
(*) Calcio carbonato attivo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.2*	g/kg	< 5
Rame *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	14,0
Ferro *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	9627

Legenda:
U.M. (unità di misura);

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segue Rapporto di prova n°: **24LA08937**

Note tecniche:
Note tecniche UNI EN 13656:2021:
- Metodo di separazione: Filtrazione
- Metodo di digestione: Microonde
- Pesata campione: 0.5359 g
- Volume mineralizzato: 50 ml
- Pretrattamento: Essiccazione e frantumazione meccanica

Note:
(*) = I metodi/prove così contrassegnati, non sono accreditati da Accredia

(#) = Dati forniti da cliente/terzi.

- I risultati contenuti nel presente Rapporto di Prova si riferiscono esclusivamente al campione sottoposto ad analisi.
- Qualora la modalità di campionamento non risulti accreditata (*), l'incertezza estesa è calcolata con livello di fidurcia al 95% e utilizzando un fattore di copertura k=2. In caso contrario, con modalità di campionamento accreditata, l'incertezza estesa è calcolata con livello di fiducia al 95%, utilizzando un fattore di copertura K=2, includendo sia l'attività di campionamento sia quella di prova.
- Nella dichiarazione di Conformità, il Laboratorio adotta come regola decisionale il confronto diretto del risultato con il limite applicato senza tenere conto dell'incertezza di misura.
- Nel caso di metodi che prevedono fasi di preparazione del campione (come estrazione, mineralizzazione, preconcentrazione o purificazione), ove non espressamente indicato, il recupero è da intendersi compreso all'interno dei limiti di accettabilità specifici previsti dal metodo di prova o dalla normativa vigente. Ove non espressamente indicato, il recupero non è stato utilizzato nei calcoli.
- Le sommatorie di più composti, ove non espressamente indicato, sono state calcolate con il criterio lower bound; il limite di quantificazione della somma si riferisce al composto meno sensibile.

Il Responsabile di Laboratorio

Dott. Stefano Gallina
Ordine dei Chimici Lazio Umbria Abruzzo Molise
Iscrizione n° 3517

Il Direttore Tecnico

Ing. Edmondo Metildi
Ordine degli Ingegneri della provincia dell'Aquila
Sezione A - n° 2739

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ECOPOINT GREEN SOLUTIONS

LAB N° 0696 L

Rapporto di prova n°: **24LA08938**

Spettabile :
Università di L'Aquila
Via Vetoio, 40
67100 L'Aquila (AQ)

Dati del campione

Identificazione campione:	(#) **Terreno agricolo PSR-S1-4**
Provenienza:	(#) **Suolo siciliano Francavilla di Sicilia (ME)**
Produttore:	(#) **Leonardi**

Dati di campionamento

Data prelievo:	(#) **08/10/2024**		
Data arrivo campione:	**05/11/2024**		
Data inizio analisi:	**05/11/2024**	Data fine analisi:	**06/12/2024**
Data RdP:	**06/12/2024**		
Prelevatore:	(#) **Committente**		

Il campionamento è stato effettuato da Committente pertanto la Ecopoint srl declina ogni responsabilità sulla modalità di campionamento adottata e sulle informazioni fornite in fase di accettazione. Le prove sono eseguite sul campione così come ricevuto.

Risultati prove

Prova *Metodo*	U.M.	Risultato
Granulometria per setacciatura ad umido e sedimentazione (Tessitura)		
(*) Sabbia (2,0-0,05 mm) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	679
(*) Limo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	193
(*) Argilla *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	128
ANALISI CHIMICO-FISICA		
(*) Scheletro *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.1 + II.3*	%	1,5
(*) Grado di reazione (pH) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	8,0
(*) Grado di reazione (pH) in KCl *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	7,1
(*) Sostanza organica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	%	1,9

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segue Rapporto di prova n°: **24LA08938**

Prova *Metodo*	U.M.	Risultato
(*) Conducibilità elettrica (su estratto acquoso 2:1) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo IV.1*	dS/m	0,251
(*) Capacità di scambio cationico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2*	meq/100g	34,6
(*) Calcio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	19,4
(*) Magnesio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	9,0
(*) Potassio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	mg/kg	824
(*) Sodio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	1,7
(*) Saturazione basica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2 + XIII.5*	%	93,4
(*) Azoto totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIV.2 + XIV.3*	g/kg	2,8
(*) Carbonio organico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	g/kg	11,2
(*) Rapporto C/N *Calcolo*	-	4,00
(*) Fosforo assimilabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XV.3*	mg/kg	32
(*) Rapporto Ca/Mg *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	3,5
(*) Rapporto Mg/K *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	0,7
(*) Calcare totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.1*	g/kg	< 10
(*) Calcio carbonato attivo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.2*	g/kg	< 5
Rame *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	31,9
Ferro *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	19150

Legenda:
U.M. (unità di misura);

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Internet: www.ecopointsrl.it

segue Rapporto di prova n°: **24LA08938**

Note tecniche:
Note tecniche UNI EN 13656:2021:
- Metodo di separazione: Filtrazione
- Metodo di digestione: Microonde
- Pesata campione: 0.4995 g
- Volume mineralizzato: 50 ml
- Pretrattamento: Essiccazione e frantumazione meccanica

Note:
(*) = I metodi/prove così contrassegnati, non sono accreditati da Accredia

(#) = Dati forniti da cliente/terzi.

- I risultati contenuti nel presente Rapporto di Prova si riferiscono esclusivamente al campione sottoposto ad analisi.
- Qualora la modalità di campionamento non risulti accreditata (*), l'incertezza estesa è calcolata con livello di fidurcia al 95% e utilizzando un fattore di copertura k=2. In caso contrario, con modalità di campionamento accreditata, l'incertezza estesa è calcolata con livello di fiducia al 95%, utilizzando un fattore di copertura K=2, includendo sia l'attività di campionamento sia quella di prova.
- Nella dichiarazione di Conformità, il Laboratorio adotta come regola decisionale il confronto diretto del risultato con il limite applicato senza tenere conto dell'incertezza di misura.
- Nel caso di metodi che prevedono fasi di preparazione del campione (come estrazione, mineralizzazione, preconcentrazione o purificazione), ove non espressamente indicato, il recupero è da intendersi compreso all'interno dei limiti di accettabilità specifici previsti dal metodo di prova o dalla normativa vigente. Ove non espressamente indicato, il recupero non è stato utilizzato nei calcoli.
- Le sommatorie di più composti, ove non espressamente indicato, sono state calcolate con il criterio lower bound; il limite di quantificazione della somma si riferisce al composto meno sensibile.

Il Responsabile di Laboratorio

Dott. Stefano Gallina
Ordine dei Chimici Lazio Umbria Abruzzo Molise
Iscrizione n° 3517

Il Direttore Tecnico

Ing. Edmondo Metildi
Ordine degli Ingegneri della provincia dell'Aquila
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ECOPOINT GREEN SOLUTIONS

LAB N° 0696 L

Rapporto di prova n°: **25LA04450**

Spettabile :
Università di L'Aquila
Via Vetoio, 40
67100 L'Aquila (AQ)

Dati del campione

Identificazione campione:	(#) **Terreno ad uso agricolo - ODA**
Provenienza:	(#) **Sicilia**
Produttore:	(#) **Orlando Daniele**

Dati di campionamento

Data prelievo:	(#) **20/05/2025**		
Data arrivo campione:	**26/05/2025**		
Data inizio analisi:	**26/05/2025**	Data fine analisi:	**13/06/2025**
Data RdP:	**18/06/2025**		
Prelevatore:	(#) **Committente**		

Il campionamento è stato effettuato da Committente pertanto la Ecopoint srl declina ogni responsabilità sulla modalità di campionamento adottata e sulle informazioni fornite in fase di accettazione. Le prove sono eseguite sul campione così come ricevuto.

Risultati prove

Prova *Metodo*	U.M.	Risultato	Classificazione
Granulometria per setacciatura ad umido e sedimentazione (Tessitura)			Argilloso-Sabbioso
(*) Sabbia (2,0-0,05 mm) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	596	
(*) Limo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	336	
(*) Argilla *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	68	
ANALISI CHIMICO-FISICA			
(*) Scheletro *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.1 + II.3*	%	< 1	
(*) Grado di reazione (pH) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	8,1	
(*) Grado di reazione (pH) in KCl *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	7,4	nd
(*) Sostanza organica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	%	3,0	

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segue Rapporto di prova n°: **25LA04450**

Prova *Metodo*	U.M.	Risultato	Classificazione
(*) Conducibilità elettrica (su estratto acquoso 2:1) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo IV.1*	dS/m	0,232	
(*) Capacità di scambio cationico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2*	meq/100g	25,2	Alta
(*) Calcio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	22,0	
(*) Magnesio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	1,6	
(*) Potassio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	mg/kg	156	
(*) Sodio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	0,1	
(*) Saturazione basica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2 + XIII.5*	%	95,8	
(*) Azoto totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIV.2 + XIV.3*	g/kg	2,8	
(*) Carbonio organico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	g/kg	17,4	
(*) Rapporto C/N *Calcolo*	-	6,15	
(*) Fosforo assimilabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XV.3*	mg/kg	5	
(*) Rapporto Ca/Mg *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	13,7	
(*) Rapporto Mg/K *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	4,0	
(*) Calcare totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.1*	g/kg	38	Poco calcareo
(*) Calcio carbonato attivo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.2*	g/kg	< 5	
Rame *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	25,7	
Ferro *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	19597	

Legenda:
U.M. (unità di misura);

ECOPOINT SRL
Sede legale e operativa: Via Cavour, 435
67051 Avezzano (AQ)
P.IVA: 01556840666

Tel.: 0863/509492 Fax: 0863/489749
e-mail: info@ecopointsrl.it
Internet: www.ecopointsrl.it

segue Rapporto di prova n°: **25LA04450**

Note tecniche:
Note tecniche UNI EN 13656:2021:
- Tipologia di pretrattamento del campione:
- Metodo di separazione: Filtrazione
- Metodo di digestione: Microonde
- Pesata campione: 0.2707 g
- Volume mineralizzato: 50 ml
- Pretrattamento: Essiccazione e frantumazione meccanica

Note:
(*) = I metodi/prove così contrassegnati, non sono accreditati da Accredia

(#) = Dati forniti da cliente/terzi.

- I risultati contenuti nel presente Rapporto di Prova si riferiscono esclusivamente al campione sottoposto ad analisi.
- Qualora la modalità di campionamento non risulti accreditata (*), l'incertezza estesa è calcolata con livello di fiducia al 95% e utilizzando un fattore di copertura k=2. In caso contrario, con modalità di campionamento accreditata, l'incertezza estesa è calcolata con livello di fiducia al 95%, utilizzando un fattore di copertura K=2, includendo sia l'attività di campionamento sia quella di prova.
- Nella dichiarazione di Conformità, il Laboratorio adotta come regola decisionale il confronto diretto del risultato con il limite applicato senza tenere conto dell'incertezza di misura.
- Nel caso di metodi che prevedono fasi di preparazione del campione (come estrazione, mineralizzazione, preconcentrazione o purificazione), ove non espressamente indicato, il recupero è da intendersi compreso all'interno dei limiti di accettabilità specifici previsti dal metodo di prova o dalla normativa vigente. Ove non espressamente indicato, il recupero non è stato utilizzato nei calcoli.
- Le sommatorie di più composti, ove non espressamente indicato, sono state calcolate con il criterio lower bound; il limite di quantificazione della somma si riferisce al composto meno sensibile.

Il Responsabile di Laboratorio

Dott. Stefano Gallina
Ordine dei Chimici Lazio Umbria Abruzzo Molise
Iscrizione n° 3517

Il Direttore Tecnico

Ing. Edmondo Metildi
Ordine degli Ingegneri della provincia dell'Aquila
Sezione A - n° 2739

ECOPOINT SRL
Sede legale e operativa: Via Cavour, 435
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P.IVA: 01556840666

Tel.: 0863/509492 Fax: 0863/489749
e-mail: info@ecopointsrl.it
Internet: www.ecopointsrl.it

LAB N° 0696 L

Rapporto di prova n°: **25LA04451**

Spettabile :
Università di L'Aquila
Via Vetoio, 40
67100 L'Aquila (AQ)

Dati del campione

Identificazione campione:	(#) **Terreno ad uso agricolo - ODB**
Provenienza:	(#) **Sicilia**
Produttore:	(#) **Orlando Daniele**

Dati di campionamento

Data prelievo:	(#) **20/05/2025**		
Data arrivo campione:	**26/05/2025**		
Data inizio analisi:	**26/05/2025**	Data fine analisi:	**13/06/2025**
Data RdP:	**18/06/2025**		
Prelevatore:	(#) **Committente**		

Il campionamento è stato effettuato da Committente pertanto la Ecopoint srl declina ogni responsabilità sulla modalità di campionamento adottata e sulle informazioni fornite in fase di accettazione. Le prove sono eseguite sul campione così come ricevuto.

Risultati prove

Prova *Metodo*	U.M.	Risultato	Classificazione
Granulometria per setacciatura ad umido e sedimentazione (Tessitura)			Argilloso-Sabbioso
(*) Sabbia (2,0-0,05 mm) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	159	
(*) Limo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	759	
(*) Argilla *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	82	
ANALISI CHIMICO-FISICA			
(*) Scheletro *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.1 + II.3*	%	< 1	
(*) Grado di reazione (pH) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	7,6	
(*) Grado di reazione (pH) in KCl *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	7,1	nd
(*) Sostanza organica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	%	4,2	

ECOPOINT SRL
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Internet: www.ecopointsrl.it

segue Rapporto di prova n°: **25LA04451**

Prova *Metodo*	U.M.	Risultato	Classificazione
(*) Conducibilità elettrica (su estratto acquoso 2:1) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo IV.1*	dS/m	0,361	
(*) Capacità di scambio cationico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2*	meq/100g	24,9	Alta
(*) Calcio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	20,3	
(*) Magnesio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	1,5	
(*) Potassio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	mg/kg	208	
(*) Sodio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	0,1	
(*) Saturazione basica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2 + XIII.5*	%	90,1	
(*) Azoto totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIV.2 + XIV.3*	g/kg	2,3	
(*) Carbonio organico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	g/kg	24,4	
(*) Rapporto C/N *Calcolo*	-	10,4	
(*) Fosforo assimilabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XV.3*	mg/kg	7	
(*) Rapporto Ca/Mg *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	13,6	
(*) Rapporto Mg/K *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	2,8	
(*) Calcare totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.1*	g/kg	< 10	Non calcareo
(*) Calcio carbonato attivo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.2*	g/kg	< 5	
Rame *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	29,8	
Ferro *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	22268	

Legenda:
U.M. (unità di misura);

ECOPOINT SRL
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Internet: www.ecopointsrl.it

segue Rapporto di prova n°: **25LA04451**

Note tecniche:
Note tecniche UNI EN 13656:2021:
- Tipologia di pretrattamento del campione:
- Metodo di separazione: Filtrazione
- Metodo di digestione: Microonde
- Pesata campione: 0.2374 g
- Volume mineralizzato: 50 ml
- Pretrattamento: Essiccazione e frantumazione meccanica

Note:
(*) = I metodi/prove così contrassegnati, non sono accreditati da Accredia

(#) = Dati forniti da cliente/terzi.

- I risultati contenuti nel presente Rapporto di Prova si riferiscono esclusivamente al campione sottoposto ad analisi.
- Qualora la modalità di campionamento non risulti accreditata (*), l'incertezza estesa è calcolata con livello di fiducia al 95% e utilizzando un fattore di copertura k=2. In caso contrario, con modalità di campionamento accreditata, l'incertezza estesa è calcolata con livello di fiducia al 95%, utilizzando un fattore di copertura K=2, includendo sia l'attività di campionamento sia quella di prova.
- Nella dichiarazione di Conformità, il Laboratorio adotta come regola decisionale il confronto diretto del risultato con il limite applicato senza tenere conto dell'incertezza di misura.
- Nel caso di metodi che prevedono fasi di preparazione del campione (come estrazione, mineralizzazione, preconcentrazione o purificazione), ove non espressamente indicato, il recupero è da intendersi compreso all'interno dei limiti di accettabilità specifici previsti dal metodo di prova o dalla normativa vigente. Ove non espressamente indicato, il recupero non è stato utilizzato nei calcoli.
- Le sommatorie di più composti, ove non espressamente indicato, sono state calcolate con il criterio lower bound; il limite di quantificazione della somma si riferisce al composto meno sensibile.

Il Responsabile di Laboratorio

Dott. Stefano Gallina
Ordine dei Chimici Lazio Umbria Abruzzo Molise
Iscrizione n° 3517

Il Direttore Tecnico

Ing. Edmondo Metildi
Ordine degli Ingegneri della provincia dell'Aquila
Sezione A - n° 2739

ECOPOINT SRL
Sede legale e operativa: Via Cavour, 435
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P.IVA: 01556840666

Tel.: 0863/509492 Fax: 0863/489749
e-mail: info@ecopointsrl.it
Internet: www.ecopointsrl.it

Rapporto di prova n°: **25LA04452**

Spettabile :
Università di L'Aquila
Via Vetoio, 40
67100 L'Aquila (AQ)

Dati del campione

Identificazione campione:	(#) **Terreno ad uso agricolo - ODC**
Provenienza:	(#) **Sicilia**
Produttore:	(#) **Orlando Daniele**

Dati di campionamento

Data prelievo:	(#) **20/05/2025**		
Data arrivo campione:	**26/05/2025**		
Data inizio analisi:	**26/05/2025**	Data fine analisi:	**13/06/2025**
Data RdP:	**18/06/2025**		
Prelevatore:	(#) **Committente**		

Il campionamento è stato effettuato da Committente pertanto la Ecopoint srl declina ogni responsabilità sulla modalità di campionamento adottata e sulle informazioni fornite in fase di accettazione. Le prove sono eseguite sul campione così come ricevuto.

Risultati prove

Prova *Metodo*	U.M.	Risultato	Classificazione
Granulometria per setacciatura ad umido e sedimentazione (Tessitura)			Argilloso-Sabbioso
(*) Sabbia (2,0-0,05 mm) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	159	
(*) Limo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	771	
(*) Argilla *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	70	
ANALISI CHIMICO-FISICA			
(*) Scheletro *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.1 + II.3*	%	< 1	
(*) Grado di reazione (pH) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	8,0	
(*) Grado di reazione (pH) in KCl *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	6,7	nd
(*) Sostanza organica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	%	4,4	

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Internet: www.ecopointsrl.it

segue Rapporto di prova n°: **25LA04452**

Prova *Metodo*	U.M.	Risultato	Classificazione
(*) Conducibilità elettrica (su estratto acquoso 2:1) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo IV.1*	dS/m	0,363	
(*) Capacità di scambio cationico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2*	meq/100g	19,4	Media
(*) Calcio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	16,6	
(*) Magnesio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	1,4	
(*) Potassio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	mg/kg	242	
(*) Sodio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	0,1	
(*) Saturazione basica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2 + XIII.5*	%	96,4	
(*) Azoto totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIV.2 + XIV.3*	g/kg	3,1	
(*) Carbonio organico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	g/kg	25,5	
(*) Rapporto C/N *Calcolo*	-	8,16	
(*) Fosforo assimilabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XV.3*	mg/kg	6	
(*) Rapporto Ca/Mg *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	11,7	
(*) Rapporto Mg/K *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	2,3	
(*) Calcare totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.1*	g/kg	< 10	Non calcareo
(*) Calcio carbonato attivo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.2*	g/kg	6	
Rame *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	43,1	
Ferro *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	29734	

Legenda:
U.M. (unità di misura);

ECOPOINT SRL
Sede legale e operativa: Via Cavour, 435
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Internet: www.ecopointsrl.it

segue Rapporto di prova n°: **25LA04452**

Note tecniche:
Note tecniche UNI EN 13656:2021:
- Tipologia di pretrattamento del campione:
- Metodo di separazione: Filtrazione
- Metodo di digestione: Microonde
- Pesata campione: 0.2066 g
- Volume mineralizzato: 50 ml
- Pretrattamento: Essiccazione e frantumazione meccanica

Note:
(*) = I metodi/prove così contrassegnati, non sono accreditati da Accredia

(#) = Dati forniti da cliente/terzi.

- I risultati contenuti nel presente Rapporto di Prova si riferiscono esclusivamente al campione sottoposto ad analisi.
- Qualora la modalità di campionamento non risulti accreditata (*), l'incertezza estesa è calcolata con livello di fiducia al 95% e utilizzando un fattore di copertura k=2. In caso contrario, con modalità di campionamento accreditata, l'incertezza estesa è calcolata con livello di fiducia al 95%, utilizzando un fattore di copertura K=2, includendo sia l'attività di campionamento sia quella di prova.
- Nella dichiarazione di Conformità, il Laboratorio adotta come regola decisionale il confronto diretto del risultato con il limite applicato senza tenere conto dell'incertezza di misura.
- Nel caso di metodi che prevedono fasi di preparazione del campione (come estrazione, mineralizzazione, preconcentrazione o purificazione), ove non espressamente indicato, il recupero è da intendersi compreso all'interno dei limiti di accettabilità specifici previsti dal metodo di prova o dalla normativa vigente. Ove non espressamente indicato, il recupero non è stato utilizzato nei calcoli.
- Le sommatorie di più composti, ove non espressamente indicato, sono state calcolate con il criterio lower bound; il limite di quantificazione della somma si riferisce al composto meno sensibile.

Il Responsabile di Laboratorio

Dott. Stefano Gallina
Ordine dei Chimici Lazio Umbria Abruzzo Molise
Iscrizione n° 3517

Il Direttore Tecnico

Ing. Edmondo Metildi
Ordine degli Ingegneri della provincia dell'Aquila
Sezione A - n° 2739

ECOPOINT SRL
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Tel.: 0863/509492 Fax: 0863/489749
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Internet: www.ecopointsrl.it

ECOPOINT GREEN SOLUTIONS

LAB N° 0696 L

Rapporto di prova n°: **25LA04453**

Spettabile :
Università di L'Aquila
Via Vetoio, 40
67100 L'Aquila (AQ)

Dati del campione

Identificazione campione:	(#) **Terreno ad uso agricolo - LA**
Provenienza:	(#) **Sicilia**
Produttore:	(#) **Leonardi**

Dati di campionamento

Data prelievo:	(#) **20/05/2025**		
Data arrivo campione:	**26/05/2025**		
Data inizio analisi:	**26/05/2025**	Data fine analisi:	**13/06/2025**
Data RdP:	**18/06/2025**		
Prelevatore:	(#) **Committente**		

Il campionamento è stato effettuato da Committente pertanto la Ecopoint srl declina ogni responsabilità sulla modalità di campionamento adottata e sulle informazioni fornite in fase di accettazione. Le prove sono eseguite sul campione così come ricevuto.

Risultati prove

Prova *Metodo*	U.M.	Risultato	Classificazione
Granulometria per setacciatura ad umido e sedimentazione (Tessitura)			Argilloso-Sabbioso
(*) Sabbia (2,0-0,05 mm) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	53	
(*) Limo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	825	
(*) Argilla *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	122	
ANALISI CHIMICO-FISICA			
(*) Scheletro *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.1 + II.3*	%	< 1	
(*) Grado di reazione (pH) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	7,8	
(*) Grado di reazione (pH) in KCl *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	6,8	nd
(*) Sostanza organica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	%	4,3	

ECOPOINT SRL
Sede legale e operativa: Via Cavour, 435
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e-mail: info@ecopointsrl.it
Internet: www.ecopointsrl.it

segue Rapporto di prova n°: **25LA04453**

Prova *Metodo*	U.M.	Risultato	Classificazione
(*) Conducibilità elettrica (su estratto acquoso 2:1) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo IV.1*	dS/m	0,329	
(*) Capacità di scambio cationico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2*	meq/100g	22,6	Alta
(*) Calcio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	12,1	
(*) Magnesio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	6,6	
(*) Potassio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	mg/kg	421	
(*) Sodio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	0,7	
(*) Saturazione basica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2 + XIII.5*	%	90,2	
(*) Azoto totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIV.2 + XIV.3*	g/kg	3,2	
(*) Carbonio organico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	g/kg	25,1	
(*) Rapporto C/N *Calcolo*	-	7,72	
(*) Fosforo assimilabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XV.3*	mg/kg	54	
(*) Rapporto Ca/Mg *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	1,8	
(*) Rapporto Mg/K *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	6,1	
(*) Calcare totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.1*	g/kg	< 10	Non calcareo
(*) Calcio carbonato attivo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.2*	g/kg	< 5	
Rame *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	44,7	
Ferro *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	23704	

Legenda:
U.M. (unità di misura);

ECOPOINT SRL
Sede legale e operativa: Via Cavour, 435
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Internet: www.ecopointsrl.it

segue Rapporto di prova n°: **25LA04453**

Note tecniche:
Note tecniche UNI EN 13656:2021:
- Tipologia di pretrattamento del campione:
- Metodo di separazione: Filtrazione
- Metodo di digestione: Microonde
- Pesata campione: 0.2449 g
- Volume mineralizzato: 50 ml
- Pretrattamento: Essiccazione e frantumazione meccanica

Note:
(*) = I metodi/prove così contrassegnati, non sono accreditati da Accredia

(#) = Dati forniti da cliente/terzi.

- I risultati contenuti nel presente Rapporto di Prova si riferiscono esclusivamente al campione sottoposto ad analisi.
- Qualora la modalità di campionamento non risulti accreditata (*), l'incertezza estesa è calcolata con livello di fiducia al 95% e utilizzando un fattore di copertura k=2. In caso contrario, con modalità di campionamento accreditata, l'incertezza estesa è calcolata con livello di fiducia al 95%, utilizzando un fattore di copertura K=2, includendo sia l'attività di campionamento sia quella di prova.
- Nella dichiarazione di Conformità, il Laboratorio adotta come regola decisionale il confronto diretto del risultato con il limite applicato senza tenere conto dell'incertezza di misura.
- Nel caso di metodi che prevedono fasi di preparazione del campione (come estrazione, mineralizzazione, preconcentrazione o purificazione), ove non espressamente indicato, il recupero è da intendersi compreso all'interno dei limiti di accettabilità specifici previsti dal metodo di prova o dalla normativa vigente. Ove non espressamente indicato, il recupero non è stato utilizzato nei calcoli.
- Le sommatorie di più composti, ove non espressamente indicato, sono state calcolate con il criterio lower bound; il limite di quantificazione della somma si riferisce al composto meno sensibile.

Il Responsabile di Laboratorio

Dott. Stefano Gallina
Ordine dei Chimici Lazio Umbria Abruzzo Molise
Iscrizione n° 3517

Il Direttore Tecnico

Ing. Edmondo Metildi
Ordine degli Ingegneri della provincia dell'Aquila
Sezione A - n° 2739

ECOPOINT SRL
Sede legale e operativa: Via Cavour, 435
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Internet: www.ecopointsrl.it

ECOPOINT GREEN SOLUTIONS

LAB N° 0696 L

Rapporto di prova n°: **25LA04454**

Spettabile :
Università di L'Aquila
Via Vetoio, 40
67100 L'Aquila (AQ)

Dati del campione

Identificazione campione:	(#) **Terreno ad uso agricolo - LB**
Provenienza:	(#) **Sicilia**
Produttore:	(#) **Leonardi**

Dati di campionamento

Data prelievo:	(#) **20/05/2025**		
Data arrivo campione:	**26/05/2025**		
Data inizio analisi:	**26/05/2025**	Data fine analisi:	**13/06/2025**
Data RdP:	**18/06/2025**		
Prelevatore:	(#) **Committente**		

Il campionamento è stato effettuato da Committente pertanto la Ecopoint srl declina ogni responsabilità sulla modalità di campionamento adottata e sulle informazioni fornite in fase di accettazione. Le prove sono eseguite sul campione così come ricevuto.

Risultati prove

Prova *Metodo*	U.M.	Risultato	Classificazione
Granulometria per setacciatura ad umido e sedimentazione (Tessitura)			
(*) Sabbia (2,0-0,05 mm) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	743	
(*) Limo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	257	
(*) Argilla *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	< 1	
ANALISI CHIMICO-FISICA			
(*) Scheletro *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.1 + II.3*	%	< 1	
(*) Grado di reazione (pH) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	7,8	
(*) Grado di reazione (pH) in KCl *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	7,1	nd
(*) Sostanza organica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	%	1,9	

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Internet: www.ecopointsrl.it

segue Rapporto di prova n°: **25LA04454**

Prova *Metodo*	U.M.	Risultato	Classificazione
(*) Conducibilità elettrica (su estratto acquoso 2:1) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo IV.1*	dS/m	0,307	
(*) Capacità di scambio cationico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2*	meq/100g	23,2	Alta
(*) Calcio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	13,2	
(*) Magnesio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	6,8	
(*) Potassio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	mg/kg	376	
(*) Sodio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	0,5	
(*) Saturazione basica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2 + XIII.5*	%	92,8	
(*) Azoto totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIV.2 + XIV.3*	g/kg	3,0	
(*) Carbonio organico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	g/kg	10,9	
(*) Rapporto C/N *Calcolo*	-	3,68	
(*) Fosforo assimilabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XV.3*	mg/kg	58	
(*) Rapporto Ca/Mg *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	1,9	
(*) Rapporto Mg/K *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	7,1	
(*) Calcare totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.1*	g/kg	< 10	Non calcareo
(*) Calcio carbonato attivo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.2*	g/kg	< 5	
Rame *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	43,6	
Ferro *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	22717	

Legenda:
U.M. (unità di misura);

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segue Rapporto di prova n°: **25LA04454**

Note tecniche:
Note tecniche UNI EN 13656:2021:
- Tipologia di pretrattamento del campione:
- Metodo di separazione: Filtrazione
- Metodo di digestione: Microonde
- Pesata campione: 0.2634 g
- Volume mineralizzato: 50 ml
- Pretrattamento: Essiccazione e frantumazione meccanica

Note:
(*) = I metodi/prove così contrassegnati, non sono accreditati da Accredia

(#) = Dati forniti da cliente/terzi.

- I risultati contenuti nel presente Rapporto di Prova si riferiscono esclusivamente al campione sottoposto ad analisi.
- Qualora la modalità di campionamento non risulti accreditata (*), l'incertezza estesa è calcolata con livello di fiducia al 95% e utilizzando un fattore di copertura k=2. In caso contrario, con modalità di campionamento accreditata, l'incertezza estesa è calcolata con livello di fiducia al 95%, utilizzando un fattore di copertura K=2, includendo sia l'attività di campionamento sia quella di prova.
- Nella dichiarazione di Conformità, il Laboratorio adotta come regola decisionale il confronto diretto del risultato con il limite applicato senza tenere conto dell'incertezza di misura.
- Nel caso di metodi che prevedono fasi di preparazione del campione (come estrazione, mineralizzazione, preconcentrazione o purificazione), ove non espressamente indicato, il recupero è da intendersi compreso all'interno dei limiti di accettabilità specifici previsti dal metodo di prova o dalla normativa vigente. Ove non espressamente indicato, il recupero non è stato utilizzato nei calcoli.
- Le sommatorie di più composti, ove non espressamente indicato, sono state calcolate con il criterio lower bound; il limite di quantificazione della somma si riferisce al composto meno sensibile.

Il Responsabile di Laboratorio

Dott. Stefano Gallina
Ordine dei Chimici Lazio Umbria Abruzzo Molise
Iscrizione n° 3517

Il Direttore Tecnico

Ing. Edmondo Metildi
Ordine degli Ingegneri della provincia dell'Aquila
Sezione A - n° 2739

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LAB N° 0696 L

Rapporto di prova n°: **25LA04455**

Spettabile :
Università di L'Aquila
Via Vetoio, 40
67100 L'Aquila (AQ)

Dati del campione

Identificazione campione:	(#) **Terreno ad uso agricolo - LC**
Provenienza:	(#) **Sicilia**
Produttore:	(#) **Leonardi**

Dati di campionamento

Data prelievo:	(#) **20/05/2025**		
Data arrivo campione:	**26/05/2025**		
Data inizio analisi:	**26/05/2025**	Data fine analisi:	**13/06/2025**
Data RdP:	**18/06/2025**		
Prelevatore:	(#) **Committente**		

Il campionamento è stato effettuato da Committente pertanto la Ecopoint srl declina ogni responsabilità sulla modalità di campionamento adottata e sulle informazioni fornite in fase di accettazione. Le prove sono eseguite sul campione così come ricevuto.

Risultati prove

Prova *Metodo*	U.M.	Risultato	Classificazione
Granulometria per setacciatura ad umido e sedimentazione (Tessitura)			
(*) Sabbia (2,0-0,05 mm) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	619	
(*) Limo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	381	
(*) Argilla *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	< 1	
ANALISI CHIMICO-FISICA			
(*) Scheletro *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.1 + II.3*	%	< 1	
(*) Grado di reazione (pH) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	7,9	
(*) Grado di reazione (pH) in KCl *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	6,9	nd
(*) Sostanza organica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	%	3,3	

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segue Rapporto di prova n°: **25LA04455**

Prova *Metodo*	U.M.	Risultato	Classificazione
(*) Conducibilità elettrica (su estratto acquoso 2:1) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo IV.1*	dS/m	0,33	
(*) Capacità di scambio cationico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2*	meq/100g	20,4	Alta
(*) Calcio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	11,8	
(*) Magnesio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	6,2	
(*) Potassio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	mg/kg	468	
(*) Sodio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	0,4	
(*) Saturazione basica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2 + XIII.5*	%	96,3	
(*) Azoto totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIV.2 + XIV.3*	g/kg	3,5	
(*) Carbonio organico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	g/kg	19,3	
(*) Rapporto C/N *Calcolo*	-	5,49	
(*) Fosforo assimilabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XV.3*	mg/kg	44	
(*) Rapporto Ca/Mg *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	1,9	
(*) Rapporto Mg/K *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	5,2	
(*) Calcare totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.1*	g/kg	< 10	Non calcareo
(*) Calcio carbonato attivo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.2*	g/kg	7	
Rame *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	48,0	
Ferro *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	26423	

Legenda:
U.M. (unità di misura);

ECOPOINT SRL
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Internet: www.ecopointsrl.it

segue Rapporto di prova n°: **25LA04455**

Note tecniche:
Note tecniche UNI EN 13656:2021:
- Tipologia di pretrattamento del campione:
- Metodo di separazione: Filtrazione
- Metodo di digestione: Microonde
- Pesata campione: 0.2051 g
- Volume mineralizzato: 50 ml
- Pretrattamento: Essiccazione e frantumazione meccanica

Note:
(*) = I metodi/prove così contrassegnati, non sono accreditati da Accredia

(#) = Dati forniti da cliente/terzi.

- I risultati contenuti nel presente Rapporto di Prova si riferiscono esclusivamente al campione sottoposto ad analisi.
- Qualora la modalità di campionamento non risulti accreditata (*), l'incertezza estesa è calcolata con livello di fiducia al 95% e utilizzando un fattore di copertura k=2. In caso contrario, con modalità di campionamento accreditata, l'incertezza estesa è calcolata con livello di fiducia al 95%, utilizzando un fattore di copertura K=2, includendo sia l'attività di campionamento sia quella di prova.
- Nella dichiarazione di Conformità, il Laboratorio adotta come regola decisionale il confronto diretto del risultato con il limite applicato senza tenere conto dell'incertezza di misura.
- Nel caso di metodi che prevedono fasi di preparazione del campione (come estrazione, mineralizzazione, preconcentrazione o purificazione), ove non espressamente indicato, il recupero è da intendersi compreso all'interno dei limiti di accettabilità specifici previsti dal metodo di prova o dalla normativa vigente. Ove non espressamente indicato, il recupero non è stato utilizzato nei calcoli.
- Le sommatorie di più composti, ove non espressamente indicato, sono state calcolate con il criterio lower bound; il limite di quantificazione della somma si riferisce al composto meno sensibile.

Il Responsabile di Laboratorio

Dott. Stefano Gallina
Ordine dei Chimici Lazio Umbria Abruzzo Molise
Iscrizione n° 3517

Il Direttore Tecnico

Ing. Edmondo Metildi
Ordine degli Ingegneri della provincia dell'Aquila
Sezione A - n° 2739

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ECOPOINT GREEN SOLUTIONS

LAB N° 0696 L

Rapporto di prova n°: **25LA04456**

Spettabile :
Università di L'Aquila
Via Vetoio, 40
67100 L'Aquila (AQ)

Dati del campione

Identificazione campione:	(#) **Terreno ad uso agricolo - LD**
Provenienza:	(#) **Sicilia**
Produttore:	(#) **Leonardi**

Dati di campionamento

Data prelievo:	(#) **20/05/2025**		
Data arrivo campione:	**26/05/2025**		
Data inizio analisi:	**26/05/2025**	Data fine analisi:	**18/06/2025**
Data RdP:	**25/06/2025**		
Prelevatore:	(#) **Committente**		

Il campionamento è stato effettuato da Committente pertanto la Ecopoint srl declina ogni responsabilità sulla modalità di campionamento adottata e sulle informazioni fornite in fase di accettazione. Le prove sono eseguite sul campione così come ricevuto.

Risultati prove

Prova *Metodo*	U.M.	Risultato
Granulometria per setacciatura ad umido e sedimentazione (Tessitura)		
(*) Sabbia (2,0-0,05 mm) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	443
(*) Limo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	357
(*) Argilla *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.5*	g/kg	200
ANALISI CHIMICO-FISICA		
(*) Scheletro *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo II.1 + II.3*	%	< 1
(*) Grado di reazione (pH) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	8,1
(*) Grado di reazione (pH) in KCl *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo III.1*	unità pH	6,9
(*) Sostanza organica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	%	3,4

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segue Rapporto di prova n°: **25LA04456**

Prova *Metodo*	U.M.	Risultato
(*) Conducibilità elettrica (su estratto acquoso 2:1) *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo IV.1*	dS/m	0,205
(*) Capacità di scambio cationico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2*	meq/100g	19,5
(*) Calcio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	11,1
(*) Magnesio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	6,1
(*) Potassio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	mg/kg	376
(*) Sodio scambiabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	meq/100g	0,5
(*) Saturazione basica *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.2 + XIII.5*	%	95,8
(*) Azoto totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIV.2 + XIV.3*	g/kg	3,1
(*) Carbonio organico *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo VII.3*	g/kg	19,5
(*) Rapporto C/N *Calcolo*	-	6,23
(*) Fosforo assimilabile *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XV.3*	mg/kg	38
(*) Rapporto Ca/Mg *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	1,8
(*) Rapporto Mg/K *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo XIII.5*	-	6,4
(*) Calcare totale *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.1*	g/kg	179
(*) Calcio carbonato attivo *D.M. 13/09/1999 SO GU n° 248 21/10/1999 Metodo V.2*	g/kg	66
Rame *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	48,9
Ferro *UNI EN 13656:2021 + UNI EN ISO 11885:2009*	mg/kg su s.s.	25907

Legenda:
U.M. (unità di misura);

ECOPOINT SRL
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segue Rapporto di prova n°: **25LA04456**

Note tecniche:
Note tecniche UNI EN 13656:2021:
- Tipologia di pretrattamento del campione:
- Metodo di separazione: Filtrazione
- Metodo di digestione: Microonde
- Pesata campione: 0.2118 g
- Volume mineralizzato: 50 ml
- Pretrattamento: Essiccazione e frantumazione meccanica

Note:
(*) = I metodi/prove così contrassegnati, non sono accreditati da Accredia

(#) = Dati forniti da cliente/terzi.

- I risultati contenuti nel presente Rapporto di Prova si riferiscono esclusivamente al campione sottoposto ad analisi.
- Qualora la modalità di campionamento non risulti accreditata (*), l'incertezza estesa è calcolata con livello di fiducia al 95% e utilizzando un fattore di copertura k=2. In caso contrario, con modalità di campionamento accreditata, l'incertezza estesa è calcolata con livello di fiducia al 95%, utilizzando un fattore di copertura K=2, includendo sia l'attività di campionamento sia quella di prova.
- Nella dichiarazione di Conformità, il Laboratorio adotta come regola decisionale il confronto diretto del risultato con il limite applicato senza tenere conto dell'incertezza di misura.
- Nel caso di metodi che prevedono fasi di preparazione del campione (come estrazione, mineralizzazione, preconcentrazione o purificazione), ove non espressamente indicato, il recupero è da intendersi compreso all'interno dei limiti di accettabilità specifici previsti dal metodo di prova o dalla normativa vigente. Ove non espressamente indicato, il recupero non è stato utilizzato nei calcoli.
- Le sommatorie di più composti, ove non espressamente indicato, sono state calcolate con il criterio lower bound; il limite di quantificazione della somma si riferisce al composto meno sensibile.

Il Responsabile di Laboratorio

Dott. Stefano Gallina
Ordine dei Chimici Lazio Umbria Abruzzo Molise
Iscrizione n° 3517

Il Direttore Tecnico

Ing. Edmondo Metildi
Ordine degli Ingegneri della provincia dell'Aquila
Sezione A - n° 2739

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