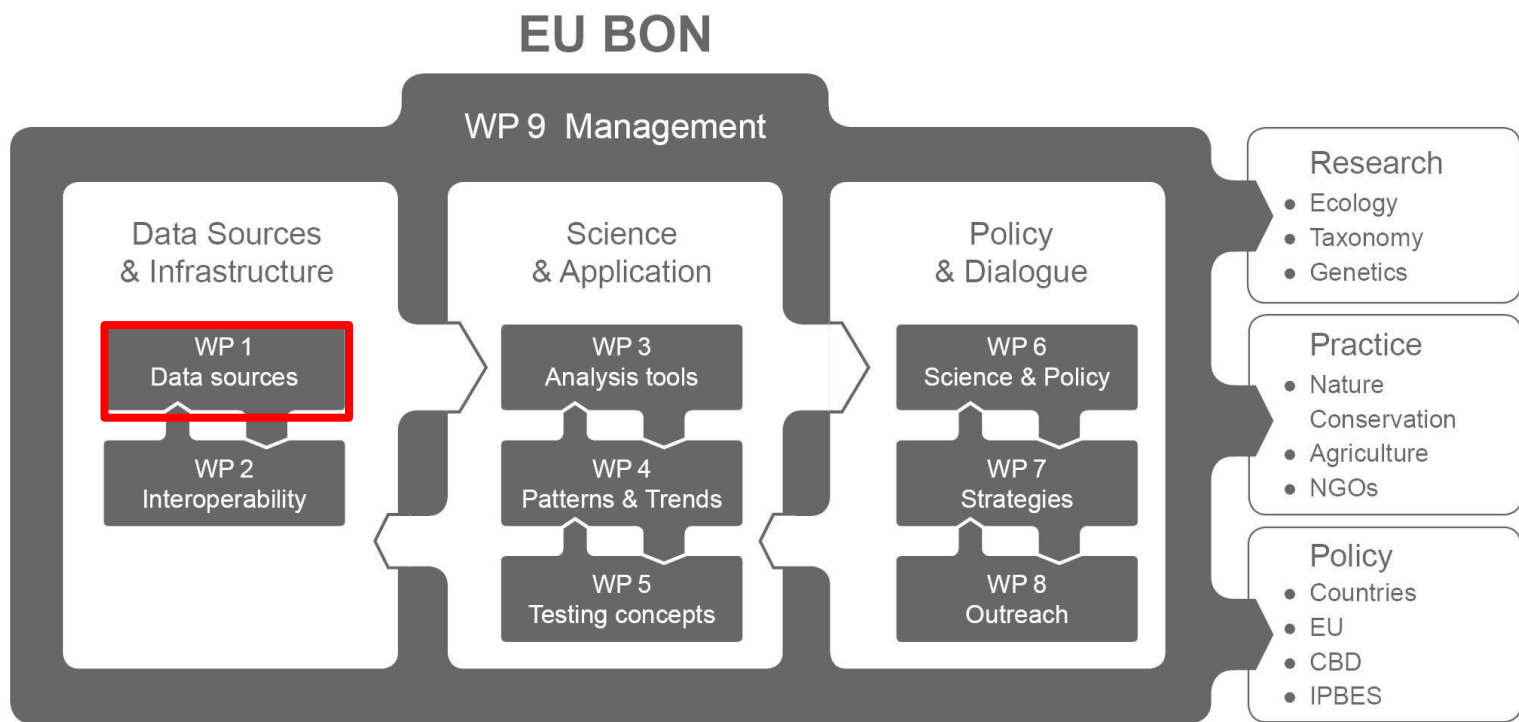


Data Mobilization strategy and show case



WP products

M9	Data mobilisation strategy	3 June, 9.30-11.00, Riley Auditorium
M18	Data Mobilisation Examples	3 June, 14.00-16.00, Elton room
M21	Horizon 2020 on Citizen Science	4 June, 11.30-13.00, Elton room
M22	Discussion on upcoming 3rd Stakeholder Roundtable on test sites & writing session (D1.1)	4 June, 11.30-13.00, Bowring room
M25 & M29	Citizen Science gateway workshop (MS153) including hands on training	4 June, 14.00-17.30, Elton room

The Unified Taxonomic Information Service (UTIS)



EU BON taxonomic backbone

The Unified Taxonomic Information Service (UTIS) is the taxonomic backbone for the EU BON project

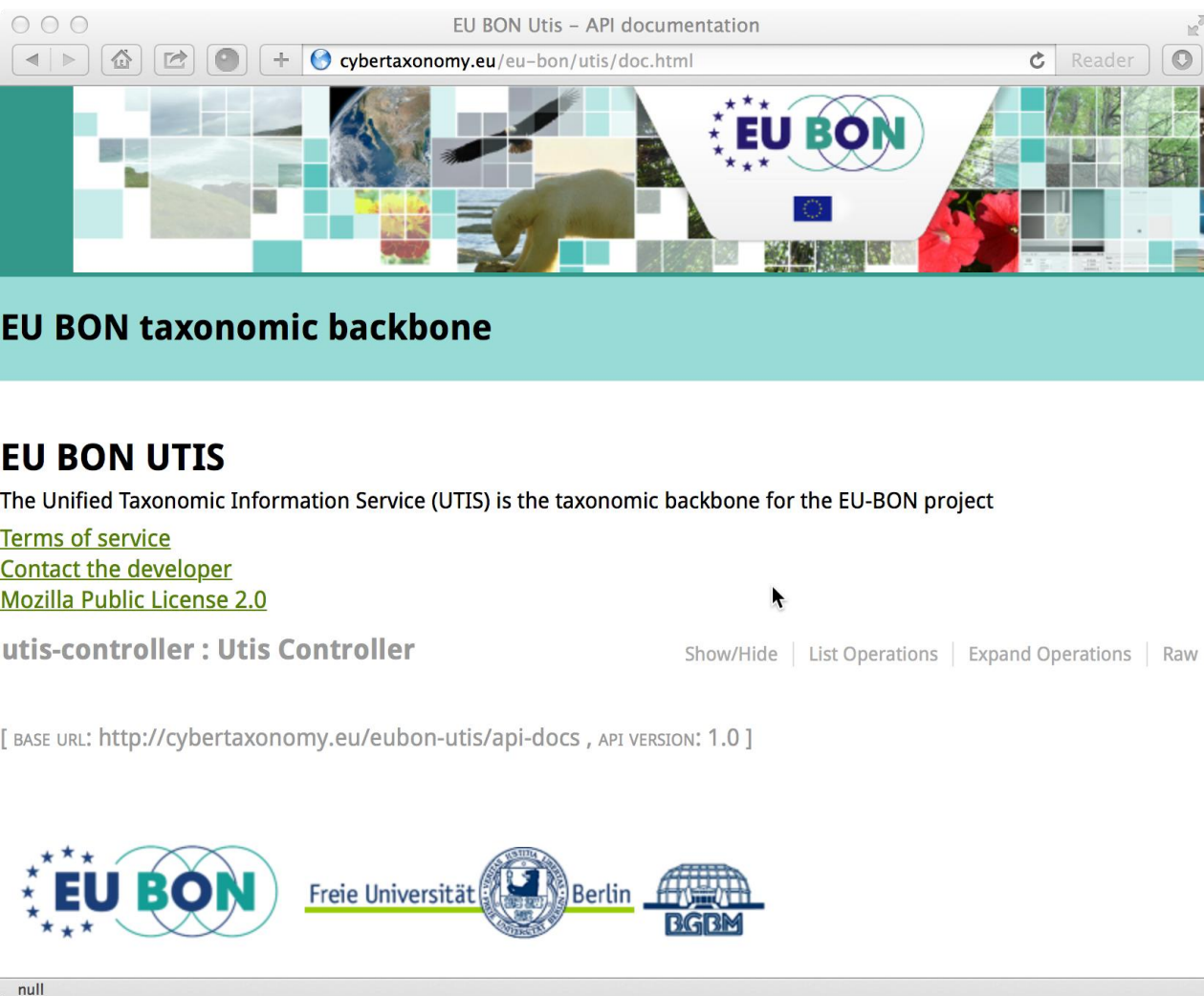
The [EU BON](#) Taxonomic backbone allows running a federated search on multiple European checklists and returns a unified result set of the individual responses of the various checklists.

The current implementation of the UTIS is still a prototype, which means that the API and data model may be changed until final release. It connects the web services of the [Pan-European Species directories Infrastructure, PESI](#) CoL, the [Catalogue of Life](#) and of the [World Register of Marine Species \(WoRMS\)](#). In future it will connect more data providers like [EUNIS](#) and [Natura2000](#) in order to be compliant with the [INSPIRE directive](#). Currently it is possible to **search for taxa and synonyms by a scientific name or vernacular name string**. In case of matching synonyms the according accepted taxon is resolved. The search results always include information on the classification and optionally on related taxa as far as this data is delivered by the connected checklist providers.

[Documentation of the RESTful UTIS service api.](#)

The service is being developed by the [Department of Research and Biodiversity Informatics](#) of the Botanic Garden and Botanical Museum Berlin-Dahlem.

The Unified Taxonomic Information Service (UTIS)



EU BON Utis - API documentation
 cybertaxonomy.eu/eu-bon/utis/doc.html




EU BON taxonomic backbone

EU BON UTIS
 The Unified Taxonomic Information Service (UTIS) is the taxonomic backbone for the EU-BON project

[Terms of service](#)
[Contact the developer](#)
[Mozilla Public License 2.0](#)

utis-controller : Utis Controller Show/Hide | List Operations | Expand Operations | Raw

[BASE URL: http://cybertaxonomy.eu/eubon-utis/api-docs , API VERSION: 1.0]

null

- Simultaneous and harmonised access to relevant distributed taxonomic information services.
- Up to now, UTIS provides access to
 - Catalogue of Life
 - PESI (:= ERMS + E+M + FauEu + IF)
 - Worms
- Additional checklists in the pipeline.

Integration, annotation and mobilization of biodiversity data - Show case

Integration of EU BON targeted data types

- Taxonomic backbone – PESI (IF).
- Genetic data – INSD and UNITE open access datasets (rDNA ITS)
- Specimen data – institutional and personal datasets.
- Ecological data – published and personal datasets.
- Species profile data – published and personal datasets.

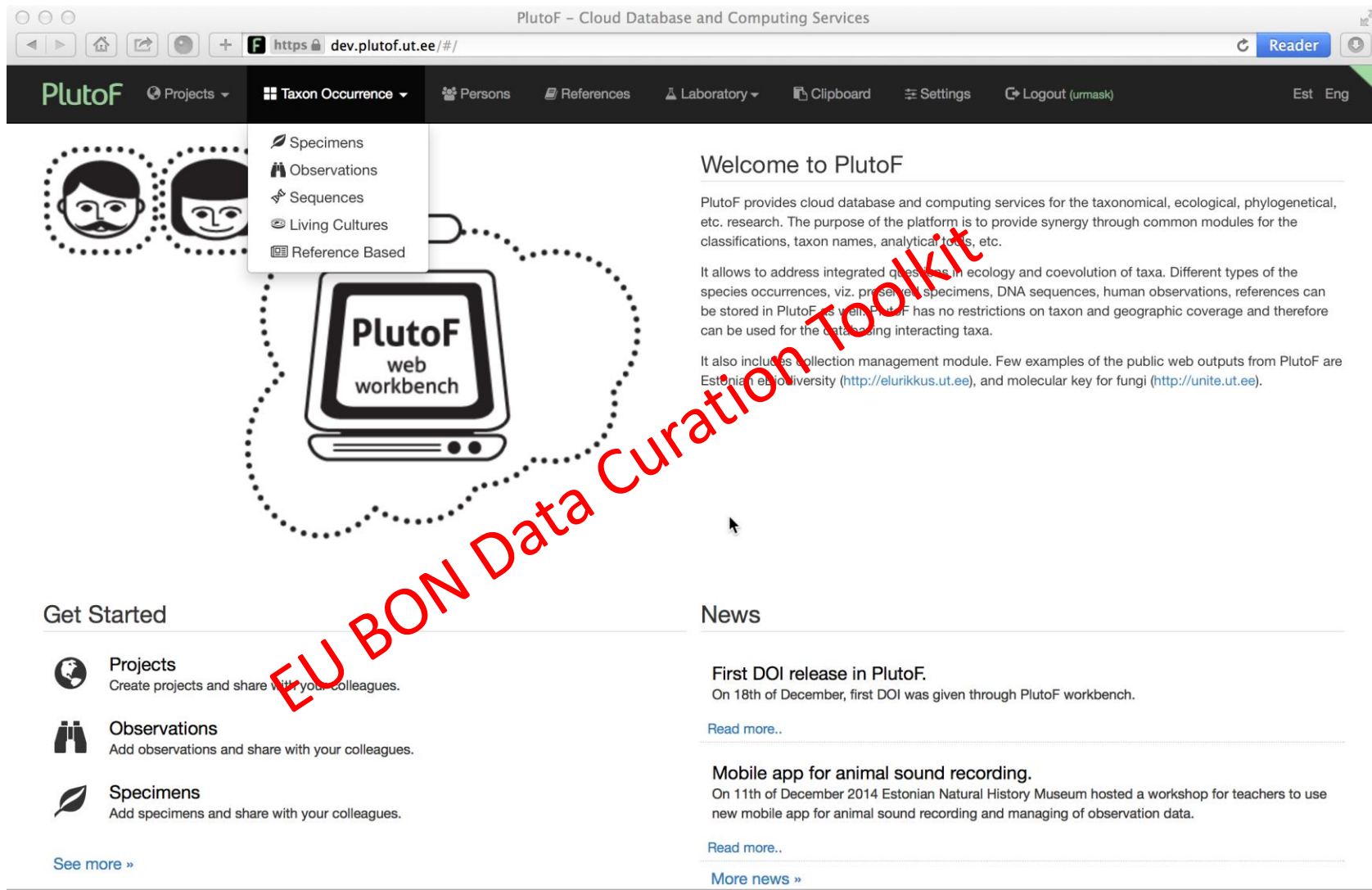
Integration, annotation and mobilization of biodiversity data - Show case

Integration of EU BON targeted datasets

- Taxonomic backbone – PESI (IP)
- Specimen data – in datasets.
- Ecological – personal datasets.
- – published and personal datasets.
- Genetic data – INSD and UNITE open access datasets (rDNA ITS)

**Online annotation of integrated datasets
by (citizen) scientists**

Integration, annotation and mobilization of biodiversity data - Show case



PlutoF - Cloud Database and Computing Services

https://dev.plutof.ut.ee/#/ Reader

PlutoF Projects Taxon Occurrence Persons References Laboratory Clipboard Settings Logout (umask) Est Eng

- Specimens
- Observations
- Sequences
- Living Cultures
- Reference Based

PlutoF web workbench

Welcome to PlutoF

PlutoF provides cloud database and computing services for the taxonomical, ecological, phylogenetical, etc. research. The purpose of the platform is to provide synergy through common modules for the classifications, taxon names, analytical tools, etc.

It allows to address integrated questions in ecology and coevolution of taxa. Different types of the species occurrences, viz. preserved specimens, DNA sequences, human observations, references can be stored in PlutoF as well. PlutoF has no restrictions on taxon and geographic coverage and therefore can be used for the data on interacting taxa.

It also includes collection management module. Few examples of the public web outputs from PlutoF are Estonian biodiversity (<http://elurikkus.ut.ee>), and molecular key for fungi (<http://unite.ut.ee>).

Get Started

- Projects**
Create projects and share with your colleagues.
- Observations**
Add observations and share with your colleagues.
- Specimens**
Add specimens and share with your colleagues.

[See more »](#)

News

First DOI release in PlutoF.
On 18th of December, first DOI was given through PlutoF workbench.
[Read more..](#)

Mobile app for animal sound recording.
On 11th of December 2014 Estonian Natural History Museum hosted a workshop for teachers to use new mobile app for animal sound recording and managing of observation data.
[Read more..](#)

[More news »](#)



Integration, annotation and mobilization of biodiversity data - Show case

Integration of EU BON

- Taxonomic backbone
- Species

Result:
>500 000 Species Hypotheses based on genetic data and enriched with specimen, ecological, species profile data and connected to the PESI taxonomic backbone

and personal datasets.

and UNITE open access datasets (rDNA ITS)





Username Log in

UNITE Species Hypotheses ver. 7 taxonomy browser

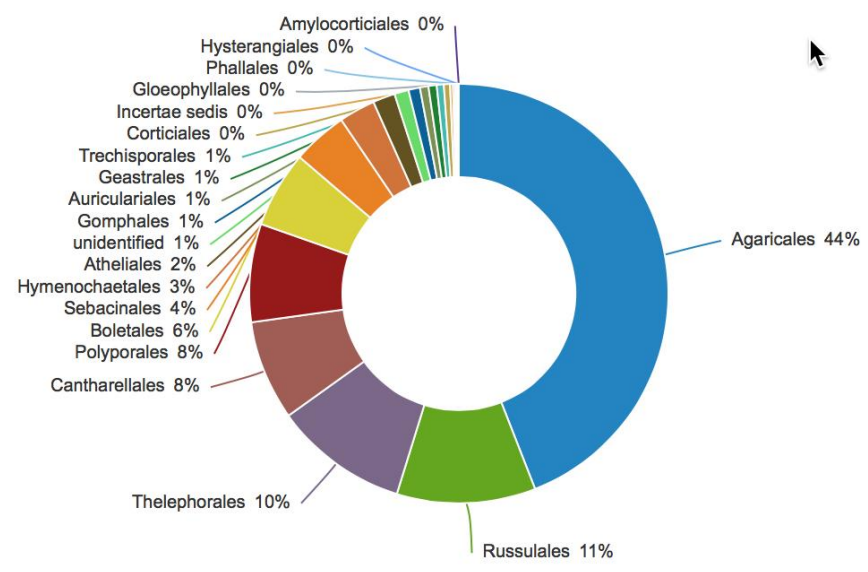
Select distance and dataset to browse:

1.5% (default) Only non-singleton SH-s Go

Fungi; Basidiomycota; Agaricomycetes

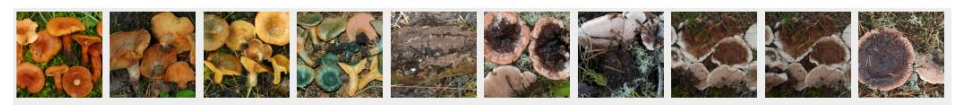
- Agaricales** (3887)
- Amylocorticiales** (2)
- Atheliales** (151)
- Auriculariales** (58)
- Boletales** (520)
- Cantharellales** (679)
- Corticiales** (42)
- Geastrales** (56)
- Gloeophyllales** (14)
- Gomphales** (78)
- Hymenochaetales** (247)
- Hysterangiales** (9)
- Incertae sedis** (20)
- Phallales** (14)
- Polyporales** (667)
- Russulales** (945)
- Sebacinales** (375)
- Theleporales** (911)
- Trechisporales** (48)
- unidentified** (22)

SH graph: cls Agaricomycetes



Open in a new window

Illustrative photos: cls Agaricomycetes



Lactarius imperceptus | SH005435.07FU

Reference sequence

Accession numbers: JQ272401

Chosen by: María Paz Martín Esteban

Date: 2015-03-27 18:17:43

Taxonomy

Placement in classification: Fungi: Basidiomycota; Agaricomycetes; Russulales; Russulaceae; Lactarius;

See [Lactarius imperceptus in Index Fungorum](#)

Identifications

Lactarius (12); Lactarius eucalypti (14); Lactarius imperceptus (1); Lactarius lacunarum (5);

Statistics

Minimum distance to the closest SH: 3.0

No. of sequences in SH: 42

Distribution of distances:

Distribution map

Locations without exact coordinates are displayed as country polygons

Ecology

Interacting taxa: Anthophyta (1); Castanea dentata (1); Cyperidium acule (1); Eucalyptus regnata (1); Monotropa uniflora (1); Nothofagus cumingiihami (1); Nothofagus menziesii (8); Pinus taeda (6); Pomadouria spetala (1); Quercus (1); Quercus suber (1); Tsuga canadensis (2); Tsuga diversifolia (1);

Metadata

DOI

<https://doi.org/10.15156/BIOSH/SH005435.07FU>

Dataset

Köjalg, Umas; Abarenkov, Kessy; Nilsson, Henrik; Larsson, Karl-Henrik; Aas, Anders Bjørnsgaard; Adams, Rachel; Alves, Artur; Ammirati, Joseph F.; Arnold, A. Elizabeth; Bahram, Mohammad; Bengtsson-Palme, Johanna; Berlin, Anna; Bothner, Synneve; Bourlat, Sarah; Cheek, Tanya; Dima, Bălinț; Drenkhan, Rein; Duarte, Camilla; Dufrays, Margaritha; Eberhardt, Hanna; Fibiger, Hanna; Fresco, Tobias G.; Gamica, Sigfredo; Gent, József; Ghobad-Nejhad, Masoomeh; Grebenec, Tine; Griffith, Gareth W.; Hampel, Felix; Kennedy, Peter; Khomich, Mariya; Kohout, Petr; Kolom, Anu; Larsson, Ellen; Lastdo, Iriny; Leavitt, Steven; Limätäinen, Kare; Lindahl, Björn; Lodge, D. Jean; Lumbsch, H. Thorsten; Martin Esteban, María Paz; Meyer, Wieland; Miettinen, Otto; Nguyen, Nhu; Niskanen, Tuula; Oton, Ryoiko; Opik, Margat Ordynets; Alexander; Pawłowska, Julia; Peintner, Ursula; Pereira, Olinto; Liparini, Pinho, Danilo Batista; Pöglmaa, Kadri; Runnel, Kadri; Ryberg, Martin; Saar, Iga; Santl, Kermit; Scott, James; Spirin, Viacheslav; Suja, Aye; Svantesson, Sten; Tadych, Mariusz; Takamatsu, Susumu; Tamm, Heidi; Taylor, Andy; F.S.; Tedersoo, Leho; Telleria, M. Teresa; Udayanga, Dhanushka; Unterseher, Martin; Voibuev, Sergey; Weiss, Michael; Wurzbacher, Christian (2015): SH005435.07FU. UNITE Community. 10.15156/BIOSH/SH005435.07FU

Publisher

UNITE Community

Publication year

2015

Creators

Umas Köjalg; Kessy Abarenkov; Henrik Nilsson; Karl-Henrik Larsson; Anders Bjørnsgaard Aas; Rachel Adams; Artur Alves; Joseph F. Ammirati; A. Elizabeth Arnold; Mohammad Bahram; Johanna Bengtsson-Palme; Anna Berlin; Synneve Bothner; Sarah Bourlat; Tanya Cheek; Bălinț Dima; Rein Drenkhan; Camilla Duarte; Margaritha Dufrays; Hanna Eberhardt; Hanna Fibiger; Tobias G. Fresco; Sigfredo Gamica; József Gent; Masoomeh Ghobad-Nejhad; Tine Grebenec; Gareth W. Griffith; Felix Hampel; Peter Kennedy; Mariya Khomich; Petr Kohout; Anu Kolom; Ellen Larsson; Iriny Lastdo; Steven Leavitt; Kare Limätäinen; Björn Lindahl; D. Jean Lodge; H. Thorsten Lumbsch; María Paz Martín Esteban; Wieland Meyer; Otto Miettinen; Nhu Nguyen; Tuula Niskanen; Ryoiko Oton; Margat Opik; Alexander Ordynets; Julia Pawłowska; Ursula Peintner; Olinto Liparini; Pinho, Danilo Batista; Kadri Pöglmaa; Kadri Runnel; Martin Ryberg; Iga Saar; Kermit Santl; James Scott; Viacheslav Spirin; Aye Suja; Sten Svantesson; Mariusz Tadych; Susumu Takamatsu; Heidi Tamm; Andy F.S. Taylor; Leho Tedersoo; M. Teresa Telleria; Dhanushka Udayanga; Martin Unterseher; Sergey Voibuev; Michael Weiss; Christian Wurzbacher;

Document(s)

SH005435.07FU_graph.png; SH005435.07FU.json;

Detailed information

SH graphical view Metadata Media Distribution map

Seq ID	UNITE taxon name	INSD taxon name	Country	DNA source	Interacting taxa
AB828027	Lactarius	uncultured ectomycorrhizal ...	Japan		Tsuga diversifolia
JF727350	Lactarius	Lactarius sp EMP28	China	Ectomycorrhiza	
KF432002	Lactarius	Lactarius sp KW18	Thailand		
JQ981753	Lactarius	uncultured Lactarius	China		
AY456344	Lactarius	Lactarius sp NC_2_8345	United States	Ectomycorrhiza	Pinus taeda
AY456343	Lactarius	Lactarius sp NC_2_72782	United States	Ectomycorrhiza	Pinus taeda
AY456347	Lactarius	Lactarius sp NC_3_8345	United States	Ectomycorrhiza	Pinus taeda
AY456345	Lactarius	Lactarius sp NC_2_8346	United States	Ectomycorrhiza	Pinus taeda
F.901331	Lactarius imperceptus	uncultured Lactarius	United States	Ectomycorrhiza	Tsuga canadensis
EU819485	Lactarius imperceptus	Lactarius imperceptus	United States	Fruitlet	Anthophyta
AY456350	Lactarius imperceptus	Lactarius sp NC_1_5999	United States	Ectomycorrhiza	Pinus taeda
DD777991	Lactarius imperceptus	uncultured Russulaceae	United States	Ectomycorrhiza	Monotropa uniflora
QQ240489	Lactarius imperceptus	uncultured Lactarius	United States	Ectomycorrhiza	Castanea dentata
AY456351	Lactarius imperceptus	Lactarius sp NC_1_6000	United States	Ectomycorrhiza	Pinus taeda
JQ272401	Lactarius imperceptus	Lactarius imperceptus	United States		Pinus taeda
HE804555	Lactarius imperceptus	uncultured ectomycorrhizal ...			
HE804544	Lactarius imperceptus	uncultured ectomycorrhizal ...			
F.901317	Lactarius imperceptus	uncultured Russulaceae	United States	Ectomycorrhiza	Tsuga canadensis
J0897291	Lactarius imperceptus	uncultured fungus	United States		Cyperidium acule
J2217612	Lactarius	Lactarius sp CO_2012	New Zealand		
F.897202	Lactarius	uncultured mycorrhizal fung...	Portugal	Ectomycorrhiza	Quercus
JN235951	Lactarius	Hydnangium australiense	New Zealand		
KF386753	Lactarius	Acrogelium sp AWC480	Australia		
F.904864	Lactarius lacunarum	uncultured ectomycorrhizal ...	Spain	Ectomycorrhiza	Quercus suber
UD000036	Lactarius lacunarum		Belgium	Fruitlet	
GQ404991	Lactarius lacunarum	uncultured fungus	Czech Republic	Ectomycorrhiza	
JF90577	Lactarius lacunarum	Lactarius lacunarum	Italy		
KF432973	Lactarius lacunarum	Lactarius lacunarum	Italy		
EF834124	Lactarius eucalypti	uncultured Lactarius	New Zealand	Ectomycorrhiza	Nothofagus menziesii
EF834128	Lactarius eucalypti	uncultured Lactarius	New Zealand	Ectomycorrhiza	Nothofagus menziesii
EF834130	Lactarius eucalypti	uncultured Lactarius	New Zealand	Ectomycorrhiza	Nothofagus menziesii
EF834129	Lactarius eucalypti	uncultured Lactarius	New Zealand	Ectomycorrhiza	Nothofagus menziesii
EF834123	Lactarius eucalypti	uncultured Lactarius	New Zealand	Ectomycorrhiza	Nothofagus menziesii
EF834122	Lactarius eucalypti	uncultured Lactarius	New Zealand	Ectomycorrhiza	Nothofagus menziesii
EF834127	Lactarius eucalypti	uncultured Lactarius	New Zealand	Ectomycorrhiza	Nothofagus menziesii
EF834126	Lactarius eucalypti	uncultured Lactarius	New Zealand	Ectomycorrhiza	Nothofagus menziesii
EF834125	Lactarius eucalypti	uncultured Lactarius	New Zealand	Ectomycorrhiza	Nothofagus menziesii
JF960798	Lactarius eucalypti	uncultured Lactarius	Australia		
UD000070	Lactarius eucalypti		Australia	Fruitlet	
UD000071	Lactarius eucalypti	uncultured Zelleromyces	Australia	Ectomycorrhiza	Eucalyptus regnata ...
JF960852	Lactarius eucalypti		Australia		
HF685093	Lactarius eucalypti	uncultured Lactarius	Italy		

● chimeric
● low quality
● EX = sequence to be excluded from the next version of global key



Each species level DOI is a combination of datasets including:

- taxonomic backbone
- specimens
- genetic data (rDNA ITS: Sanger and NGS)
- ecology
- species profile (multimedia, distribution, functional traits, etc.)

EU BON General Meeting
1-4 July 2015, Cambridge





Tuber whetstonense | SH001616.07FU

Species Hypothesis pages version 7 unite

Reference sequence

Accession numbers AY830855

Chosen by Matthew E. Smith

Date 2014-11-09 23:04:55

Taxonomy

Placement in classification
Fungi; Ascomycota; Pezizomycetes; Pezizales; Tuberales; Tuber;

[See Tuber whetstonense in Index Fungorum](#)

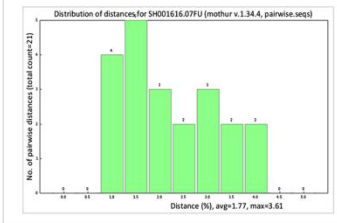
Identifications
Tuber (4); Tuber whetstonense (3);

Statistics

Minimum distance to the closest SH 3.0

No. of sequences in SH 7

Distribution of distances



Distribution map

*Locations without exact coordinates are displayed as country polygons

Ecology

Interacting taxa
Quercus (4); Quercus douglasii (1);

Metadata

DOI
<http://dx.doi.org/10.15156/BIO/SH001616.07FU>

Dataset
Köjalg, Urmas; Abarenkov, Kessy; Nilsson, Henrik; Larsson, Karl-Henrik; Aas, Anders Bjørnsgard; Adams, Rachel; Alves, Artur; Ammirati, Joseph F.; Arnold, A. Elizabeth; Bahram, Mohammad; Bengtsson-Palme, Johan; Berlin, Anna; Botnen, Synnøve; Bourlat, Sarah; Cheeke, Tanya; Dima, Bálint; Drenkhan, Rein; Duarte, Camila; Dueñas, Margarita; Eberhardt, Ursula; Friberg, Hanna; Frøeslev, Tobias G.; Garnica, Sigisfredo; Geml, József; Ghobad-Nejhad, Masoomeh; Grebenc, Tine; Griffith, Gareth W.; Hampe, Felix; Kennedy, Peter; Khomich, Maryia; Kohout, Petr; Kollom, Anu; Larsson, Ellen; Laszlo, Irinyi; Leavitt, Steven; Liimatainen, Kare; Lindahl, Björn; Lodge, D. Jean; Lumbsch, H. Thorsten; Martín Esteban, María Paz; Meyer, Wieland; Miettinen, Otto; Nguyen, Nhu; Niskanen, Tuula; Oono, Ryoko; Öpik, Maarja; Ordynets, Alexander; Pawłowska, Julia; Peintner, Ursula; Pereira, Olinto Liparini; Pinho, Danilo Batista; Pöldmaa, Kadri; Runnel, Kadri; Ryberg, Martin; Saar, Irja; Sanli, Kemal; Scott, James; Spirin, Viacheslav; Sujja, Ave; Svantesson, Sten; Tadych, Mariusz; Takamatsu, Susumu; Tamm, Heidi; Taylor, Andy F.S.; Tedersoo, Leho; Telleria, M. Teresa; Udayanga, Dhanushka; Unterseher, Martin; Volobuev, Sergey; Weiss, Michael; Wurzbacher, Christian (2015): SH001616.07FU. UNITE Community. 10.15156/BIO/SH001616.07FU

Publisher
UNITE Community

Publication year
2015

Creators
Urmas Köjalg, Kessy Abarenkov, Henrik Nilsson, Karl-Henrik Larsson, Anders Bjørnsgard Aas, Rachel Adams, Artur Alves, Joseph F. Ammirati, A. Elizabeth Arnold, Mohammad Bahram. [Show more](#)

Document(s)
SH001616.07FU_graph.png; SH001616.07FU.json;

From data mobilization to open access service:
Identification and communication

Detailed information

SH graphical view [Metadata](#) [Media](#) [Distribution map](#)

Seq ID	UNITE taxon name	INSD taxon name	Country	DNA source	Interacting taxa
GQ221620	Tuber	uncultured Tuber	United States	Ectomycorrhiza	
EF559286	Tuber	uncultured Tuberales	United States	Ectomycorrhiza	Quercus
JF419244	Tuber whetstonense	Tuber whetstonense	United States		
EF411131	Tuber	uncultured Tuber	United States	Ectomycorrhiza	Quercus
AY830855	Tuber whetstonense	Tuber whetstonense	United States	Fruitbody (Holotype)	Quercus
HM485392	Tuber whetstonense	Tuber whetstonense	United States	Fruitbody (Paratype)	
DQ974800	Tuber	uncultured Tuber	United States	Ectomycorrhiza	Quercus ...

♦ chimeric
● low quality
✖ EX = sequence to be excluded from the next version of global key





Unified system for the DNA based fungal species linked to the classification
Ver. 7.0

Home Run Analysis Search Pages Workbench **Resources** Notes and news UNITE Board Acknowledgements

Downloads

Reference/representative sequences

Following Kõljalg et al. (2013), each terminal fungal taxon for which two or more ITS sequences are available is referred to as a *species hypothesis* (SH). One sequence is chosen automatically by the computer and reference sequence is chosen by hand.

Downloads - https://unite.ut.ee

There are four releases of the keys/keys set: special files pre-formatted for **QIIME**, **mothur**, and **CRIST** use, and one **general** FASTA release for, e.g., local BLAST searches.

There is a brand new release of **UNITE/INSDC representative/reference sequences** for use in reference-based chimera detection of fungal ITS sequences in **UCHIME** and similar programs.

QIIME release (download)

Three sets of QIIME files are released, corresponding to the SHs resulting from clustering at the 97% and 99% threshold levels. The third set of files is the result of a dynamic use of clustering thresholds, such that some SHs are delimited at the 97% level, some at the 97.5% level, some at the 98% level, and so on; these choices were made manually by experts of those particular lineages of fungi. The syntax is the same throughout the three sets of files.

Each SH is given a stable name of the accession number type, here shown in the FASTA file of the dynamic set:

```
>SH099456.05FU_FJ357315_refs
CACAAATATGAAGGCGGGCTGGCCTCTTGTGAGAGGACCGGC...
```

```
SH099456 = accession number of the SH
05FU = global key release 5, organism group FUNgi
FJ357315 = GenBank/UNITE accession number of sequence chosen to represent the SH
refs = this is a manually designated RefS
(reps = this is an automatically chosen RepS)
```

In the corresponding text file, the classification string of the SH is found:

```
SH099456.05FU_FJ357315_refs k__Fungi;p__Ascomycota;c__Dothideomycetes;o__Pleosporales;f__Pleosporaceae;g__Embellisia;s__Embellisia_planif
```

This specifies the hierarchical classification of the sequence. k = kingdom; p = phylum; c = class; o = order; f = family; g = genus; and s = species. Missing information is indicated as "unidentified" item; "f__unidentified;" means that no family name for the sequence exists.



Fork me on GitHub



Quantitative Insights Into Microbial Ecology

- Home
- Install
- Tutorials
- Scripts
- Help
- Resources
- File Formats
- Workshops
- Blog
- Developer
- Articles Citing QIIME

What is QIIME?

QIIME (canonically pronounced *chime*) stands for Quantitative Insights Into Microbial Ecology.

QIIME is an open-source bioinformatics pipeline for performing microbiome analysis from raw DNA sequencing data. QIIME is designed to take users from raw sequencing data generated on the Illumina or other platforms through publication quality graphics and statistics. This includes demultiplexing and quality filtering, OTU picking, taxonomic assignment, and phylogenetic reconstruction, and diversity analyses and visualizations. QIIME has been applied to studies based on billions of sequences from tens of thousands of samples.

Getting started with QIIME

Installing: The quickest way to get started using QIIME is with [MacQIIME](#) (if you're running Mac OS X), the [QIIME VirtualBox](#) or the [QIIME Amazon EC2 image](#) (if you're using Windows, Mac OS X, or Linux), or [pip](#) (if you're using Linux or Mac OS X). See the [QIIME install documentation](#) for details.

Running: Once you've installed QIIME, move on to the [QIIME Tutorials](#). The [Illumina](#)

Forum Documentation

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CLC GENOMICS WORKBENCH

A comprehensive and user-friendly analysis package for analyzing, comparing, and visualizing next generation sequencing data.

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Introduction

Analyze, compare and visualize NGS data

Dominating the high-throughput sequencing data analysis challenge

Feature overview



Integration, annotation and mobilization of biodiversity data - Show case

Example of the full chain of EU BON data mobilization (except remote sd)

Different data types
Integrated
Enriched with annotations
Mobilized
Open access (DOI)
Utilized by the community
(identifications and communication)

Integration, annotation and mobilization of biodiversity data - Show case

Strategy different from GBIF, INSD, etc.



Thank you!

