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Conference Abstract

The UNITE Database for Molecular Identification and for Communicating Fungal Species

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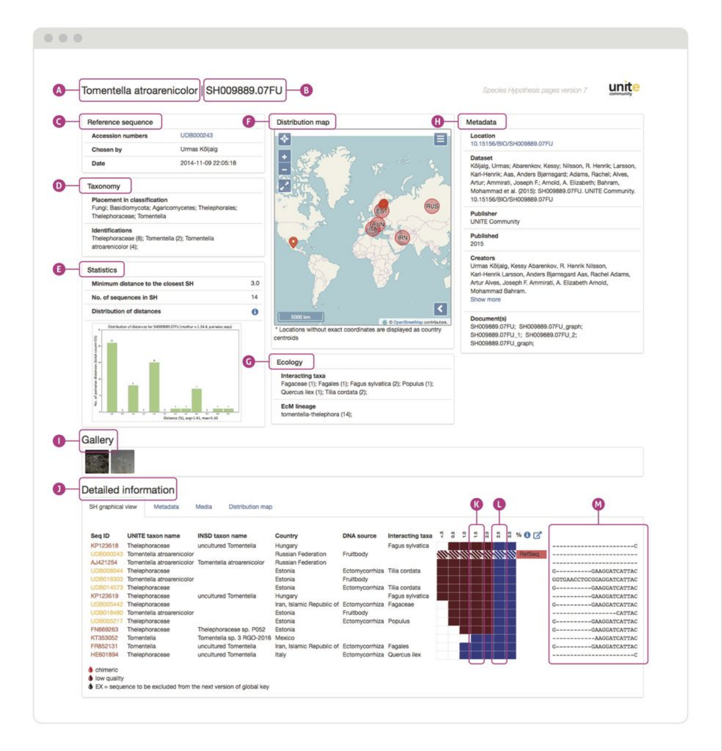
Abstract

UNITE (https://unite.ut.ee; Nilsson et al. 2018) is an international community of scientists and citizen scientists established in 2001. The ambition of UNITE is to develop: 1) datasets and tools for robust and reproducible molecular identification; 2) Persistent Identifiers based system for the communicating fungal species. Datasets of the nuclear ribosomal internal transcribed spacer (ITS) region, form the basis for UNITE. The current version includes nearly 1 million public fungal ITS sequences. Datasets are curated and annotated by community members. During the past 15 years, they made more than 275 000 improvements. In the complete absence of Latin names for species, UNITE offers a unique system where species hypotheses (SH) are provided with Digital Object Identifiers (DOIs). The current version 8 of UNITE offers more than 800 000 DOI-based SHs. One such SH DOI page is shown in Fig. 1. These DOI identifiers are also incorporated into the taxonomic backbone, making communication of taxa seamless in both directions. DOI identifiers of species hypotheses are also used by GBIF (Global Biodiversity Information Facility) in order to publish high-throughput sequencing taxon occurrence data in their data portal.


A
B
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Species Hypothesis pages version 7
unite community
RUS
EST
HUN
ITA
IRN
5000 km
© OpenStreetMap contributors.
Distribution of distances for SH009889.07FU (mothur v.1.34.4, pairwise.seqs)
No. of pairwise distances (total count=55)
Distance (%), avg=1.41, max=5.43
<.5
0.5
1.0
1.5
2.0
2.5
3.0
%
RefSeq

Tomentella atroarenicolor | SH009889.07FU

Reference sequence

Accession numbers	UDB000243
Chosen by	Urmas Kõljalg
Date	2014-11-09 22:05:18

Taxonomy

Placement in classification
Fungi; Basidiomycota; Agaricomycetes; Thelephorales; Thelephoraceae; Tomentella

Identifications
Thelephoraceae (8); Tomentella (2); Tomentella atroarenicolor (4);

Statistics

Minimum distance to the closest SH	3.0
No. of sequences in SH	14
Distribution of distances	

Distribution map

* Locations without exact coordinates are displayed as country centroids

Metadata

Location
10.15156/BIO/SH009889.07FU

Dataset
Kõljalg, Urmas; Abarenkov, Kessy; Nilsson, R. Henrik; Larsson, Karl-Henrik; Aas, Anders Bjørnsgard; Adams, Rachel; Alves, Artur; Ammirati, Joseph F.; Arnold, A. Elizabeth; Bahram, Mohammad et al. (2015): SH009889.07FU. UNITE Community. 10.15156/BIO/SH009889.07FU

Publisher
UNITE Community

Published
2015

Creators
Urmas Kõljalg, Kessy Abarenkov, R. Henrik Nilsson, Karl-Henrik Larsson, Anders Bjørnsgard Aas, Rachel Adams, Artur Alves, Joseph F. Ammirati, A. Elizabeth Arnold, Mohammad Bahram.
Show more

Document(s)
SH009889.07FU; SH009889.07FU_graph; SH009889.07FU_1; SH009889.07FU_2; SH009889.07FU_graph;

Ecology

Interacting taxa
Fagaceae (1); Fagales (1); Fagus sylvatica (2); Populus (1); Quercus ilex (1); Tilia cordata (2);

EcM lineage
tomentella-thelephora (14);

Gallery

Detailed information

SH graphical view | Metadata | Media | Distribution map

Seq ID	UNITE taxon name	INSD taxon name	Country	DNA source	Interacting taxa
KP123618	Thelephoraceae	uncultured Tomentella	Hungary		Fagus sylvatica
UDB000243	Tomentella atroarenicolor		Russian Federation	Fruitbody	
AJ421254	Tomentella atroarenicolor	Tomentella atroarenicolor	Russian Federation		
UDB008044	Thelephoraceae		Estonia	Ectomycorrhiza	Tilia cordata
UDB016303	Tomentella atroarenicolor		Estonia	Fruitbody	
UDB014573	Thelephoraceae		Estonia	Ectomycorrhiza	Tilia cordata
KP123619	Thelephoraceae	uncultured Tomentella	Hungary		Fagus sylvatica
UDB005442	Thelephoraceae		Iran, Islamic Republic of	Ectomycorrhiza	Fagaceae
UDB018480	Tomentella atroarenicolor		Estonia	Fruitbody	
UDB005217	Thelephoraceae		Estonia	Ectomycorrhiza	Populus
FN669263	Thelephoraceae	Thelephoraceae sp. P052	Estonia		
KT353052	Tomentella	Tomentella sp. 3 RGO-2016	Mexico		
FR852131	Tomentella	uncultured Tomentella	Iran, Islamic Republic of	Ectomycorrhiza	Fagales
HE601894	Thelephoraceae	uncultured Tomentella	Italy	Ectomycorrhiza	Quercus ilex

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-----------------------C
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------------------------
G----------GAAGGATCATTAC
GGTGAACCTGCGGAGGATCATTAC
G----------GAAGGATCATTAC
-----------GAAGGATCATTAC
G----------GAAGGATCATTAC
------------------CATTAC
G----------GAAGGATCATTAC
G----------GAAGGATCATTAC
------------AAGGATCATTAC
G----------GAAGGATCATTAC
-----------------------C
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- chimeric
- low quality
- EX = sequence to be excluded from the next version of global key

Figure 1.

A screenshot of a UNITE SH Digital Object Identifier (DOI) page for *Tomentella atroarenicolor* (https://plutof.ut.ee/#/datacite/10.15156%2FBIO%2FSH009889.07FU). (**A**) The most accurate taxon name chosen automatically (or manually, if the default were overridden by an expert) from the available sequence identifications; (**B**) short ID of the DOI; (**C**) Data on reference sequence chosen to represent this SH; (**D**) placement of the SH in the fungal classification and identification records for individual sequences; the number after the taxon name indicates how many sequences carry that name. (**E**) Select statistics on the SH. The minimum distance 3.0% is the mandatory genetic difference between sister SHs. (**F**) Distribution map of the individual sequences. (**G**) Information on ecology (interacting taxa) if associated with the individual sequences. (**H**) DataCite-specific data on the DOI. (**I**) Images of the specimen or sample from which the DNA was extracted. Only a limited number of sequences have images attached to them. (**J**) Graphical overview of the SH with detailed information. (**K**) SH inclusiveness across sequence similarity threshold values. A threshold value (= minimum distance) of 1.5% will split these sequences into two SHs, shown here in different colours. (**L**) A threshold value of 2.5% will lump all sequences into a single SH. Each such SH is hyperlinked to its own unique web page. (**M**) Scrollable multiple sequence alignment of the SH. ‘RefSeq’ indicates that the sequence was selected manually to be the representative sequence for the SHs. RefSeqs stem from type specimens or other authentic and particularly trustworthy material. This particular SH contains both International Nucleotide Sequence Database Collaboration sequences (brown) and sequences that are only found in UNITE (yellow).

UNITE serves as a data provider for a range of metabarcoding software pipelines and regularly exchanges data with all major fungal sequence databases and other community resources.

Recent improvements include ITS-based species hypotheses for all eukaryotes and aggregation of full-length, high-quality ITS sequences generated by the PacBio Sequel system (https://www.pacb.com/products-and-services/sequel-system) from diverse material samples.

Keywords

molecular identification, persistent identifiers, fungi, taxonomy

Presenting author

Kessy Abarenkov

Presented at

Biodiversity_Next 2019

References

- Nilsson RH, Larsson K, Taylor AFS, Bengtsson-Palme J, Jeppesen TS, Schigel D, Kennedy P, Picard K, Glöckner FO, Tedersoo L, Saar I, Kõljalg U, Abarenkov K (2018) The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. Nucleic Acids Research 47: D259-D264. https://doi.org/10.1093/nar/gky1022