

Supplementary Figure 1. Visualization of the *Rhizopogon verii* species hypothesis (SH) in UNITE 9.0.

PlutoF DOI
doi.plutof.ut.ee/doi/10.15156/BIO/SH1219438.09FU

PlutoF
Species Hypotheses pages
unit community
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Species Hypotheses (SH)
Widescreen FASTA Curate

Rhizopogon verii | SH1219438.09FU

Communication of the SH

Digital Object Identifier (DOI) <https://dx.doi.org/10.15156/BIO/SH1219438.09FU>

Taxon name Rhizopogon verii

Placement in classification and Taxon Hypotheses

Fungi (TH068972) / Dikarya (TH069005) / Basidiomycota (TH069042) / Agaricomycotina (TH069209) / Agaricomycetes (TH069290) / Boletales (TH069632) / Rhizopogonaceae (TH072692) / Rhizopogon (TH074613)

Reference sequence

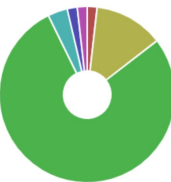
Accession number AM085531


Chosen by María Paz Martín Esteban, 26/03/2015 12:57:03

Ecology Taxonomy Statistics History

EcM lineage suillus-rhizopogon (62)

Interacting taxa Pinus radiata (1); Pinus pinaster (7); Pinus sylvestris (43); Pinus (2); Pinus strobus (1); Pinus taeda (1)





* Locations without exact coordinates are displayed as country centroids

DOI metadata

Title SH1219438.09FU

Publisher UNITE Community

Published 2023

Citation Köljalg, Urmas; Abarenkov, Kessy; Nilsson, R. Henrik; Larsson, Karl-Henrik; May, Tom W.; Taylor, A.F.S.; Frøslev, Tobias G.; Pawłowska, Julia; Lindahl, Björn; Smith, Matthew E. et al. (2023): SH1219438.09FU. UNITE Community. 10.15156/BIO/SH1219438.09FU

Downloads SH1219438.09FU, SH1219438.09FU_graph, SH1219438.09FU_3

Individuals of the current SH (total: 257, core: 81)

Level 1 (17) Level 2 (31) Level 3 (42) Level 4 (44) Level 5 (92) Level 6 (92) Level 7 (257)

Sequences within the same 1.0% SH for the same continent collapsed

Sequence ID	UNITE taxon name	INSD taxon name	Source	Interacting taxa	Area	Conservation	Sequence
UDB001618	+105 Rhizopogon verii		Fruitlet: DG05-22		United Kingdom	100%A G G A C G A T T A A T G
AM085531	+17 Rhizopogon verii	Rhizopogon verii	Fruitlet: TVER_H_AQUI		Tunisia	100%G A T T A A T G
JD075973	Rhizopogon verii	Rhizopogon verii	Plant-associated sample	Pinus pinaster	Unspecified	100%A T T G
UDB06489152	+98 Rhizopogon	uncultured fungus	Soil sample: TUE001090		Colombia	100%A T G
UDB06501607	+20 Rhizopogon		Soil sample: TUE002544		New Zealand	100%A T G
UDB06485747	Rhizopogon		Soil sample: TUE000276		Madagascar	100%A T G
UDB06485675	Rhizopogon		Soil sample: TUE000226		Estonia	100%A T G
AJ307687	Rhizopogon	ectomycorrhizal isolate ECM 12	Plant-associated sample	Pinus	France	100%
UDB06501579	Rhizopogon		Soil sample: TUE02544		New Zealand	100%
UDB06489218	Rhizopogon		Soil sample: TUE001091		Colombia	100%A T G
LN875271	Rhizopogon verii	Rhizopogon verii		Pinus sylvestris	Germany	100%G A T T A A T G
UDB06485705	Rhizopogon		Soil sample: TUE000276		Madagascar	100%
UDB06504868	Rhizopogon		Soil sample: TUE003144		South Africa	100%A T G A
UDB06507510	Rhizopogon		Soil sample: TUE003356		Estonia	100%A T G
UDB06489196	Rhizopogon		Soil sample: TUE001091		Colombia	100%A T G
UDB06507507	Rhizopogon		Soil sample: TUE003356		Estonia	100%A T G
UDB06504557	Rhizopogon		Soil sample: TUE003135		Portugal	100%A T G

Supplementary Figure 2. Visualization of the taxon hypothesis (TH) of the fungal order *Boletales* in UNITE 9.0.

Plutof DOI [10.15156/BIO/TH069632](https://doi.org/10.15156/BIO/TH069632)

Plutof Open Workbench

Boletales | TH069632

Taxon Hypothesis pages **unit** community Data hosted by **Plutof**

Taxonomy

Placement in taxonomy
Fungi (TH068972); Dikarya (TH069005); Basidiomycota (TH069042); Agaricomycetes (TH069290)

Children
Calostomataceae (TH070293); Gyrodontaceae (TH070318); Hygrophoropsidaceae (TH070698); Suillaceae (TH070720); Astraeaceae (TH071050); Paxillaceae (TH071301); Boletales *fam. incertae sedis* (TH071427); Boletaceae (TH071498); Coniophoraceae (TH071600); Duplicystaceae (TH071648) [Show more](#)

Statistics

Number of SHs	979
Number of ITS sequences	858

Ecology

Interacting taxa
Asteropeia mcphersonii (1); Fagus sylvatica (1); Quercus (7); Betula alnoides (6); Oreamunnea mexicana (5); Quercus oleoides (5); Pinus densiflora (4); Pyrolo japonica (4); Asteropeia (3); Coccoloba uvifera (3) [Show more](#)

EcM lineage
boletus (139); suillus-rhizopogon (52); paxillus-gyrodon (37); non-ectomycorrhizal (8); pisolithus-scleroderma (5)

5000 km
Leaflet | © Mapbox © OpenStreetMap

* Locations without exact coordinates are displayed as country centroids

Metadata

Location	10.15156/BIO/TH069632
Citation	Kõljalg, Urmas; Abarenkov, Kessy; Nilsson, R. Henrik; Larsson, Karl-Henrik; May, Tom W.; Taylor, A.F.S.; Frieslev, Tobias G.; Põldmaa, Kadri (2023); TH069632. UNITE Community, 10.15156/BIO/TH069632
Publisher	UNITE Community
Published	2023
Creators	Kõljalg, Urmas; Abarenkov, Kessy; Nilsson, R. Henrik; Larsson, Karl-Henrik; May, Tom W.; Taylor, A.F.S.; Frieslev, Tobias G.; Põldmaa, Kadri.
Documents	TH069632_v1.0.json

Detailed information

Title	TH069632
Subtitle	Boletales
Location	https://dx.doi.org/10.15156/BIO/TH069632
Publisher	UNITE Community
Published	2023
Resource type	Dataset/UNITE Taxon Hypothesis
Creators	Kõljalg, Urmas; Abarenkov, Kessy; Nilsson, R. Henrik; Larsson, Karl-Henrik; May, Tom W.; Taylor, A.F.S.; Frieslev, Tobias G.; Põldmaa, Kadri.
Taxa	Boletales E.-J. Gilbert, 1931
Contributors	<ul style="list-style-type: none">ContactPerson: Abarenkov, KessyDataManager: Zirk, AllanDataManager: Pirrmann, TimoDataManager: Põhönen, RalvoDataManager: Ivanov, FilipHostingInstitution: UTE - University of Tartu; Natural History Museum and Botanical Garden
Dates	<ul style="list-style-type: none">Available: 2023-08-11
Funders	
Abstract	Here we present the novel 'taxon hypothesis' (TH) concept to accommodate fungal 'species hypothesis' (SH) into existing classification frameworks for taxonomic communication. As supported with Digital Object Identifiers (DOIs), THs are flexible in time and enable direct cross-communication of higher level taxa along with evolving classification schemes. Every TH includes given number of SHs and consequently fixed number of fungal rDNA ITS sequences. DNA sequences generated by high-throughput or Sanger sequencing studies and identified against UNITE SHs will be automatically assigned to THs as well.
Formats	<ul style="list-style-type: none">application/json
Subjects/keywords	
Licence	Attribution-NonCommercial (CC BY-NC)
Citation	Kõljalg, Urmas; Abarenkov, Kessy; Nilsson, R. Henrik; Larsson, Karl-Henrik; May, Tom W.; Taylor, A.F.S.; Frieslev, Tobias G.; Põldmaa, Kadri (2023); TH069632. UNITE Community, 10.15156/BIO/TH069632
Related identifiers	
Alternate	

Supplementary Figure 3. Browsing and searching third-party curations added by the members of the UNITE community.

Example 1: Locality info and isolation source specified, taxon re-identification added for KJ180283.

UNITE - Search

Search by SH code ...

Species Hypotheses Sequences **Curations**

... or search third-party annotations:

Taxon name Include sub-taxa

Annotated by

Annotated field

Third-party annotations: 2 records found. Showing records 1 - 2

#	Accession number	Taxon name	Typification	Annotated at	Annotated by	Country	Locality text
1.	MF687864 ENA	<i>Boletus</i>		2023-01-24 09:24	Urmaz Köljalğ	China	
2.	KJ180283 ENA	<i>Sakaguchia</i>		2022-02-01 08:07	Urmaz Köljalğ	China	

ENA European Nucleotide Archive

Sequence: KJ180283.1

Uncultured eukaryote clone KJ180283.1: 285 18S ribosomal RNA gene, partial sequence; Internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

Organism: uncultured eukaryote
Accession: KJ180283
Mol Type: genomic DNA
Topology: linear
Base Count: 603
Dataclass: STD
Tax Division: ENV
Keywords: ENA
Environmental Sample: true
MIS Checksum: d98D746b4263a156e6970161567c7

3rd Party Curations

Operation	Attribute Name	Attribute Value	Assertion Method	Assertion Evidences	Provider Name	Status
Add	organism	Sakaguchia	manual assertion	evidence used in manual assertion	plutof	
Add	identified_by	Urmaz Köljalğ	manual assertion	evidence used in manual assertion	plutof	
Add	db_xref	taxon:10602	manual assertion	evidence used in manual assertion	plutof	
Add	type_material		manual assertion	evidence used in manual assertion	plutof	
Add	isolation_source	Water	manual assertion	evidence used in manual assertion	plutof	
Add	country	China:Shandong	manual assertion	evidence used in manual assertion	plutof	
Add	lat_lon	37.890 S 121.88736 E	manual assertion	evidence used in manual assertion	plutof	

ebi.ac.uk/ena/clearinghouse/api/curations/KJ180283

```

{
  "curations": [
    {
      "id": "ff850ca9-a23a-4e15-8897-c11bd62c4312",
      "recordType": "sequence",
      "recordId": "KJ180283",
      "primaryRecordId": "KJ180283.1",
      "dataIdentifier": "plutof",
      "attributePost": "organism",
      "valuePost": "Sakaguchia",
      "attributeDelete": false,
      "assertionMethod": "manual assertion",
      "assertionEvidences": [
        {
          "identifier": "ECO:0000352",
          "shortForm": "ECO_0000352",
          "label": "evidence used in manual assertion"
        }
      ]
    },
    {
      "id": "a61bd2e9-38bd-4268-ae84-501d501ba3fe",
      "recordType": "sequence",
      "recordId": "KJ180283",
      "primaryRecordId": "KJ180283.1",
      "dataIdentifier": "plutof",
      "attributePost": "identified_by",
      "valuePost": "Urmaz Köljalğ",
      "attributeDelete": false,
      "assertionMethod": "manual assertion",
      "assertionEvidences": [
        {
          "identifier": "ECO:0000352",
          "shortForm": "ECO_0000352",
          "label": "evidence used in manual assertion"
        }
      ]
    }
  ]
}
    
```

Example 2: Data on typification and newly described taxon name added for OQ073926.

UNITE - Search

Search by SH code ...

Species Hypotheses Sequences **Curations**

... or search third-party annotations:

Taxon name Include sub-taxa

Annotated by

Annotated field

Third-party annotations: 31 records found. Showing records 1 - 31

#	Accession number	Taxon name	Typification	Annotated at	Annotated by	Country	Locality text
1.	OQ073926 ENA	<i>Placopyrenium pseudocineretum</i>	Holotype	2023-08-28 01:44	Yui Fujinuma		
2.	AB540582 ENA	<i>Gliomastix tumulicola</i>	Ex-holotype	2023-05-03 01:22	Yui Fujinuma		
3.	AB709658 ENA	<i>Pochonia boninensis</i>	Ex-holotype	2023-05-01 07:06	Yui Fujinuma	Chichijima, Bonin Islands, Tokyo	
4.	AB709648 ENA	<i>Pochonia chlamydosporia</i> var. <i>ellipsoidora</i>	Ex-holotype	2023-05-01 06:55	Yui Fujinuma	Angashima Island, Tokyo	
5.	AB670709 ENA	<i>Virgaria boninensis</i>	Ex-holotype	2023-05-01 06:00	Yui Fujinuma	Chichijima, Bonin Islands, Tokyo	

ENA European Nucleotide Archive

Sequence: OQ073926.1

Placopyrenium sp. HT-2023a voucher: STU5MNS-STU-F-0002927 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.

Organism: *Placopyrenium* sp. HT-2023a
Accession: OQ073926
Mol Type: genomic DNA
Topology: linear
Base Count: 498
Dataclass: STD
Tax Division: FUN
Location: 40.38 N 141.94 E
Specimen Voucher: STU5MNS-STU-F-0002927
Country: Italy: Sardinia, Sassari Province, Burgos

3rd Party Curations

Operation	Attribute Name	Attribute Value	Assertion Method	Assertion Evidences	Provider Name	Status
Add	db_xref	taxon:3038975	manual assertion	documented statement evidence	plutof	
Add	type_material	Holotype of <i>Placopyrenium pseudocineretum</i>	manual assertion	documented statement evidence	plutof	
Add	organism	<i>Placopyrenium pseudocineretum</i>	manual assertion	documented statement evidence	plutof	
Add	identified_by	Yui Fujinuma	manual assertion	documented statement evidence	plutof	

All third-party curations pushed to European Nucleotide Archive can be fetched programmatically using the Elixir Contextual Data ClearingHouse RESTful API - <https://www.ebi.ac.uk/ena/clearinghouse/api/>.