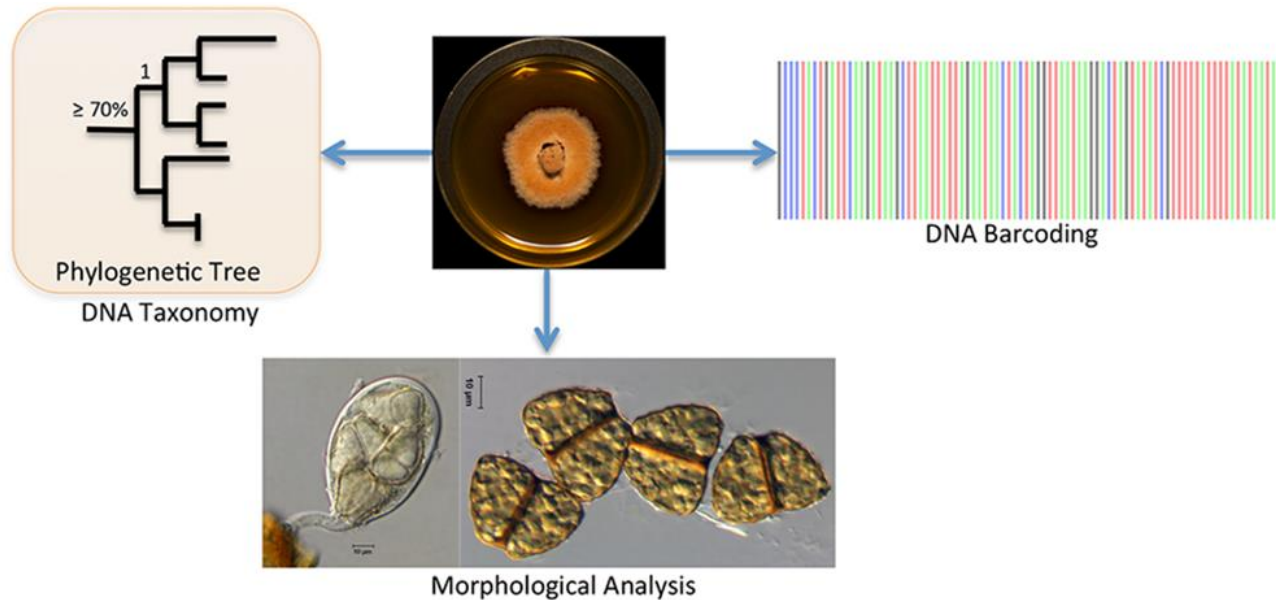


One of the possible ways
How to identify fungi
based on molecular markers



Raja & al. 2016

Ondřej Koukol

Department of Botany, Charles University, Prague, Czech Republic

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. [Learn more](#)

NEWS

BLAST+ 2.13.0 is here!
Starting with this release, we are including the blastn_vdb and tblastn_vdb executables in the BLAST+ distribution.

Thu, 17 Mar 2022 12:00:00 EST [More BLAST news...](#)

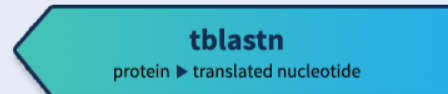
Web BLAST



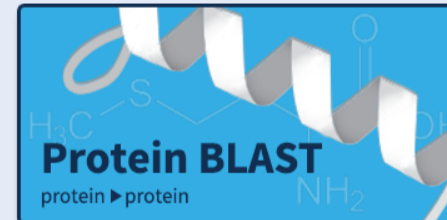
Nucleotide BLAST
nucleotide ▶ nucleotide



blastx
translated nucleotide ▶ protein



tblastn
protein ▶ translated nucleotide



Protein BLAST
protein ▶ protein

BLAST Genomes

Enter organism common name, scientific name, or tax id

Search

[Human](#)

[Mouse](#)

[Rat](#)

[Microbes](#)

BLAST!

- Basic Local Alignment **Search Tool**
(not *Identification tool*)

- fast, accurate and web-accessible
(but full of errors in sequence names and metadata)



BLAST: algorithm-based results

You: interpretation of the results for identification



Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. [Learn more](#)

NEWS

BLAST+ 2.13.0 is here!
Starting with this release, we are including the blastn_vdb and tblastn_vdb executables in the BLAST+ distribution.

Thu, 17 Mar 2022 12:00:00 EST [More BLAST news...](#)

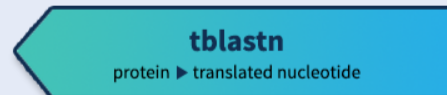
Web BLAST



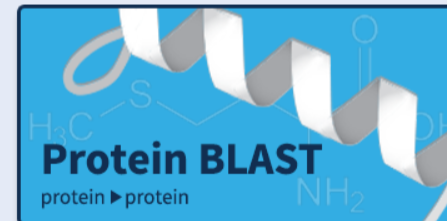
Nucleotide BLAST
nucleotide ▶ nucleotide



blastx
translated nucleotide ▶ protein



tblastn
protein ▶ translated nucleotide



Protein BLAST
protein ▶ protein

BLAST Genomes

Enter organism common name, scientific name, or tax id

Search

[Human](#)

[Mouse](#)

[Rat](#)

[Microbes](#)

blastn blastp blastx tblastn tblastx

BLASTn programs search nucleotide databases using a nucleotide query. more...

[Reset page](#) [Bookmark](#)

Enter Query Sequence

Enter accession number(s), gis(s), or FASTA sequence(s) Query subrange

CCCTGTAACCTCGAAGTGAAGCGGAAAAGCTCAAATTTGAATCTGGCA
GTCCCTGTGGCTGTCCGAGT
TGTAAATAGAGAGAGTGTTCGCCGCGTAGAAGCGTATACAAGCTCTTTGA
ATGAGCCCTCTAAAGAGGT

Or, upload file

Job Title Enter a descriptive title for your BLAST search

Choose Search Set

Database Standard databases (nr etc.) rRNA/ITS databases Genomic + transcript databases Betacoronavirus

Organism

Exclude Models (XM/XP) Uncultured/environmental sample sequences

Limit to Sequences from type material

Entrez Query

Program Selection

Optimize for Highly similar sequences (megablast) More dissimilar sequences (discontiguous megablast) Somewhat similar sequences (blastn)

Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences) Show results in a new window

[+ Algorithm parameters](#)

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Your search is limited to records that include: entrez query: Fungi NOT uncultured

Job Title **Mycena KH028**

RID [GVSBF8GM01R](#) Search expires on 06-31 18:07 pm [Download All](#)

Program **BLASTN** [Citation](#)

Database **nt** [See details](#)

Query ID **lc|Query_131329**

Description **None**

Molecule type **dna**

Query Length **888**

Other reports [Distance tree of results](#) [MSA viewer](#)

Filter Results

Organism only top 20 will appear exclude

[+ Add organism](#)

Percent Identity to E value to Query Coverage to

select all 100 sequences selected

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Pseudohydrosium floccipes voucher BRNM.751633 large subunit ribosomal RNA gene, partial sequence	Pseudohydrosium...	1637	1637	100%	0.0	100.00%	888	OM423635.1
<input checked="" type="checkbox"/> Pseudohydrosium floccipes voucher AMB_18768 large subunit ribosomal RNA gene, partial sequence	Pseudohydrosium...	1434	1434	87%	0.0	100.00%	780	OM423637.1
<input checked="" type="checkbox"/> Pseudohydrosium floccipes voucher BRNM.825631 large subunit ribosomal RNA gene, partial sequence	Pseudohydrosium...	1637	1637	100%	0.0	99.89%	1340	OM423636.1
<input checked="" type="checkbox"/> Hydroosium sp. RV98/43 25S large subunit ribosomal RNA gene, partial sequence	Hydroosium sp. RV...	1496	1496	99%	0.0	97.28%	1134	AF261369.1
<input checked="" type="checkbox"/> Hydroosium sp. strain N.L. Bougher NLB 1550 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA	Hydroosium sp.	1487	1487	99%	0.0	96.94%	2098	MT571690.1
<input checked="" type="checkbox"/> Hydroosium sp. URM 84459 large subunit ribosomal RNA gene, partial sequence	Hydroosium sp. URM...	1421	1421	99%	0.0	95.70%	1258	KC348446.1
<input checked="" type="checkbox"/> Clitocybe ulmicola isolate KUBOT-KRMK-2020-13 large subunit ribosomal RNA gene, partial sequence	Pulverinula ulmic...	1275	1275	94%	0.0	94.17%	837	MW425344.1
<input checked="" type="checkbox"/> Clitocybe ulmicola isolate TFB13871 large subunit ribosomal RNA gene, partial sequence	Pulverinula ulmic...	1343	1343	99%	0.0	94.10%	940	MT237446.1
<input checked="" type="checkbox"/> Porothelium fimbriatum strain FP102067 25S large subunit ribosomal RNA gene, partial sequence	Porothelium fim...	1338	1338	99%	0.0	94.00%	1310	AF261371.1
<input checked="" type="checkbox"/> Porothelium sp. strain G0006 large subunit ribosomal RNA gene, partial sequence	Porothelium sp.	1336	1336	99%	0.0	94.00%	1289	MK278580.1
<input checked="" type="checkbox"/> Porothelium fimbriatum isolate AFTOL-ID1725 25S large subunit ribosomal RNA gene, partial sequence	Porothelium fim...	1332	1332	99%	0.0	93.89%	1798	DQ457673.1
<input checked="" type="checkbox"/> Porothelium panoulium voucher JBSS0131802 large subunit ribosomal RNA gene, partial sequence	Porothelium par...	1304	1304	97%	0.0	93.80%	902	OM423657.1
<input checked="" type="checkbox"/> Porothelium fimbriatum strain HC-10-11/98 C 25S large subunit ribosomal RNA gene, partial sequence	Porothelium fim...	1327	1327	99%	0.0	93.78%	1343	AF261370.1
<input checked="" type="checkbox"/> Porothelium omphaliforme voucher AMB_18842 large subunit ribosomal RNA gene, partial sequence	Porothelium om...	1315	1315	99%	0.0	93.65%	892	OM423650.1
<input checked="" type="checkbox"/> Porothelium omphaliforme voucher AMB_18844 large subunit ribosomal RNA gene, partial sequence	Porothelium om...	1290	1290	97%	0.0	93.55%	896	OM423652.1
<input checked="" type="checkbox"/> Porothelium omphaliforme voucher AMB_18843 large subunit ribosomal RNA gene, partial sequence	Porothelium om...	1290	1290	97%	0.0	93.55%	898	OM423651.1
<input checked="" type="checkbox"/> Porothelium omphaliforme voucher AMB_18850 large subunit ribosomal RNA gene, partial sequence	Porothelium om...	1286	1286	97%	0.0	93.53%	896	OM423656.1
<input checked="" type="checkbox"/> Porothelium omphaliforme voucher WU.18775 large subunit ribosomal RNA gene, partial sequence	Porothelium om...	1291	1291	98%	0.0	93.46%	887	OM423654.1

Example 1

- fresh collection provisionally labelled *Mycena* sp. KH028



BLASTN programs search nucleotide databases using a nucleotide query, more...

Reset page Bookmark

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#)
CCCTAGTAACCTGGGAGTGAAGCGGGAAAAGCTCAAATTTGAAATCTGGCA
GTCCCTGTGGGTGTCGAGT
TGTAAATTTAGAGAAGTGTACCCGCGTAGACCGTATACAAGTCTTTTGA
ATGAGGCGTCATAGAGGSGT

← paste your sequence

Or, upload file Soubor nevybrán [?](#)
Job Title
Enter a descriptive title for your BLAST search [?](#)

← name your search

Choose Search Set

Database Standard databases (nr etc.): rRNA/ITS databases Genomic + transcript databases Betacoronavirus
 [?](#)
Organism exclude [Add organism](#)
Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [?](#)
Exclude Models (XM/XP) Uncultured/environmental sample sequences
Limit to Sequences from type material
Entrez Query [Create custom database](#)
Enter an Entrez query to limit search [?](#)

← limit your search
(e.g. Fungi NOT uncultured)

Program Selection

Optimize for Highly similar sequences (megablast)
 More dissimilar sequences (discontiguous megablast)
 Somewhat similar sequences (blastn)
Choose a BLAST algorithm [?](#)

BLAST

Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)
 Show results in a new window

+ Algorithm parameters

FOLLOW NCBI



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[Save Search](#)

[Search Summary](#) ▾

[How to read this report?](#)

[BLAST Help Videos](#)

[Back to Traditional Results Page](#)

i Your search is limited to records that include: entrez query: Fungi NOT uncultured

name of your search

Job Title	Mycena KH028
RID	GWZSG034016 Search expires on 09-01 05:20 am Download All ▾
Program	BLASTN ? Citation ▾
Database	nt See details ▾
Query ID	Id Query_11119
Description	None
Molecule type	dna
Query Length	887
Other reports	Distance tree of results MSA viewer ?

Filter Results

Organism only top 20 will appear exclude

Type common name, binomial, taxid or group name

[+ Add organism](#)

Percent Identity to **E value** to **Query Coverage** to

[Filter](#) [Reset](#)

Descriptions

[Graphic Summary](#)

[Alignments](#)

[Taxonomy](#)

results of your search

Sequences producing significant alignments

[Download](#) ▾

[Select columns](#) ▾

Show [?](#)

select all 100 sequences selected

[GenBank](#)

[Graphics](#)

[Distance tree of results](#)

[MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Pseudohydropus floccipes voucher BRNM 825631 internal transcribed spacer 1, partial sequence: 5.8S ribosoma... Pseudohydropus...	Pseudohydropus...	1628	1628	100%	0.0	100.00%	887	QM422760.1
<input checked="" type="checkbox"/>	Pseudohydropus floccipes voucher BRNM 751633 internal transcribed spacer 1, partial sequence: 5.8S ribosoma... Pseudohydropus...	Pseudohydropus...	1467	1467	92%	0.0	99.14%	991	QM422759.1
<input checked="" type="checkbox"/>	Pseudohydropus floccipes voucher BRNM 816173 internal transcribed spacer 1, partial sequence: 5.8S ribosoma... Pseudohydropus...	Pseudohydropus...	1363	1363	84%	0.0	99.33%	925	QM422758.1
<input checked="" type="checkbox"/>	Hydropus sp. 'IN02' isolate S.D. Russell MycoMap # 5766 internal transcribed spacer 1, partial sequence: 5.8S ri... Hydropus sp. 'IN02'	Hydropus sp. 'IN02'	1122	1122	85%	0.0	93.37%	954	ON561612.1
<input checked="" type="checkbox"/>	Agaricales sp. voucher Mushroom Observer # 282780 internal transcribed spacer 1, partial sequence: 5.8S ribos... Agaricales sp.	Agaricales sp.	985	1204	86%	0.0	93.09%	898	MK607523.1
<input checked="" type="checkbox"/>	Hydropus sp. 'IN02' isolate S.D. Russell MycoMap # 5369 internal transcribed spacer 1, partial sequence: 5.8S ri... Hydropus sp. 'IN02'	Hydropus sp. 'IN02'	750	908	69%	0.0	92.08%	750	ON561611.1
<input checked="" type="checkbox"/>	Pseudohydropus globosporus voucher BAP 661 (Holotype, SFSU) small subunit ribosomal RNA gene, partial seq... Pseudohydropus...	Pseudohydropus...	481	481	54%	3e-132	84.91%	708	MH414566.1

Results

E value (Expect value)

= number of hits one can expect to see by chance when searching a database of a particular size,

= the smaller E, the match is more significant

Score

= an indication of how good the alignment is; the higher the score, the better the alignment is

Query cover

Percent identity

= (di)similarity of sequences

Descriptions				Graphic Summary	Alignments	Taxonomy			
Sequences producing significant alignments				Download	Select columns	Show	100	?	
<input checked="" type="checkbox"/> select all	100 sequences selected			GenBank	Graphics	Distance tree of results	MSA Viewer		
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Pseudohydropus floccipes voucher BRNM 751633 large subunit ribosomal RNA gene, partial sequence	Pseudohydropus...	1637	1637	100%	0.0	100.00%	888	OM423635.1
<input checked="" type="checkbox"/>	Pseudohydropus floccipes voucher AMB 18768 large subunit ribosomal RNA gene, partial sequence	Pseudohydropus...	1434	1434	87%	0.0	100.00%	780	OM423637.1
<input checked="" type="checkbox"/>	Pseudohydropus floccipes voucher BRNM 825631 large subunit ribosomal RNA gene, partial sequence	Pseudohydropus...	1637	1637	100%	0.0	99.89%	1340	OM423636.1

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

Download

Select columns

Show 100

select all 100 sequences selected

GenBank

Graphics

Distance tree of results

MSA Viewer

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Pseudohydrops floccipes voucher BRNM 825631 internal transcribed spacer 1, partial sequence; 5.8S ribos...	Pseudohydropu...	1628	1628	100%	0.0	100.00%	887	OM422760.1
<input checked="" type="checkbox"/>	Pseudohydrops floccipes voucher BRNM 816173 internal transcribed spacer 1, partial sequence; 5.8S ribos...	Pseudohydropu...	1363	1363	84%	0.0	99.33%	925	OM422758.1
<input checked="" type="checkbox"/>	Pseudohydrops floccipes voucher BRNM 751633 internal transcribed spacer 1, partial sequence; 5.8S ribos...	Pseudohydropu...	1467	1467	92%	0.0	99.14%	991	OM422759.1
<input checked="" type="checkbox"/>	Hemimycena sp. voucher F079668 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene...	Hemimycena sp.	300	300	20%	8e-78	96.67%	626	MW540735.1
<input checked="" type="checkbox"/>	Hydropus sp. 'IN02' isolate S.D. Russell MycoMap # 5766 internal transcribed spacer 1, partial sequence; 5.8...	Hydropus sp. 'IN...	1122	1122	85%	0.0	93.37%	954	ON561612.1
<input checked="" type="checkbox"/>	Agaricales sp. voucher Mushroom Observer # 282780 internal transcribed spacer 1, partial sequence; 5.8S ri...	Agaricales sp.	985	1204	86%	0.0	93.09%	898	MK607523.1
<input checked="" type="checkbox"/>	Hydropus sp. 'IN02' isolate S.D. Russell MycoMap # 5369 internal transcribed spacer 1, partial sequence; 5.8...	Hydropus sp. 'IN...	750	908	69%	0.0	92.08%	750	ON561611.1
<input checked="" type="checkbox"/>	Hydropus funebris voucher PDD:87227 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA...	Hydropus funebris	418	418	41%	2e-113	87.63%	694	JQ694112.1
<input checked="" type="checkbox"/>	Agaricomycetes sp. 2 KM-2017 isolate SA1201E03 internal transcribed spacer 1, partial sequence; 5.8S ribos...	Agaricomycetes ...	442	442	43%	1e-120	87.34%	600	MG018162...
<input checked="" type="checkbox"/>	Tricholomataceae sp. 7-L-4-C-7(M)B.1 18S ribosomal RNA gene, partial sequence; internal transcribed spac...	Tricholomatacea...	300	300	29%	8e-78	87.18%	657	KJ654632.1
<input checked="" type="checkbox"/>	Marasmiaceae sp. KD-2017a isolate KD 16-014 small subunit ribosomal RNA gene, partial sequence; interna...	Marasmiaceae s...	300	393	37%	8e-78	86.83%	678	KY346869.1
<input checked="" type="checkbox"/>	Agaricales sp. voucher Mushroom Observer # 282780 internal transcribed spacer 1, partial sequence; 5.8S ribos...	Agaricales sp.	985	1204	86%	0.0	93.09%	898	MK607523.1
<input checked="" type="checkbox"/>	Hydropus sp. 'IN02' isolate S.D. Russell MycoMap # 5369 internal transcribed spacer 1, partial sequence; 5.8S ri...	Hydropus sp. 'IN02'	750	908	69%	0.0	92.08%	750	ON561611.1
<input checked="" type="checkbox"/>	Pseudohydrops globosporus voucher BAP 661 (Holotype, SFSU) small subunit ribosomal RNA gene, partial seq...	Pseudohydropus ...	481	481	54%	3e-132	84.91%	708	MH414566.1

- three times one name retrieved with Per. identity >99%
- other names with identity <97% (query cover!)
- reliable records?

Nucleotide

Advanced

Search

Help

GenBank

Send to:

Change region shown

Customize view

Analyze this sequence

Run BLAST

Pseudohdropus floccipes voucher BRNM 825631 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

GenBank: OM422760.1

[FASTA](#) [Graphics](#)

Go to:

LOCUS OM422760 887 bp DNA linear PLN 20-MAR-2022
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 ORGANISM [Pseudohdropus floccipes](#)
 Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Porothelaeaceae; Pseudohdropus.
 REFERENCE 1 (bases 1 to 887)
 AUTHORS Consiglio,G., Vizzini,A., Cooper,J., Marchetti,M., Angelini,C., Brugaletta,E. and Setti,L.

VERSION OM422760.1
 KEYWORDS .
 SOURCE Pseudohdropus floccipes
 ORGANISM [Pseudohdropus floccipes](#)
 Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Porothelaeaceae; Pseudohdropus.
 REFERENCE 1 (bases 1 to 887)
 AUTHORS Consiglio,G., Vizzini,A., Cooper,J., Marchetti,M., Angelini,C., Brugaletta,E. and Setti,L.
 TITLE I membri agaricoidi del Genere Porothelium (Porothelaeaceae, Agaricales), Porothelium emend., Porothelaeaceae s. stricto e nuovi Generi per Agaricus floccipes e Mycena subalpina
 JOURNAL Riv Micol 64 (2), 99-190 (2021)
 REFERENCE 2 (bases 1 to 887)
 AUTHORS Consiglio,G., Cooper,J., Angelini,C., Marchetti,M., Brugaletta,E., Campo,E., Setti,L. and Vizzini,A.
 TITLE Direct Submission
 JOURNAL Submitted (25-JAN-2022) submissions, ALVALAB, Dr. Fernando Bongera, Severo Ochoa S1.04, Oviedo 33006, Spain
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 Sequencing Technology :: Sanger dideoxy sequencing
 ##Assembly-Data-END##
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 /db_xref="taxon:2913275"
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 /collection_date="23-Jun-2019"
 /collected_by="H. Sev?ikova"
 /identified_by="H. Sev?ikova"
 misc_RNA
 <1..>887
 /note="contains internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and large subunit ribosomal RNA"
 ORIGIN
 1 ttgcagtgg ttaactggat ggaagttag ctgcttcgta gactggtctg aagcttgagt
 61 aaaaccttgc tttgtgtccc tctcagtcgc aagactggtc tgaagcatca gtaaaactgt
 121 gctttgtgtg tggatctctc gtcgcaagac tggtytggag cttgattaaa acctggctct

- sequence from a specimen in a published study!
- with a voucher!

**I membri agaricoidi del Genere *Porothelium*
(*Porothelaceae*, *Agaricales*),
Porothelium emend., *Porothelaceae* s. stricto
e nuovi Generi per
Agaricus floccipes e *Mycena subalpina***

English version, pages 152 to 179

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*Questi autori hanno contribuito a questo lavoro in egual misura
Autori ai quali inviare la corrispondenza

RIASSUNTO

Analisi morfologiche e molecolari dell'europeo *Marasmius omphaliiformis*, della nordamericana *Clitocybe ulmicola*, dell'indiana *Clitocybula albida*, dell'africano *Hydropus globosporus*, di alcuni taxa non descritti, male interpretati o provvisori, di sequenze ambientali di Asia, Estonia e USA e di sei specie agaricoidi della Nuova Zelanda e della Repubblica Dominicana descritte per la prima volta, dimostrano che essi danno origine a un clado principale assieme al Genere cyphelloide *Porothelium* (*Porothelaceae*), un clado che noi consideriamo rappresenti *Porothelaceae* s. stricto. *Marasmius omphaliiformis*, le tre specie della Repubblica Dominicana e una della Nuova Zelanda sono riconosciuti membri del Genere *Porothelium* malgrado la differente morfologia (forma, habitus) dei loro basidiomi. Di conseguenza, *Porothelium* viene emendato per includere anche taxa agaricoidi. I caratteri principali condivisi da tutte le specie delle *Porothelaceae* s. stricto sono l'habitat lignicolo e la presenza di giunti a fibbia. Elementi metacromatici (trama e/o cistidi) in blu di cresile sono presenti nella maggior parte dei taxa delle *Porothelaceae* s. stricto. Materiale francese di *Porothelium omphaliiforme* viene qui selezionato

99

Materiale studiato: Repubblica Ceca: 24/05/2013, Lanžhot, Cahnov Nature Reserve, bosco alluvionale di pianura con *Quercus*, *Fraxinus angustifolia*, *Populus*, *Carpinus*, su tronco degradato coperto di muschio di *Fraxinus angustifolia*, leg. V. Antonín V. and H. Ševčíková, BRNM 751633; 03/10/2014, Lanžhot, Ranšpurk Nature Reserve, bosco alluvionale di pianura con *Quercus*, *Fraxinus angustifolia*, *Carpinus*, *Acer campestre*, su tronco muschioso vivente di *Fraxinus*, leg. H. Ševčíková, BRNM 766596; 07/06/2019, ibidem, su tronco degradato di *Carpinus*, leg. H. Ševčíková, BRNM 816173; 23/06/2019, Grygov, Království Nature Reserve, bosco alluvionale di pianura con *Quercus*, *Fraxinus*, *Tilia*, *Carpinus*, su tronco degradato coperto di muschio di *Fraxinus*, leg. H. Ševčíková, BRNM 825631. **Italia:** 03/11/2003, Aggìus (Tempio Pausania, SS), in un bosco di *Quer-*

```

VERSION 01422/00.1
KEYWORDS .
SOURCE Pseudohydropus floccipes
ORGANISM Pseudohydropus floccipes
Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
Agaricomycetes; Agaricomycetidae; Agaricales; Porothelaceae;
Pseudohydropus.
REFERENCE 1 (bases 1 to 887)
AUTHORS Consiglio,G., Vizzini,A., Cooper,J., Marchetti,M., Angelini,C.,
Brugaletta,E. and Setti,L.
TITLE I membri agaricoidi del Genere Porothelium (Porothelaceae,
Agaricales), Porothelium emend., Porothelaceae s. stricto e nuovi
Generi per Agaricus floccipes e Mycena subalpina
JOURNAL Riv Micol 64 (2), 99-190 (2021)
REFERENCE 2 (bases 1 to 887)
AUTHORS Consiglio,G., Cooper,J., Angelini,C., Marchetti,M., Brugaletta,E.,
Campo,E., Setti,L. and Vizzini,A.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2022) submissions, ALVALAB, Dr. Fernando Bongera,
Severo Ochoa S1.04, Oviedo 33006, Spain
COMMENT ##Assembly-Data-START##
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##Assembly-Data-END##
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/specimen_voucher="BRNM 825631"
/db_xref="taxon:2913275"
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Carpinus, on decayed moss-covered trunk of Fraxinus"
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/collected_by="H. Ševčíková"
/identified_by="H. Ševčíková"
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subunit ribosomal RNA"
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121 gctttgtgtg tggatctctc gtcgcaagac tggtytggag cttgattaaa acctggtctc

```

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Pseudohydropus floccipes voucher BRNM 825631 internal transcribed spacer 1, partial sequence; 5.8S ribos...	Pseudohydropu...	1628	1628	100%	0.0	100.00%	887	OM422760.1
<input checked="" type="checkbox"/>	Pseudohydropus floccipes voucher BRNM 816173 internal transcribed spacer 1, partial sequence; 5.8S ribos...	Pseudohydropu...	1363	1363	84%	0.0	99.33%	925	OM422758.1
<input checked="" type="checkbox"/>	Pseudohydropus floccipes voucher BRNM 751633 internal transcribed spacer 1, partial sequence; 5.8S ribos...	Pseudohydropu...	1467	1467	92%	0.0	99.14%	991	OM422759.1
<input checked="" type="checkbox"/>	Hemimycena sp. voucher F079668 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene...	Hemimycena sp.	300	300	20%	8e-78	96.67%	626	MW540735.1
<input checked="" type="checkbox"/>	Hydropus sp. 'IN02' isolate S.D. Russell MycoMap # 5766 internal transcribed spacer 1, partial sequence; 5.8...	Hydropus sp. 'IN...	1122	1122	85%	0.0	93.37%	954	ON561612.1
<input checked="" type="checkbox"/>	Agaricales sp. voucher Mushroom Observer # 282780 internal transcribed spacer 1, partial sequence; 5.8S ri...	Agaricales sp.	985	1204	86%	0.0	93.09%	898	MK607523.1
<input checked="" type="checkbox"/>	Hydropus sp. 'IN02' isolate S.D. Russell MycoMap # 5369 internal transcribed spacer 1, partial sequence; 5.8...	Hydropus sp. 'IN...	750	908	69%	0.0	92.08%	750	ON561611.1
<input checked="" type="checkbox"/>	Hydropus funebris voucher PDD:87227 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA...	Hydropus funebris	418	418	41%	2e-113	87.63%	694	JQ694112.1
<input checked="" type="checkbox"/>	Agaricomycetes sp. 2 KM-2017 isolate SA1201E03 internal transcribed spacer 1, partial sequence; 5.8S ribos...	Agaricomycetes ...	442	442	43%	1e-120	87.34%	600	MG018162.1
<input checked="" type="checkbox"/>	Tricholomataceae sp. 7-L-4-C-7(M)B.1 18S ribosomal RNA gene, partial sequence; internal transcribed spac...	Tricholomatacea...	300	300	29%	8e-78	87.18%	657	KJ654632.1
<input checked="" type="checkbox"/>	Marasmiaceae sp. KD-2017a isolate KD 16-014 small subunit ribosomal RNA gene, partial sequence; interna...	Marasmiaceae s...	300	393	37%	8e-78	86.83%	678	KY346869.1
<input checked="" type="checkbox"/>	Agaricales sp. voucher Mushroom Observer # 282780 internal transcribed spacer 1, partial sequence; 5.8S ribos...	Agaricales sp.	985	1204	86%	0.0	93.09%	898	MK607523.1
<input checked="" type="checkbox"/>	Hydropus sp. 'IN02' isolate S.D. Russell MycoMap # 5369 internal transcribed spacer 1, partial sequence; 5.8S ri...	Hydropus sp. 'IN02'	750	908	69%	0.0	92.08%	750	ON561611.1
<input checked="" type="checkbox"/>	Pseudohydropus globosporus voucher BAP 661 (Holotype, SFSU) small subunit ribosomal RNA gene, partial seq...	Pseudohydropus ...	481	481	54%	3e-132	84.91%	708	MH414566.1



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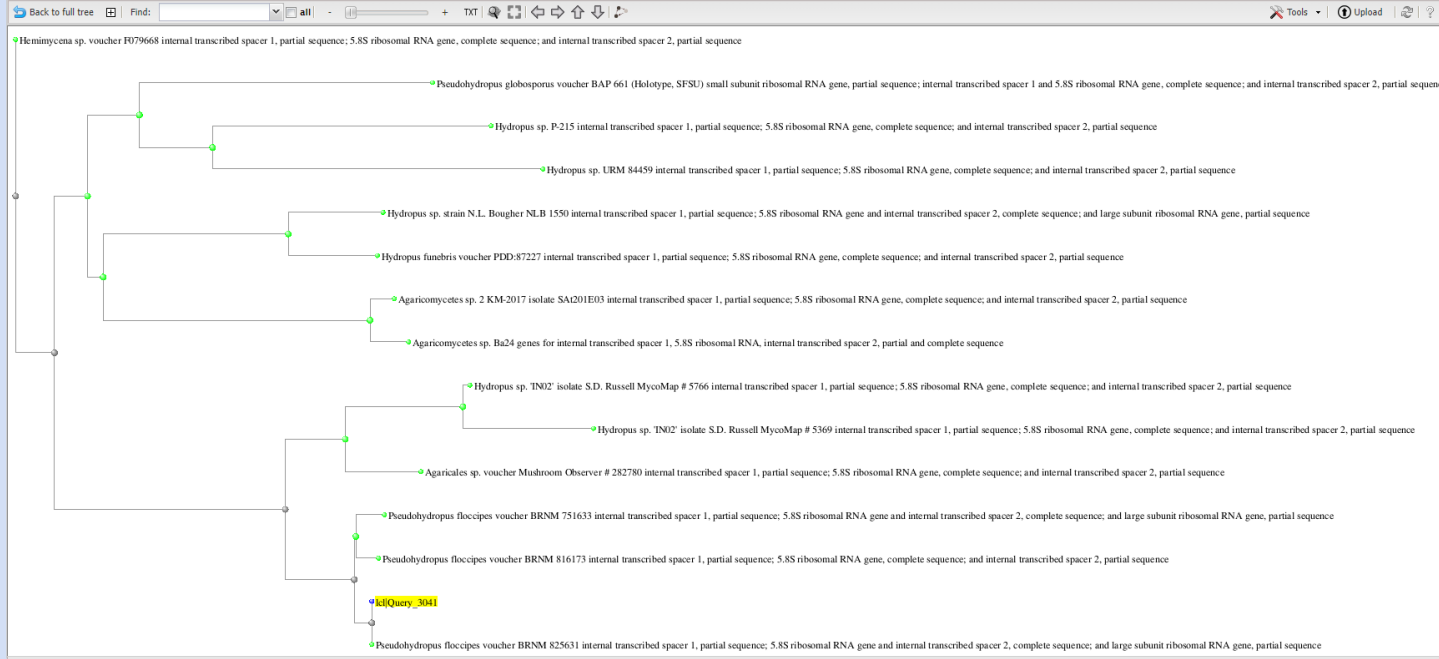
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Query ID: **lc|Query_3041**

Database: **nt**

Tree method: **Fast Minimum Evolution**
Max Seq Difference: **0.75**
Sequence Label: **Sequence Title (if avail.)**

Mouse over an internal node for a subtree or alignment. Click on tree label to select sequence to download



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Label color map

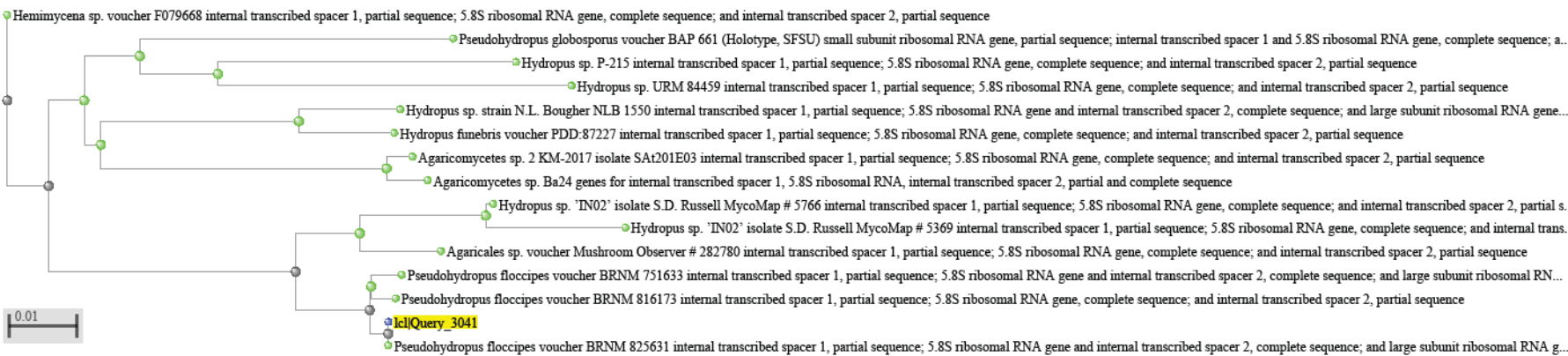
- query
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Blast names color map

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- Ascomycete Fungi
- unknown

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CCCTAGTAACTGCGGAGTGAAGCGGGAAAAGCTCAAATTTGAAATCTGGCA
GTCCCTGTGGCTGTCGAGT
TSTAAATTTAGAGAAGTGTACCCGCGTAGACCGTATACAAGTCCTTTTGA
ATGAGGCGTCATAGAGSGT

Query subrange

From

To

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Resupinatus porosus CFMR PR-5832 ITS region; from TYPE material	Resupinatus por...	281	281	19%	2e-72	96.47%	639	NR_119556.1
<input checked="" type="checkbox"/>	Resupinatus hausknechtii WU 7659 ITS region; from TYPE material	Resupinatus hau...	276	276	19%	1e-70	95.88%	654	NR_158916.1
<input checked="" type="checkbox"/>	Haloaleurodiscus mangrovei TMI 25211 ITS region; from TYPE material	Haloaleurodiscus...	270	270	18%	5e-60	95.81%	706	NR_171202.1
<input checked="" type="checkbox"/>	Haloaleurodiscus mangrovei genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 25S rRNA, partial and complete sequ...	Haloaleurodiscus...	270	270	18%	5e-60	95.81%	706	AB176453.1
<input checked="" type="checkbox"/>	Mycena griseotincta voucher HMJAU43800 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA g...	Mycena griseotin...	281	281	19%	2e-72	95.48%	749	MK309783.1
<input checked="" type="checkbox"/>	Mycena hygrophoroides voucher HMJAU43417 internal transcribed spacer 1, partial sequence; 5.8S ribosomal R...	Mycena hygroph...	281	369	26%	2e-72	95.48%	757	MK309780.1
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<input checked="" type="checkbox"/>	Mycena bicystidiata voucher HMJAU43648 small subunit ribosomal RNA gene, partial sequence; internal transcrib...	Mycena bicystidiata	281	388	27%	2e-72	95.48%	791	MK309773.1
<input checked="" type="checkbox"/>	Mycena bicystidiata HMJAU 43648 ITS region; from TYPE material	Mycena bicystidiata	281	388	27%	2e-72	95.48%	791	NR_173285.1
<input checked="" type="checkbox"/>	Mycena lumina XAL.A. Cortes-Perez 1679 ITS region; from TYPE material	Mycena lumina	268	268	19%	2e-68	95.29%	698	NR_163298.1
<input checked="" type="checkbox"/>	Mycena lumina voucher ACP1679 small subunit ribosomal RNA gene, partial sequence; internal transcribed spac...	Mycena lumina	268	268	19%	2e-68	95.29%	698	MG926687.1
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<input checked="" type="checkbox"/>	Mycena pasvikensis voucher O-F-76005 sequence	Mycena pasviken...	268	268	19%	2e-68	95.29%	671	MT216241.1
<input checked="" type="checkbox"/>	Pseudomarasmius efibulatus isolate TFB7070 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RN...	Pseudomarasmi...	279	279	20%	9e-72	94.94%	693	MK268234.1
<input checked="" type="checkbox"/>	Marasmiellus celebanticus TO HG2281 ITS region; from TYPE material	Marasmiellus cel...	279	382	27%	9e-72	94.94%	792	NR_154152.1
<input checked="" type="checkbox"/>	Marasmiellus celebanticus voucher TO HG2281 18S ribosomal RNA gene, partial sequence; internal transcribed s...	Marasmiellus cel...	279	382	27%	9e-72	94.94%	792	JF460781.1

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Resupinatus porosus CFMR PR-5832 ITS region; from TYPE material	Resupinatus por...	281	281	19%	2e-72	96.47%	639	NR_119556.1
<input checked="" type="checkbox"/>	Resupinatus hausknechtii WU 7659 ITS region; from TYPE material	Resupinatus hau...	276	276	19%	1e-70	95.88%	654	NR_158916.1
<input checked="" type="checkbox"/>	Haloaleurodiscus mangrovei TMI 25211 ITS region; from TYPE material	Haloaleurodiscus...	270	270	18%	5e-69	95.81%	706	NR_171202.1
<input checked="" type="checkbox"/>	Haloaleurodiscus mangrovei genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 25S rRNA, partial and complete sequ...	Haloaleurodiscus...	270	270	18%	5e-69	95.81%	706	AB176453.1
<input checked="" type="checkbox"/>	Mycena griseotincta voucher HMJAU43800 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA g...	Mycena griseotin...	281	281	19%	2e-72	95.48%	749	MK309783.1
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<input checked="" type="checkbox"/>	Mycena miscanthi voucher HMJAU43584 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA ge...	Mycena miscanthi	281	281	19%	2e-72	95.48%	762	MK309779.1
<input checked="" type="checkbox"/>	Mycena bicystidiata voucher HMJAU43648 small subunit ribosomal RNA gene, partial sequence; internal transcrib...	Mycena bicystidiata	281	388	27%	2e-72	95.48%	791	MK309773.1
<input checked="" type="checkbox"/>	Mycena bicystidiata HMJAU 43648 ITS region; from TYPE material	Mycena bicystidiata	281	388	27%	2e-72	95.48%	791	NR_173285.1
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<input checked="" type="checkbox"/>	Mycena lumina voucher ACP1679 small subunit ribosomal RNA gene, partial sequence; internal transcribed spac...	Mycena lumina	268	268	19%	2e-68	95.29%	698	MG926687.1
<input checked="" type="checkbox"/>	Mycena nivicola voucher SFSU:DED 5075 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA g...	Mycena nivicola	268	268	19%	2e-68	95.29%	457	KX513843.1
<input checked="" type="checkbox"/>	Mycena pasvikensis voucher O-F-76005 sequence	Mycena pasviken...	268	268	19%	2e-68	95.29%	671	MT216241.1
<input checked="" type="checkbox"/>	Pseudomarasmius efibulatus isolate TFB7070 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RN...	Pseudomarasmi...	279	279	20%	9e-72	94.94%	693	MK268234.1
<input checked="" type="checkbox"/>	Marasmiellus celebanticus TO HG2281 ITS region; from TYPE material	Marasmiellus cel...	279	382	27%	9e-72	94.94%	792	NR_154152.1
<input checked="" type="checkbox"/>	Marasmiellus celebanticus voucher TO HG2281 18S ribosomal RNA gene, partial sequence; internal transcribed s...	Marasmiellus cel...	279	382	27%	9e-72	94.94%	792	JF460781.1

Blast Tree View

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BLAST RID: **GW5V6XHQ13**

Query ID: **lc|Query_3041**

Database: **nt**

Tree method: **Fast Minimum Evolution**
Max Seq Difference: **0.75**
Sequence Label: **Sequence Title (if avail.)**

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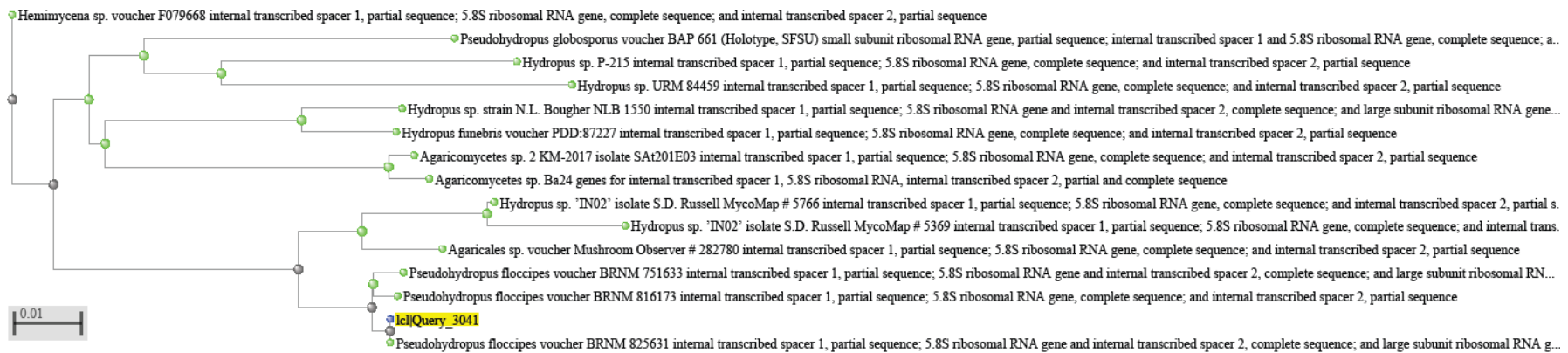
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from type material

Blast names color map
Basidiomycete Fungi
Ascomycete Fungi
unknown



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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Pseudohydrops floccipes voucher BRNM 825631 internal transcribed spacer 1, partial sequence: 5.8S ribosoma...	Pseudohydrops...	1628	1628	100%	0.0	100.00%	887	OM422760.1
<input checked="" type="checkbox"/>	Pseudohydrops floccipes voucher BRNM 751633 internal transcribed spacer 1, partial sequence: 5.8S ribosoma...	Pseudohydrops...	1467	1467	92%	0.0	99.14%	991	OM422759.1
<input checked="" type="checkbox"/>	Pseudohydrops floccipes voucher BRNM 816173 internal transcribed spacer 1, partial sequence: 5.8S ribosoma...	Pseudohydrops...	1363	1363	84%	0.0	99.33%	925	OM422758.1
<input type="checkbox"/>	Agaricales sp. voucher Mushroom Observer # 282780 internal transcribed spacer 1, partial sequence: 5.8S ribos...	Agaricales sp.	985	1204	86%	0.0	93.09%	898	MK607523.1
<input checked="" type="checkbox"/>	Pseudohydrops globosporus voucher BAP 661 (Holotype, SFSU) small subunit ribosomal RNA gene, partial seq...	Pseudohydrops...	481	481	54%	2e-132	84.91%	708	MH414566.1
<input type="checkbox"/>	Hydropus sp. P-215 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA gene, complete sequen...	Hydropus sp. P...	468	468	48%	2e-128	86.47%	624	KR135357.1
<input type="checkbox"/>	Agaricomycetes sp. 2 KM-2017 isolate SAI201E03 internal transcribed spacer 1, partial sequence: 5.8S ribosom...	Agaricomycetes ...	442	442	43%	1e-120	87.34%	600	MG018162.1
<input type="checkbox"/>	Hydropus sp. URM 84459 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA gene, complete s...	Hydropus sp. UR...	435	435	52%	2e-118	83.30%	527	KC348452.1
<input type="checkbox"/>	Hydropus sp. strain N.L. Bougher NLB 1550 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA...	Hydropus sp.	429	657	62%	9e-117	85.35%	2098	MT571660.1
<input checked="" type="checkbox"/>	Hydropus funebris voucher PDD:87227 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA gen...	Hydropus funebris	418	418	41%	2e-113	87.63%	694	JQ694112.1
<input type="checkbox"/>	Tricholomataceae sp. 29 YS-2010 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA gene, co...	Tricholomatacea...	337	337	45%	6e-89	82.16%	584	HM007087.1
<input type="checkbox"/>	Trogia aff. furcata voucher SFSU:DED 8260 small subunit ribosomal RNA gene, partial sequence: internal transcr...	Trogia aff. furcata	335	335	45%	2e-88	81.95%	670	MF100962.1
<input checked="" type="checkbox"/>	Clitocybe ulmicola isolate TFB13871 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA gene, c...	Pulverulina ulmic...	333	333	45%	7e-88	82.08%	616	MT237476.1
<input checked="" type="checkbox"/>	Clitocybe ulmicola isolate KUBOT-KRMK-2020-13 internal transcribed spacer 1, partial sequence: 5.8S ribosomal...	Pulverulina ulmic...	333	417	51%	7e-88	82.08%	668	MW425325.1
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<input checked="" type="checkbox"/>	Porothelium fimbriatum voucher CLZhao 1145 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribo...	Porothelium fim...	329	421	48%	9e-87	83.33%	659	MG231800.1
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<input type="checkbox"/>	Marasmiellus sp. voucher FLAS-F-68717 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA ge...	Marasmiellus sp.	327	327	40%	3e-86	83.16%	449	OM672927.1
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<input type="checkbox"/>	Agaricales sp. isolate TU10 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA gene, complete...	Agaricales sp.	326	326	41%	1e-85	82.99%	574	MN537673.1
<input type="checkbox"/>	Agaricales sp. isolate TU09 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA gene, complete...	Agaricales sp.	326	326	41%	1e-85	82.99%	574	MN537672.1
<input type="checkbox"/>	Agaricales sp. isolate TU06 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA gene, complete...	Agaricales sp.	326	326	41%	1e-85	82.99%	567	MN537669.1
<input type="checkbox"/>	Agaricales sp. isolate MD71 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA gene, complete...	Agaricales sp.	326	326	41%	1e-85	82.99%	567	MN537654.1



- [Agaricales sp. isolate lv](#)
- [Agaricales sp. isolate lv](#)
- [Porothelium fimbriatum](#)
- [Tricholomataceae sp. is](#)
- [Trichocomaceae sp. isr](#)
- [Sidera vulgaris culture i](#)
- [Porothelium omphaliif](#)
- [Porothelium omphaliif](#)

Descriptions
Graphic Summary
Alignments
Taxonomy

Sequences producing significant alignments

select all 11 sequences selected

	Description	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Pseudohydrops floccipes voucher BRNM 825631 internal transcribed spacer 1, partial sequence: 5.8S ribosoma...	100%	0.0	100.00%	887	OM422760.1
<input checked="" type="checkbox"/>	Pseudohydrops floccipes voucher BRNM 751633 internal transcribed spacer 1, partial sequence: 5.8S ribosoma...	92%	0.0	99.14%	991	OM422759.1
<input checked="" type="checkbox"/>	Pseudohydrops floccipes voucher BRNM 816173 internal transcribed spacer 1, partial sequence: 5.8S ribosoma...	84%	0.0	99.33%	925	OM422758.1
<input type="checkbox"/>	Agaricales sp. voucher Mushroom Observer # 282780 internal transcribed spacer 1, partial sequence: 5.8S ribos...	86%	0.0	93.09%	898	MK607523.1
<input checked="" type="checkbox"/>	Pseudohydrops globosporus voucher BAP 661 (Holotype, SFSU) small subunit ribosomal RNA gene, partial seq...	54%	2e-132	84.91%	708	MH414566.1
<input type="checkbox"/>	Hydropus sp. P-215 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA gene, complete sequen...	48%	2e-128	86.47%	624	KR135357.1
<input type="checkbox"/>	Agaricomycetes sp. 2 KM-2017 isolate SAI201E03 internal transcribed spacer 1, partial sequence: 5.8S ribosom...	43%	1e-120	87.34%	600	MG018162.1
<input type="checkbox"/>	Hydropus sp. URM 84459 internal transcribed spacer 1, partial sequence: 5.8S ribosomal RNA gene, complete s...	52%	2e-118	83.30%	527	KC348452.1

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GenBank (complete sequence)
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Descriptions Table (CSV)
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ASN.1



>OM422760.1 *Pseudohydropus floccipes* voucher BRNM 825631
internal transcribed spacer 1, partial sequence; 5.8S
ribosomal RNA gene and internal transcribed spacer 2,
complete sequence; and large subunit ribosomal RNA gene,
partial sequence

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AAAACCTTGCTTTGTGTCCC...



>OM422760_*Pseudohydropus floccipes*_BRNM825631

TTGCAGTTGGTTAACTGGATGGAAGTTTAGCTCGTTCGTAGACTGGTCTGAAGCTTGAGT
AAAACCTTGCTTTGTGTCCC...

>OM422760_Pseudohydropus_floccipes_BRNM825631

TTGCAGTTGGTTAACTGGATGGAAGTTTAGCTCGTTCGTAGACTGGTCTGAAGCTTGAGT
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>Pseudohydropus_floccipes_KH028

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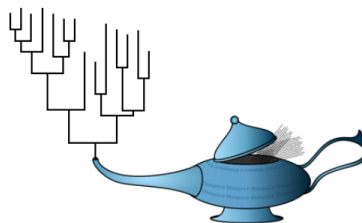
CATTACTGAAAGATAGATGGGATTGATGCTGGCTCTTGACTGAGTACGTGCTCGTCCTAT
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>OM422758_Pseudohydropus_floccipes_BRNM816173

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CGTTTTTCTATCTACCCACTGTGCACCTTTTGTAGGCTCTATGATACTTCTCAGTCGATG
CAGTAATCACTGGCAGCGCACAATGGTCACTAGTTGTCCA...

...

Phylogeny.fr Robust Phylogenetic Analysis For The Non-Specialist



If you use results from this site for publication, as I am managing it alone since years, could you please add this to the acknowledgments section (and [let me know](#)):
Sebastien Santini (CNRS/AMU IGS UMR7256) and the PACA Bioinfo platform for the availability and management of the phylogeny.fr website used to

Moreover, please cite:
[Dereeper A.*, Guignon V.*, Blanc G., Audic S., Buffet S., Chevenet F., Dufayard J.F., Guindon S., Lefort V., Lescot M., Claverie J.M., Gascuel O. *Phylogeny.fr: robust phylogenetic analysis for the non-specialist*. *Nucleic Acids Res.* 2008 Jul 1;36\(Web Server issue\):W465-9. Epub 2008 Apr 19. \(PubMed\)](#) * joint first authors

And if you use blast-explorer:
[Dereeper A., Audic S., Claverie J.M., Blanc G. *BLAST-EXPLORER helps you building datasets for phylogenetic analysis*. *BMC Evol Biol.* 2010 Jan 12;10:8. \(PubMed\)](#)

=====[Mirror site](#)=====

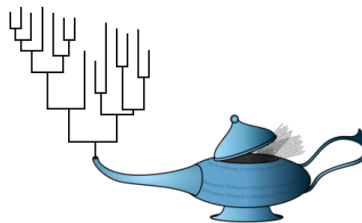
Phylogeny.fr is a free, simple to use web service dedicated to reconstructing and analysing phylogenetic relationships between molecular sequences.
Phylogeny.fr runs and connects various bioinformatics programs to reconstruct a **robust phylogenetic tree from a set of sequences**.

Regarding the constantly growing number of users and the limited space on our server, results will not be conserved for more than one week and ser accounts have been disabled. Moreover, jobs that generate more than 100 Mo of data, will be killed and deleted without notification.

http://phylogeny.lirmm.fr/phylo_cgi/index.cgi

Phylogeny.fr

Robust Phylogenetic Analysis For The Non-Specialist



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Methodes et Algorithmes pour la Bio-informatique LIRMM

Information Genomique et Structurale

Home Phylogeny Analysis Blast Explorer Online Programs Your Workspace Documentation Downloads Contacts



1. Workflow Setup

Workflow Settings

Name of the analysis (optional):

Choose processing steps to run:

- Multiple Alignment: **MUSCLE**
- Alignment curation: **Gblocks**
- Construction of phylogenetic tree: **PhyML**
- Visualisation of phylogenetic tree: **TreeDyn**



Run workflow:

- all at once
- step by step

[Create workflow](#)



Input Data

Upload your set of sequences in FASTA, EMBL or NEXUS format from a file:

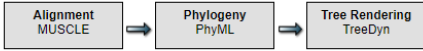
Or paste it here [load example of sequences](#)

Maximum number of sequences is 200 for proteins and 200 for nucleic acids.
Maximum length of sequences is 2000 for proteins and 6000 for nucleic acids.

Alignment: MUSCLE

[► Advanced Settings...](#)

Advanced Mode



- 1. Overview
- 2. Data & Settings
- 3. Alignment
- 4. Phylogeny
- 5. Tree Rendering

Tree Rendering results

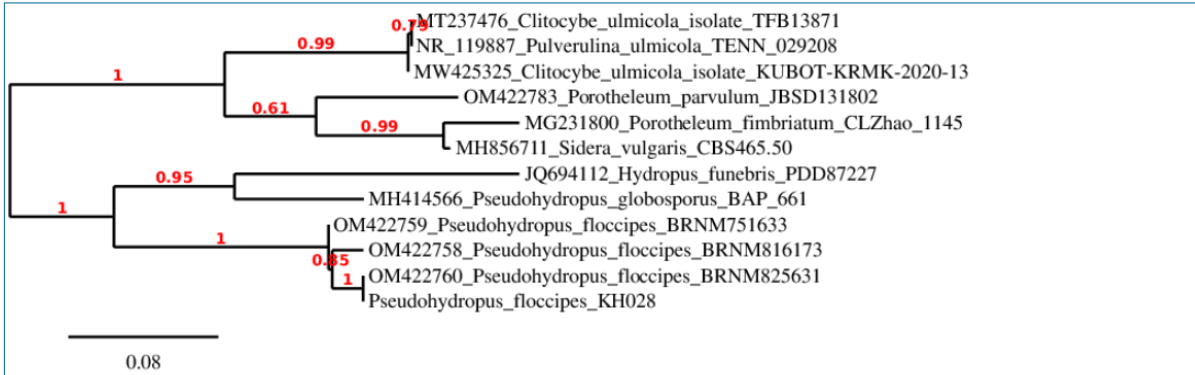


Figure 1: Phylogenetic tree.

==> Download the tree: PNG - PDF - SVG - TGF (TreeDyn format) - Newick - Text

Select an action:

- Reset (cancel all changes)
- Mid-point rooting
- Use Genbank information to automatically rename leaves by: species and gi species only colorize
- Collapse branches having branch support value smaller than % or a number of bootstraps smaller than

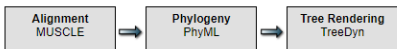
Select an action and click leaf or internal branch:

- Colorize leaf branch choose a color and a legend label
- Reroot (outgroup)
- Flip (flip an entire tree at a node)
- Swap (flip two branches at a node)
- Change leaf name
- Add leaf annotations color

Display:

- Branch support values Branch lengths None color:
- Display branch support values in %

Advanced Mode



- 1. Overview
- 2. Data & Settings
- 3. Alignment
- 4. Phylogeny
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Tree Rendering results

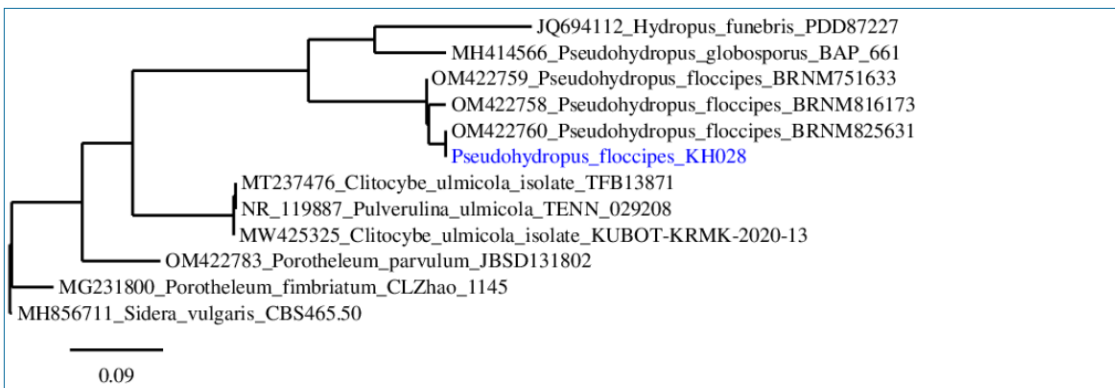


Figure 1: Phylogenetic tree.

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Select an action:

- Reset (cancel all changes)
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Select an action and click leaf or internal branch:

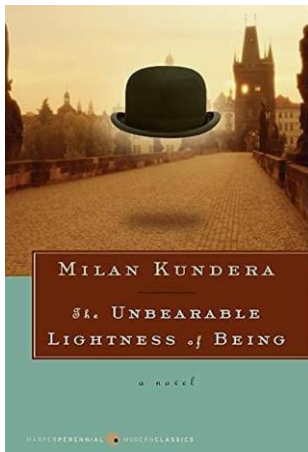
- Colorize leaf branch choose a color and a legend label
- Reroot (outgroup)
- Flip (flip an entire tree at a node)
- Swap (flip two branches at a node)
- Change leaf name
- Add leaf annotations color

Display:

- Branch support values Branch lengths None color:
- Display branch support values in %
- Display legend

Do not forget!



- results of BLAST are based on algorithm, check metadata/literature for additional information
- the interpretation is yours
- do not forget the phenotype data



Fungal Diversity
<https://doi.org/10.1007/s13225-019-00428-3>



The unbearable lightness of sequenced-based identification

Valérie Hofstetter¹  · Bart Buyck²  · Guillaume Eyssartier³ · Sylvain Schnee¹ · Katia Gindro²

Received: 20 February 2019 / Accepted: 8 May 2019
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Examples for you

- download file **Test_fasta_and_form.txt** from the webpage of the course
- try to identify the three collections of *Mycena* with the ITS rDNA sequences
- submit the most probable name(s) and your explanation (optional), why you decided for that based on the BLAST search(es)