



Is a new species description science or data release?

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my MEM lab team



Significance of new species publishing

Fungal Diversity (2021) 109:155–179
<https://doi.org/10.1007/s13225-021-00486-6>

REVIEW



Integrative approaches for species delimitation in Ascomycota

Sajeewa S. N. Maharachchikumbura^{1,2} · Yanpeng Chen¹ · Hiran A. Ariyawansa³ · Kevin D. Hyde⁴ · Danny Haelewaters^{5,6} · Rekhan H. Perera⁴ · Milan C. Samarakoon⁴ · Dhanushka N. Wanasinghe⁷ · Danilo E. Bustamante^{8,9} · Jian-Kui Liu¹ · Daniel P. Lawrence¹⁰ · Ratchadawan Cheewangkoon² · Marc Stadler^{11,12}

„Biodiversity loss from disturbances caused by human activities means that species are disappearing at an ever increasing rate. The high number of species that have yet to be described have generated extreme crisis to the taxonomist. Therefore, more than in any other era, effective ways to discover and delimitate species are needed.“

Integrative approaches are crucial for understanding species boundaries within Ascomycota.

Fungal Diversity (2022) 116:547–614
<https://doi.org/10.1007/s13225-022-00510-3>

REVIEW



Ten decadal advances in fungal biology leading towards human well-being

Ausana Mapook¹ · Kevin D. Hyde^{1,2,17,19,20,23} · Khadija Hassan³ · Blondelle Matio Kemkuignou³ · Adéla Čmoková⁵ · Frank Surup^{3,4} · Eric Kuhnert⁶ · Pathompong Paomephan^{3,7} · Tian Cheng^{3,5} · Sybren de Hoog^{8,9,10} · Yinggai Song¹¹ · Ruvishika S. Jayawardena^{1,2} · Abdullah M. S. Al-Hatmi^{8,12} · Tokameh Mahmoudi¹³ · Nadia Ponts¹⁴ · Lena Studt-Reinhold¹⁵ · Florence Richard-Forget¹⁴ · K. W. Thilini Chethana^{1,2} · Dulanjalee L. Harishchandra^{1,2,16} · Peter E. Mortimer^{17,18} · Huili Li^{17,18} · Saisamorm Lumyong^{19,20,21} · Worawoot Aiduang²⁰ · Jaturong Kumla^{19,20} · Nakarin Suwannarach^{19,20} · Chitrabhanu S. Bhunjun^{1,2} · Feng-Ming Yu^{1,2,22} · Qi Zhao²² · Doug Schaefer¹⁸ · Marc Stadler^{3,4}

Fungi are important as a potential industrial resource and for human well-being.

Fungal diversity and new species description trends

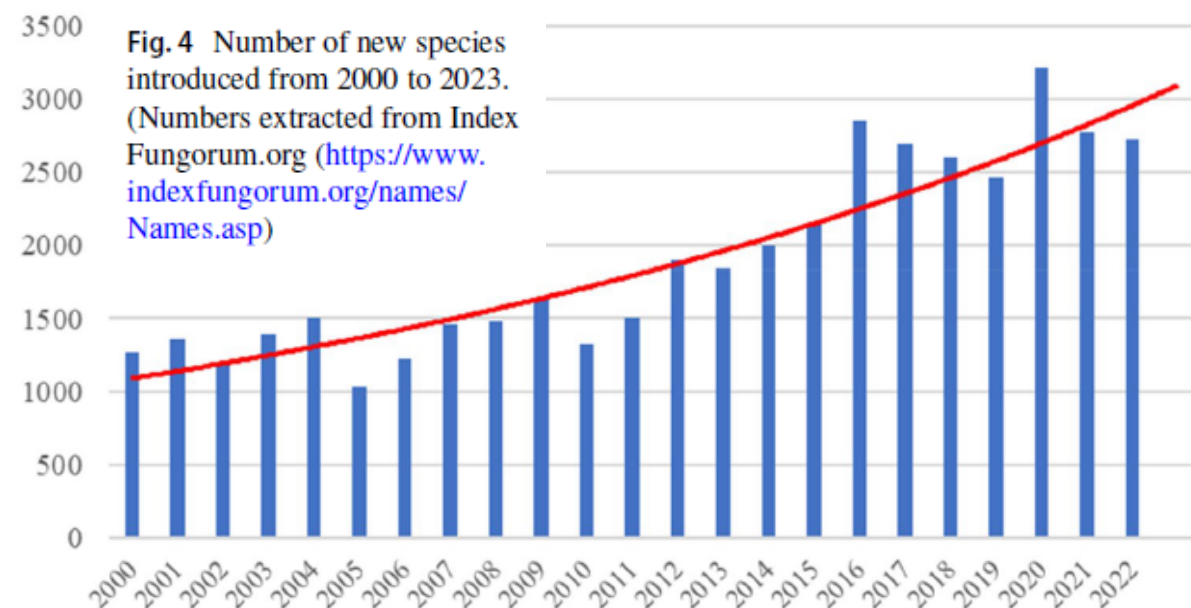
Fungal Diversity (2024) 125:1–71
<https://doi.org/10.1007/s13225-023-00532-5>



Current trends, limitations and future research in the fungi?

Kevin D. Hyde^{1,2,3,4,5} · Petr Baldrian⁶ · Yanpeng Chen⁷ · K. W. Thilini Chethana^{2,8} · Sybren De Hoog⁹ · Mingkwan Doilom⁴ · Antonio R. Gomes de Farias² · Micael F. M. Gonçalves^{10,11} · Didsanutda Gonkhom^{2,8} · Heng Guj^{1,12} · Sandra Hilário^{10,13} · Yuwei Hu^{1,12} · Ruvishika S. Jayawardena^{2,8,14} · Sabin Khyaju^{2,8} · Paul M. Kirk¹⁵ · Petr Kohout⁶ · Thatsanee Luangharn² · Sajeewa S. N. Maharachchikumbura^{7,16} · Ishara S. Manawasinghe^{4,5} · Peter E. Mortimer^{1,12} · Allen Grace T. Niego¹⁷ · Monthien Phonemany^{2,8} · Birthe Sandargo^{18,19} · Indunil C. Senanayake^{4,20} · Marc Stadler^{18,19} · Frank Surup^{18,19} · Naritsada Thongklang^{2,8} · Dhanushka N. Wanasinghe^{1,12} · Ali H. Bahkali³ · Arttapon Walker^{2,8}

Species Numbers



Fungal Diversity (2024) 128:191–225
<https://doi.org/10.1007/s13225-024-00545-8>

REVIEW



Fungal numbers: global needs for a realistic assessment

Kevin D. Hyde^{1,2,3} · Alwasel Saleh⁴ · Herbert Dustin R. Aumentado^{2,5} · Teun Boekhout^{4,13} · Ishika Bera² · Sabin Khyaju^{2,5} · Chitrabhanu S. Bhunjun^{2,5} · K. W. Thilini Chethana^{2,5} · Chayanard Phukhamsakda² · Mingkwan Doilom⁶ · Vinodhini Thiyagaraja¹ · Peter E. Mortimer^{7,14,15} · Sajeewa S. N. Maharachchikumbura⁸ · Sinang Hongsan⁹ · Ruvishika S. Jayawardena^{2,5} · Wei Dong⁶ · Rajesh Jeewon^{10,11} · Fatimah Al-Otibi³ · Subodini N. Wijesinghe^{2,5} · Dhanushka N. Wanasinghe^{7,12}

Estimates for global fungal species richness range from 2.2 to 13.2 million.



MYCOSPHERE 15(1): 5146–6239 (2024)
Doi 10.5943/mycosphere/15/1/25

www.mycosphere.org

ISSN 2077 7019

ARTICLE

The 2024 Outline of *Fungi* and fungus-like taxa

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Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand
Innovative Institute for Plant Health, College of Agriculture and Biology, Zhongkai University of Agriculture and Engineering, Guangzhou 510225, Guangdong, P.R. China

Fungal estimates for individual higher rank fungal taxa and specifically for *icertae sedis* are provided.

Standards

Aime et al. *IMA Fungus* (2021) 12:11
<https://doi.org/10.1186/s43008-021-00063-1>



IMA Fungus

NOMENCLATURE

Open Access

How to publish a new fungal species, or name, version 3.0



M. Catherine Aime^{1*}, Andrew N. Miller², Takayuki Aoki³, Konstanze Bensch⁴, Lei Cai⁵, Pedro W. Crous⁴, David L. Hawksworth^{6,7,8}, Kevin D. Hyde⁹, Paul M. Kirk¹⁰, Robert Lücking¹¹, Tom W. May¹², Elaine Malosso¹³, Scott A. Redhead¹⁴, Amy Y. Rossman¹⁵, Marc Stadler¹⁶, Marco Thines^{17,18}, Andrey M. Yurkov¹⁹, Ning Zhang²⁰ and Conrad L. Schoch²¹

Minimal requirements and recommendations for good practices.

Fungal Diversity (2021) 109:181–237
<https://doi.org/10.1007/s13225-021-00479-5>

REVIEW



Delimiting species in Basidiomycota: a review

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Mycological Progress (2022) 21: 40
<https://doi.org/10.1007/s11557-022-01796-y>



ORIGINAL ARTICLE



How good are we at describing a new fungal species? A case study based on the family *Botryosphaeriaceae* (*Dothideomycetes*)

Eduardo Batista¹ · Anabela Lopes¹ · Artur Alves¹

Received: 27 September 2021 / Revised: 3 December 2021 / Accepted: 6 December 2021 / Published online: 4 April 2022
© German Mycological Society and Springer-Verlag GmbH Germany, part of Springer Nature 2022

In *Botryosphaeriaceae*, 60% of the descriptions are outdated or only meet the minimal requirements for publication and 50% of the authors do not provide enough accessible and reproducible information.

Recommended application of integrative taxonomy combining group specific approach.

Singletons

WHEN SHOULD WE DESCRIBE SPECIES?

Two intense debates are underway in fungal taxonomy, one more public than the other, with little consideration that one debate may inform the other. The more public debate, which continues in this issue of *IMA Fungus* (see p. 213), concerns possible mechanisms for typification of, and the attendant wisdom of accepting, DNA-only species. The quieter debate, occurring more among editors, often to the frustration of authors of rejected papers, concerns the acceptability of papers

taxonomy. My question is whether this process actually discovers new species, or simply indicates that there are new species to be found? In modern ecology, when you have a substrate in your hand that contains DNA sequences of a thousand species, half of them unknown, have you discovered 500 new species or have you picked up a handful of dirt?

In conventional taxonomy, a specimen in hand allows measurement and descriptions of characters and character states,



EDITORIAL

Species discovery vs. new species descriptions

IMA Fungus 2017, Keith A. Seifert 2017

Cazabonne et al. *IMA Fungus* (2024) 15:7
<https://doi.org/10.1186/s43008-023-00137-2>



IMA Fungus

MYCOLENS

Open Access

Singleton-based species names and fungal rarity: Does the number really matter?



Jonathan Cazabonne^{1,2*}, Allison K. Walker³, Jonathan Lesven^{4,5} and Danny Haelewaters^{6,7,8,9*} 

„If multiple independent sources of data support the existence of a new taxon, we encourage mycologists to proceed with formal description, irrespective of the number of specimens at hand. Although the description of singleton-based species may not be considered best practice, it does represent responsible science in the light of closing the Linnean biodiversity shortfall.“

Old names

Koukol and Delgado *IMA Fungus* (2021) 12:26
<https://doi.org/10.1186/s43008-021-00073-z>



NOMENCLATURE

Open Access

Why morphology matters: the negative consequences of hasty descriptions of putative novelties in asexual ascomycetes

Ondřej Koukol^{1*} and Gregorio Delgado²

Overlooking of old names when publishing new species due to relying strictly on sequence data

IMA Fungus



Mycosphere 7 (11): 1622–1648 (2016) www.mycosphere.org ISSN 2077 7019

Article – special issue

Doi 10.5943/mycosphe/7/11/2

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Taxonomic utility of old names in current fungal classification and nomenclature: Conflicts, confusion & clarifications

Dayarathne MC^{1,2}, Boonmee S^{1,2}, Braun U⁷, Crous PW⁸, Daranagama DA¹, Dissanayake AJ^{1,6}, Ekanayaka H^{1,2}, Jayawardena R^{1,6}, Jones EBG¹⁰, Maharachchikumbura SSN⁵, Perera RH¹, Phillips AJL⁹, Stadler M¹¹, Thambugala KM^{1,3}, Wanasinghe DN^{1,2}, Zhao Q^{1,2}, Hyde KD^{1,2}, Jeewon R^{12*}

Old names in current fungal classification and nomenclature: difficulties in loaning specimens and lack of expertise from specialist mycologists

Highlights

Yurkov et al. *IMA Fungus* (2021) 12:18
<https://doi.org/10.1186/s43008-021-00067-x>



IMA Fungus

NOMENCLATURE

Open Access

Nomenclatural issues concerning cultured yeasts and other fungi: why it is important to avoid unneeded name changes



Andrey Yurkov^{1*}, Artur Alves², Feng-Yan Bai³, Kyria Boundy-Mills⁴, Pietro Buzzini⁵, Neža Čadež⁶, Gianluigi Cardinali⁷, Serge Casaregola⁸, Vishnu Chaturvedi⁹, Valérie Collin¹⁰, Jack W. Fell¹¹, Victoria Girard¹⁰, Marizeth Groenewald¹², Ferry Hagen¹², Chris Todd Hittinger¹³, Aleksey V. Kachalkin^{14,15}, Markus Kostrzewa¹⁶, Vassili Kouvelis¹⁷, Diego Libkind¹⁸, Xinzhan Liu³, Thomas Maier¹⁶, Wieland Meyer^{19,20,21,22}, Gábor Péter²³, Marcin Piątek²⁴, Vincent Robert¹², Carlos A. Rosa²⁵, Jose Paulo Sampaio^{26,27}, Matthias Sipiczki²⁸, Marc Stadler²⁹, Takashi Sugita³⁰, Junta Sugiyama^{31,32}, Hiroshi Takagi³³, Masako Takashima³⁴, Benedetta Turchetti⁵, Qi-Ming Wang^{3,35} and Teun Boekhout^{12,36}

Importance of nomenclatural stability for communicating scientific finds

PLOS BIOLOGY

ESSAY

Tightening the requirements for species diagnoses would help integrate DNA-based descriptions in taxonomic practice

Frank E. Rheindt^{1*}, Patrice Bouchard², Richard L. Pyle³, Francisco Welter-Schultes⁴, Erna Aesch⁵, Shane T. Ahyong^{6,7}, Alberto Ballerio⁸, Thierry Bourgoin⁹, Luis M. P. Ceriaco¹⁰, Dmitry Dmitriev¹¹, Neal Evenhuis³, Mark J. Grygier¹², Mark S. Harvey¹³, Maurice Kottelat¹⁴, Nikita Kluge¹⁵, Frank-T. Krell¹⁶, Jun-ichi Kojima¹⁷, Sven O. Kullander¹⁸, Paulo Lucinda¹⁹, Christopher H. C. Lyal²⁰, Cristina Luisa Scioscia²¹, Daniel Whitmore²², Douglas Yanega²³, Zhi-Qiang Zhang^{24,25}, Hong-Zhang Zhou²⁶, Thomas Pape^{27*}

contrastive and state specific diagnosis

Contrastive diagnoses

A contrastive diagnosis presents distinguishing characters or character states in direct comparison to at least one other species, for example:

...Diagnosis: New Species X differs in leg colour from Species Y...

State-specific diagnoses

A state-specific diagnosis is one in which an author not only presents a distinguishing character but also specifies its character state. For example:

...Diagnosis: The new species has green legs...

Species concepts

Species concept based on integrated (polyphasic) approach is recommended, with good practice task list and group specific recommendations.

Combining

- phylogenetic (sequence or genome) component
- phenotype (morphological) component
- biological (reproductive) component

Sequence-based species concepts require publicly available and validated references

Fungal Diversity (2021) 109:27–55
<https://doi.org/10.1007/s13225-021-00475-9>

REVIEW



The evolving species concepts used for yeasts: from phenotypes and genomes to speciation networks

Teun Boekhout^{1,2} · M. Catherine Almeida³ · Dominik Begerow⁴ · Toni Gabaldón^{5,6,7} · Joseph Heitman⁸ · Martin Kemler⁴ · Kantarawee Khayhan⁹ · Marc-André Lachance¹⁰ · Edward J. Louis¹¹ · Sheng Sun⁸ · Duong Vu¹ · Andrey Yurkov¹²

Fungal Diversity (2021) 109:239–266
<https://doi.org/10.1007/s13225-021-00484-8>

REVIEW



What is a species in fungal plant pathogens?

Ruvishika S. Jayawardena^{1,2,7} · Kevin D. Hyde^{1,2,7,8} · Antonio Roberto Gomes de Farias^{2,3} · Chitrabhanu S. Bhunjun^{2,7} · Himashi S. Fernandez⁴ · Dimuthu S. Manamgoda⁴ · Dhanushka Udayanga⁵ · Indunil S. Herath⁵ · Kasun M. Thambugala⁶ · Ishara S. Manawasinghe¹ · Achala J. Gajanayake^{2,7} · Binu C. Samarakoon^{2,7} · Digvijayini Bundhun^{2,7} · Deeksha Gomdola^{2,7} · Naruemon Huanraluek² · Ya-ru Sun^{2,7} · Xia Tang^{2,7} · Itthayakorn Promputtha⁸ · Marco Thines^{9,10}

Fungal Diversity (2021) 109:99–154
<https://doi.org/10.1007/s13225-021-00477-7>

REVIEW



Species in lichen-forming fungi: balancing between conceptual and practical considerations, and between phenotype and phylogenomics

Robert Lücking¹ · Steven D. Leavitt^{2,3} · David L. Hawksworth^{4,5}

Plant Disease • 2022 • 106:1573–1596 • <https://doi.org/10.1094/PDIS-09-21-2083-SR>

Special Report

<https://doi.org/10.1094/PDIS-09-21-2083-SR>

e-Xtra*

Publicly Available and Validated DNA Reference Sequences Are Critical to Fungal Identification and Global Plant Protection Efforts: A Use-Case in *Colletotrichum*

Aaron H. Kennedy,^{1,†} Conrad L. Schoch,² Glorimar Marrero,¹ Vyacheslav Brover,² and Barbara Robbertse²

Soil fungi and agarics in fungal diversity based on eDNA

Received: 8 July 2022 | Accepted: 9 August 2022

DOI: 10.1111/gcb.16398

RESEARCH ARTICLE



WILEY

Global patterns in endemism and vulnerability of soil fungi

Leho Tedersoo¹ | Vladimir Mikryukov² | Alexander Zizka³ | Mohammad Bahram⁴ | Niloufar Hagh-Doust² | Sten Anslan² | Oleh Prylutskyi⁵ | Manuel Delgado-Baquerizo⁶ | Fernando T. Maestre⁷ | Jaan Pärn² | Maarja Öpik² | Mari Moora² | Martin Zobel² | Mikko Espenberg² | Ülo Mander² | Abdul Nasir Khalid⁸ | Adriana Corrales⁹ | Ahto Agan¹⁰ | Aida-M. Vasco-Palacios¹¹ | Alessandro Saitta¹² | Andrea C. Rinaldi¹³ | Annemieke Verbeken¹⁴ | Bobby P. Sulisty¹⁵ | Boris Tamgnoe¹⁶ | Brendan Furneaux¹⁷ | Camila Duarte Ritter¹⁸ | Casper Nyamukondiwa¹⁹ | Cathy Sharp²⁰ | César Marín²¹ | Daniyal Gohar¹ | Darta Klavina²² | Dipon Sharmah²³ | Dong Qin Dai²⁴ | Eduardo Nouhra²⁵ | Elisabeth Machteld Biersma²⁶ | Elisabeth Rähn¹⁰ | Erin K. Cameron²⁷ | Eske De Crop¹⁴ | Eveli Otsing¹ | Evgeny A. Davydov²⁸ | Felipe E. Alborno²⁹ | Francis Q. Brearley³⁰ | Franz Buegger³¹ | Geoffrey Zahn³² | Gregory Bonito³³ | Inga Hiiesalu² | Isabel C. Barrio³⁴ | Jacob Heilmann-Clausen³⁵ | Jelena Ankuda³⁶ | John Y. Kupagme¹ | Jose G. Maciá-Vicente³⁷ | Joseph Djeugap Fovo¹⁶ | József Geml³⁸ | Juha M. Alatalo³⁹ | Julieta Alvarez-Manjarrez⁴⁰ | Kadri Pöldmaa² | Kadri Runnel² | Kalev Adamson¹⁰ | Kari Anne Bråthen⁴¹ | Karin Pritsch³¹ | Kassim I. Tchan⁴² | Kęstutis Armolaitis³⁶ | Kevin D. Hyde⁴³ | Kevin K. Newsham⁴⁴ | Kristel Panksep⁴⁵ | Adebola A. Lateef⁴⁶ | Liis Tiirmann¹ | Linda Hansson⁴⁷ | Louis J. Lamit^{48,49} | Malka Saba⁵⁰ | Maria Tuomi⁴¹ | Marieka Gryzenhout⁵¹ | Marijn Bauters⁵² | Meike Piepenbrink⁵³ | Nalin Wijayawardene²⁴ | Nourou S. Yorou⁴² | Olavi Kurina⁵⁴ | Peter E. Mortimer⁵⁵ | Peter Meidl⁵⁶ | Petr Kohout⁵⁷ | Rolf Henrik Nilsson⁵⁸ | Rasmus Puusepp¹ | Rein Drenkhan¹⁰ | Roberto Garibay-Orijel⁵⁹ | Roberto Godoy⁶⁰ | Saad Alkahtani⁶¹ | Saleh Rahimlou¹ | Sergey V. Dudov⁶² | Sergei Pölme¹ | Soumya Ghosh⁵¹ | Sunil Mundra⁶³ | Talaat Ahmed³⁹ | Tarquin Netherway⁴ | Terry W. Henkel⁶⁴ | Tomas Roslin⁴ | Vincent Ntezirayo⁶⁵ | Vladimir E. Fedosov⁶² | Vladimir G. Onipchenko⁶² | W. A. Erandi Yasanthika⁴³ | Young Woon Lim⁶⁶ | Nadejda A. Soudzilovskaia⁶⁷ | Alexandre Antonelli⁶⁸ | Urmas Köljal² | Kessy Abarenkov⁶⁹

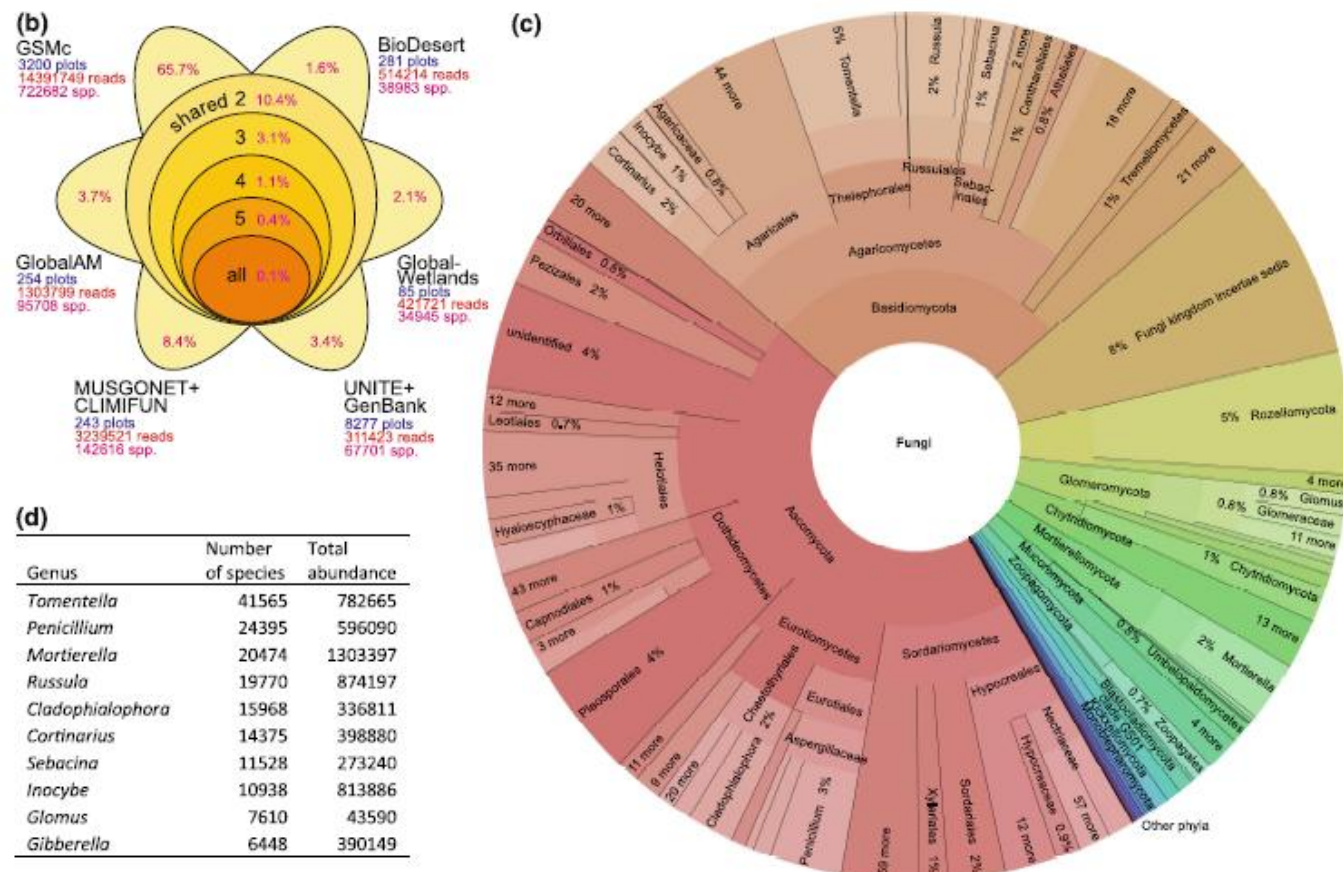


FIGURE 1 Distribution of samples and fungal species across data sets. (a) Global sampling map, with different colours representing different data sets; (b) species distribution of fungi among data sets, with the proportion of unique and shared species indicated; (c) Krona chart indicating the taxonomic distribution of fungal species (interactive chart can be browsed at <https://plutof.ut.ee/#/doi/10.15156/B/O/2483900>); and (d) species richness and total read abundance of the top 10 most diverse fungal genera.

Three ectomycorrhizal genera as a model

2020-2024

Amanita



Cortinarius s.l.



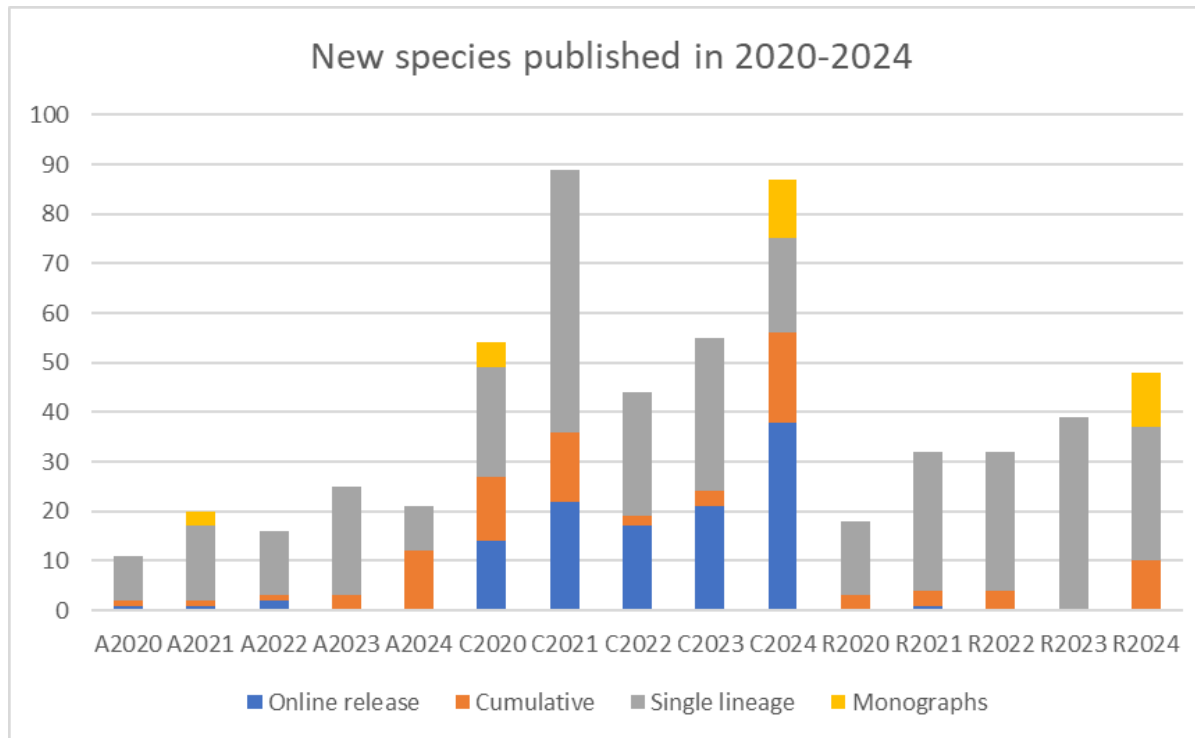
Russula



New species descriptions in publications

2020-2024	Amanita	Cortinarius	Russula	Total
Online Release	4	112	1	117
Cumulative	18	50	20	88
Single lineage	68	150	137	355
Monographs	3	17	11	31
Total	93	329	169	591

Michaela
Caboňová



Types of scientific publications with new species

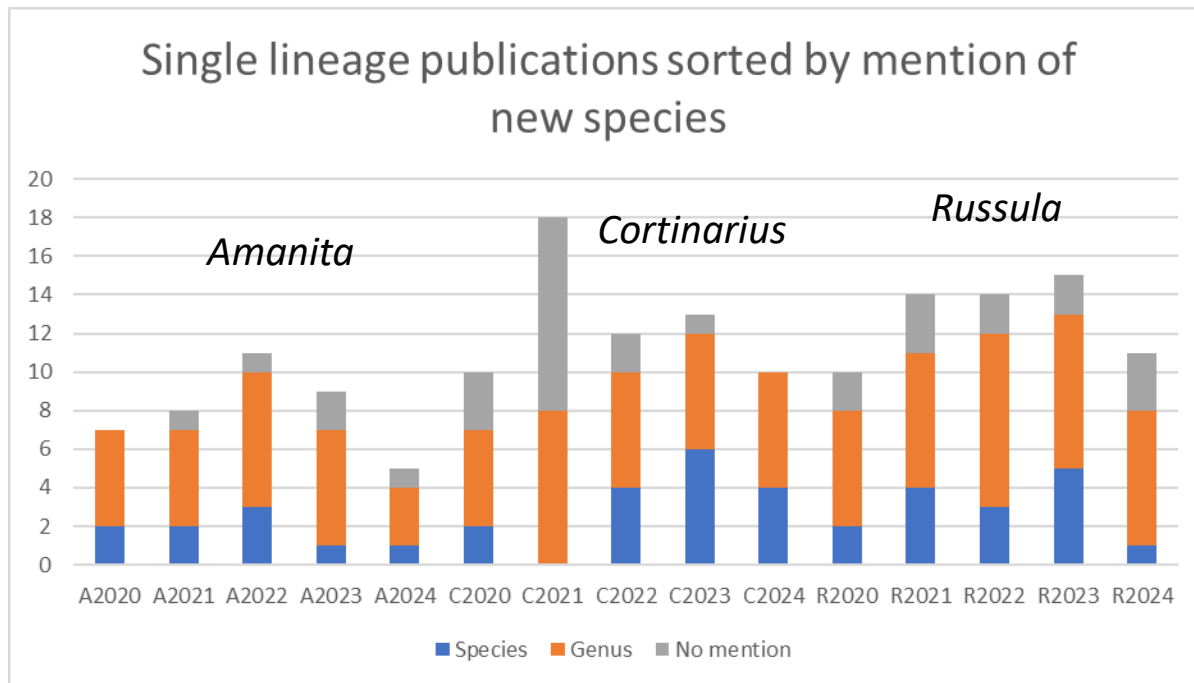
- A. Online release (Index fungorum)
- B. Cumulative publications (Fungal diversity profiles, Fungal planet description sheets, etc.)
- C. Single lineage publications
- D. Monographic books

Species hypothesis in single lineage taxonomic publications

219 publications with new species descriptions for all three genera in 2020-2024

167 of them are single lineage publications

Michaela
Caboňová



2020-2024	Amanita	Cortinarius	Russula	Total
Species	9	16	15	40
Genus	26	31	37	94
No mention	5	16	12	33
Total	40	63	64	167

Introductions sorting:

- A. a mention of new species names
- B. a mention of new species described
- C. no mention about taxa described

What is a difference between research and data release publication?



Research Ideas and Outcomes 3: e12431
doi: [10.3897/rio.3.e12431](https://doi.org/10.3897/rio.3.e12431)



Guidelines

Strategies and guidelines for scholarly publishing of biodiversity data

Lyubomir Penev[‡], Daniel Mietchen[§], Vishwas Shravan Chavan[‡], Gregor Hagedorn[‡], Vincent Stuart Smith[#], David Shotton[□], Éamonn Ó Tuama[“], Viktor Senderov^{”^}, Teodor Georgiev[”], Pavel Stoev[✓], Quentin John Groom[‡], David Remsen[?], Scott C. Edmunds[§]

A data paper is a scholarly journal publication whose primary purpose is to describe a dataset or a group of datasets, rather than to report a research investigation (Newman and Corke 2009, Chavan and Ingwersen 2009, Chavan and Penev 2011). As such, it contains facts about data, not hypotheses and arguments in support of those hypotheses based upon data, as found in a conventional research article.



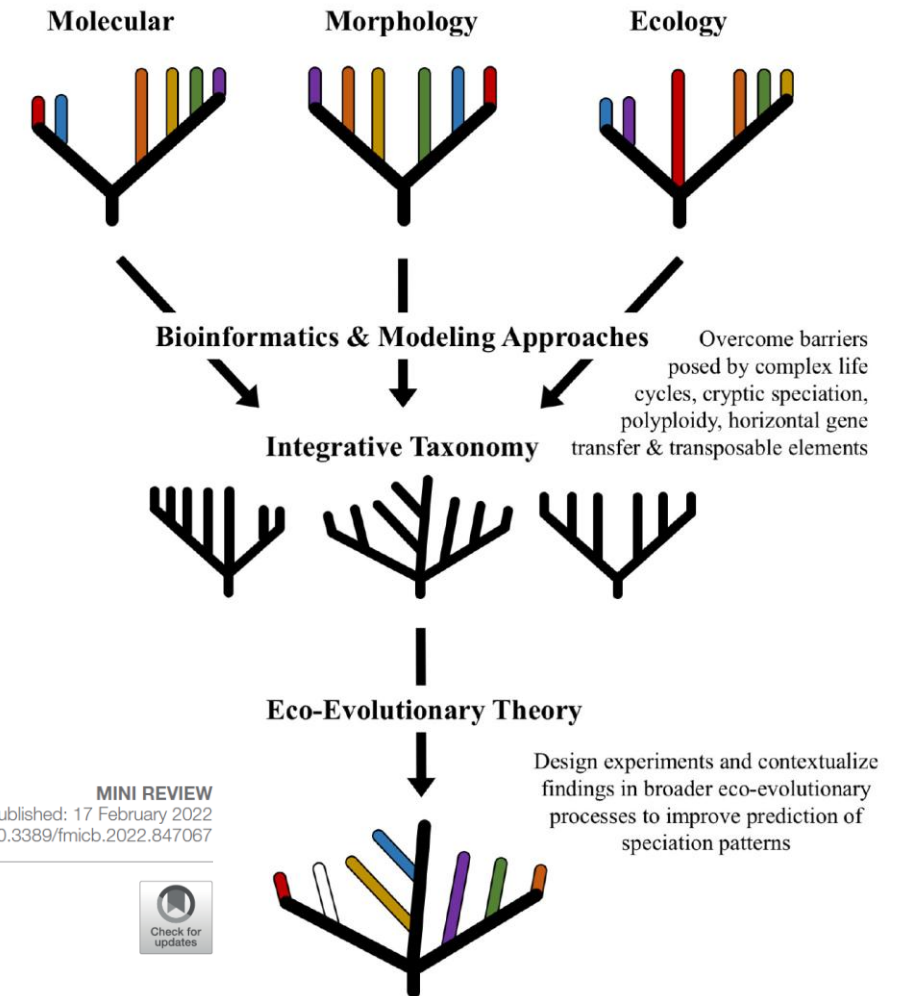
Species hypothesis

- sequence based
- morphology based
- geography based
- ecology based
- evolutionary hypothesis



Improving Taxonomic Delimitation of Fungal Species in the Age of Genomics and Phenomics

Ashley Stenge^{1,2,3*}, Kimberly M. Stanke^{1,4}, Amanda C. Quattrone^{1,5,6} and Joshua R. Herr^{3,5,6*}



Sequence based hypothesis

Hodophilus foetens complex

Katarína Adamčíková and Soňa Jančovičová

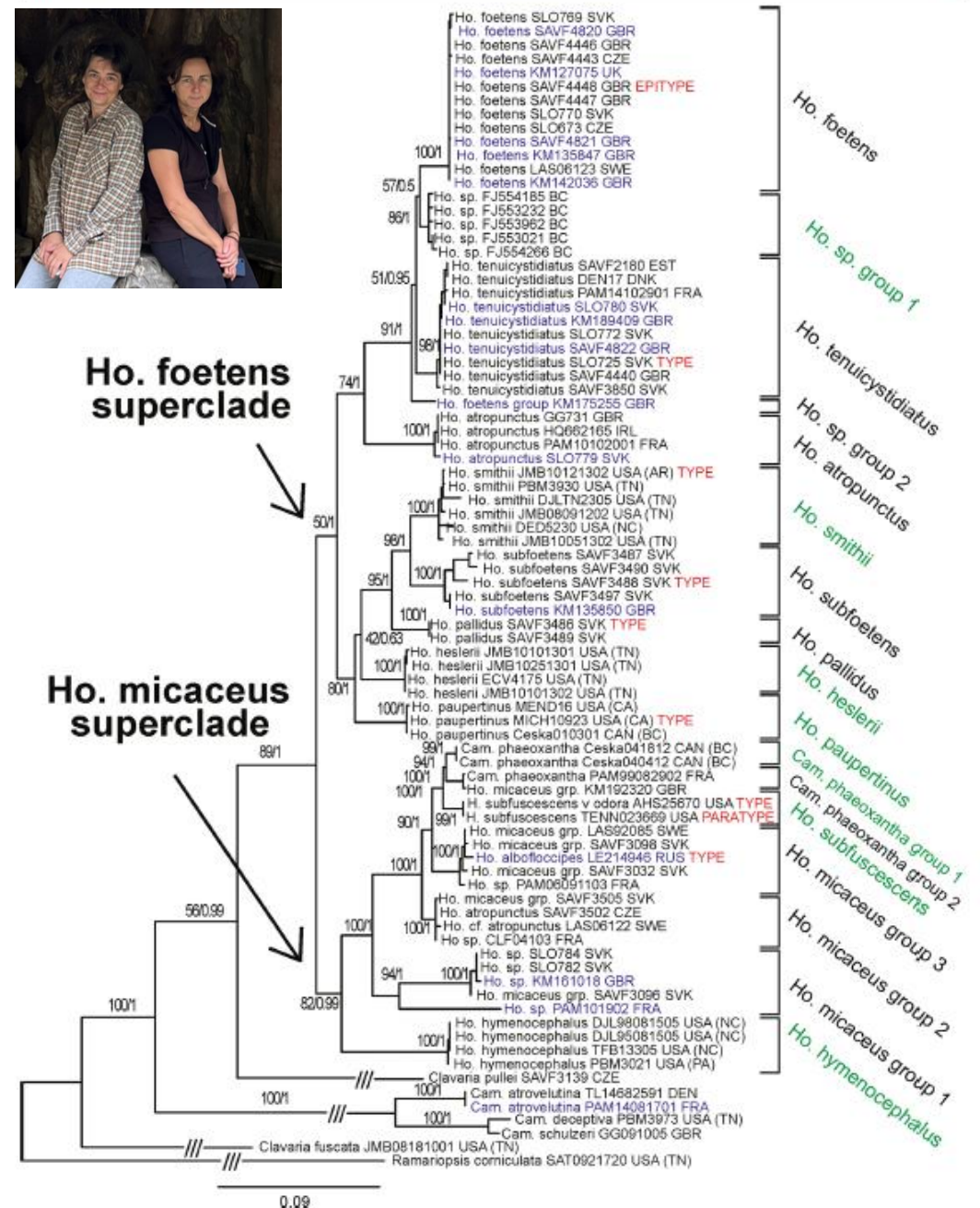
Mycol Progress (2017) 16:47–62

55



Mycol Progress (2017) 16:47–62

51



Sequence based hypothesis

Dermoloma

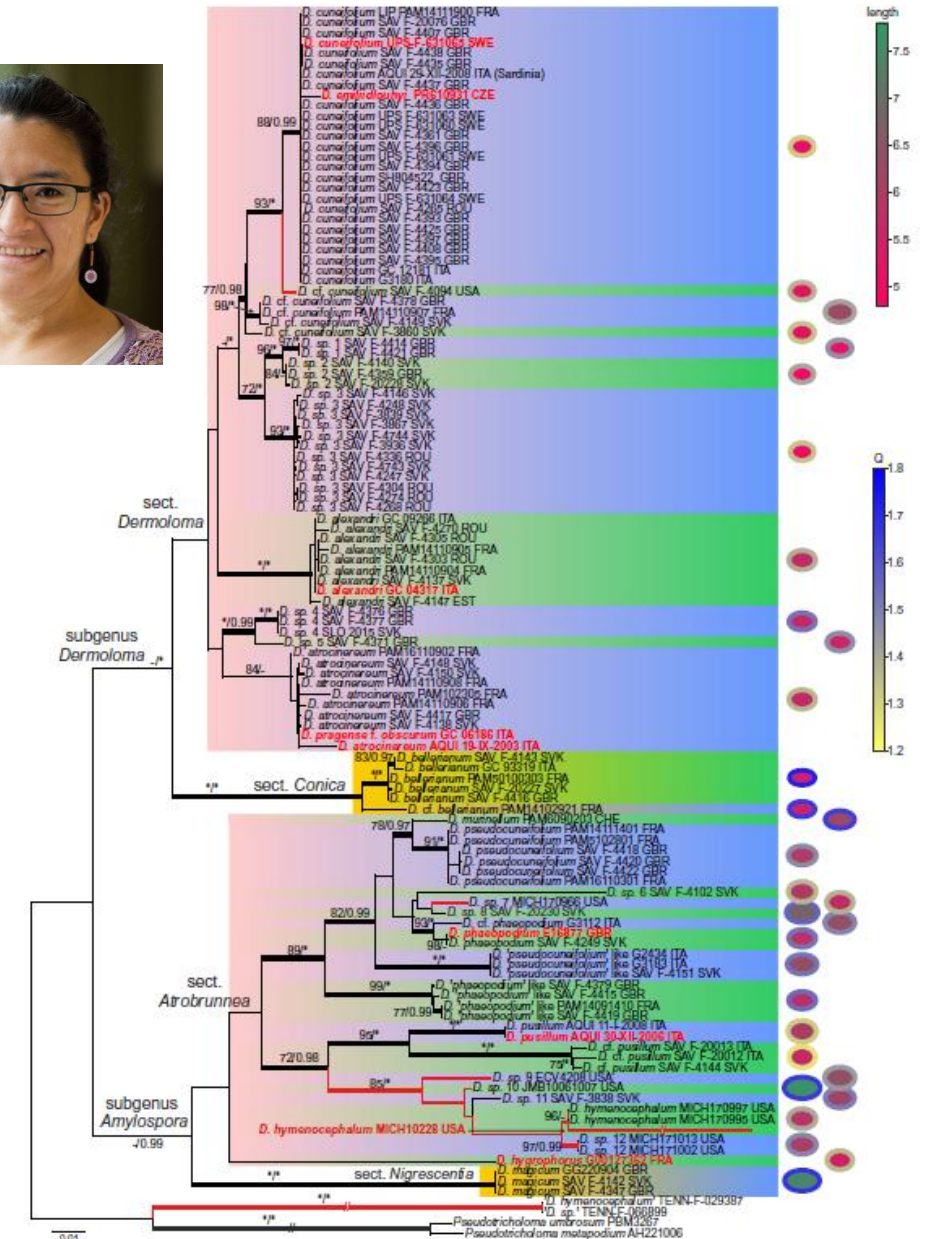
Marisol
Sánchez-García



Fig. 3 Examples of *Dermoloma* morphology. a Inamyloid spores of subgenus *Dermoloma* (*D. cuneifolium*, SAV F-4423). b Amyloid spores of subgenus *Amylospora* (*D. pseudocuneifolium*, SAV F-4422). c Basidiomata of section *Dermoloma* (*D. cuneifolium*, SAV F-4436). d Basidiomata of section *Conica* (*D. bellierianum*, SAV F-4416). e Basidiomata of section *Atrobrunnea* (*D. pseudocuneifolium*, SAV F-4420). f Basidiomata of section *Nigrescentia* (*D. magicum*, SAV F-4242). Scale of 10 mm represents for basidiomata



Katarína Adamčíková
and Soňa Jančovičová



Sequence based hypothesis

Dermoloma



IMA Fungus 16: e157337 (2025)
DOI: 10.3897/imafungus.16.157337

Research Article

A phylogenetic and morphological study of the genus *Dermoloma* (Agaricales, Tricholomataceae) in Europe and North America exposes inefficiency of opportunistic species descriptions

Katarína Adamčíková¹, Munazza Kiran^{2,3}, Miroslav Caboň², Brandon P. Matheny⁴, Marisol Sánchez-García⁵, Eef Arnolds⁶, Michaela Caboňová², Gilles Corriol⁷, Bálint Dima⁸, Gernot Friebeš⁹, Gareth W. Griffith¹⁰, Django Grootmyers⁴, David Harries¹¹, Alexander Karich¹², Armin Mešić¹³, Martin Mihaljević¹⁴, Pierre-Arthur Moreau¹⁵, Ana Pošta¹³, Vasilii Shapkin², Zdenko Tkalcčec¹³, Alfredo Vizzini¹⁶, Lenka Vondrovicová¹⁴, Slavomir Adamčík^{2,17}, Soňa Jančovičová¹⁷

Biodiversity Data Journal 13: e158080
doi: 10.3897/BDJ.13.e158080

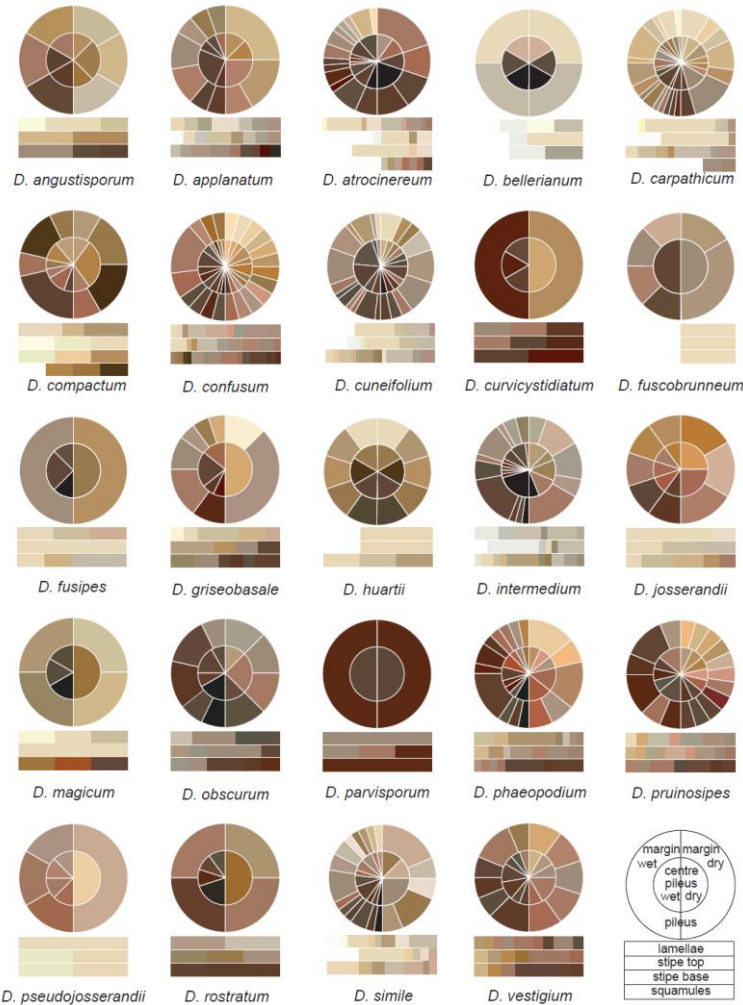


Taxonomy & Inventories

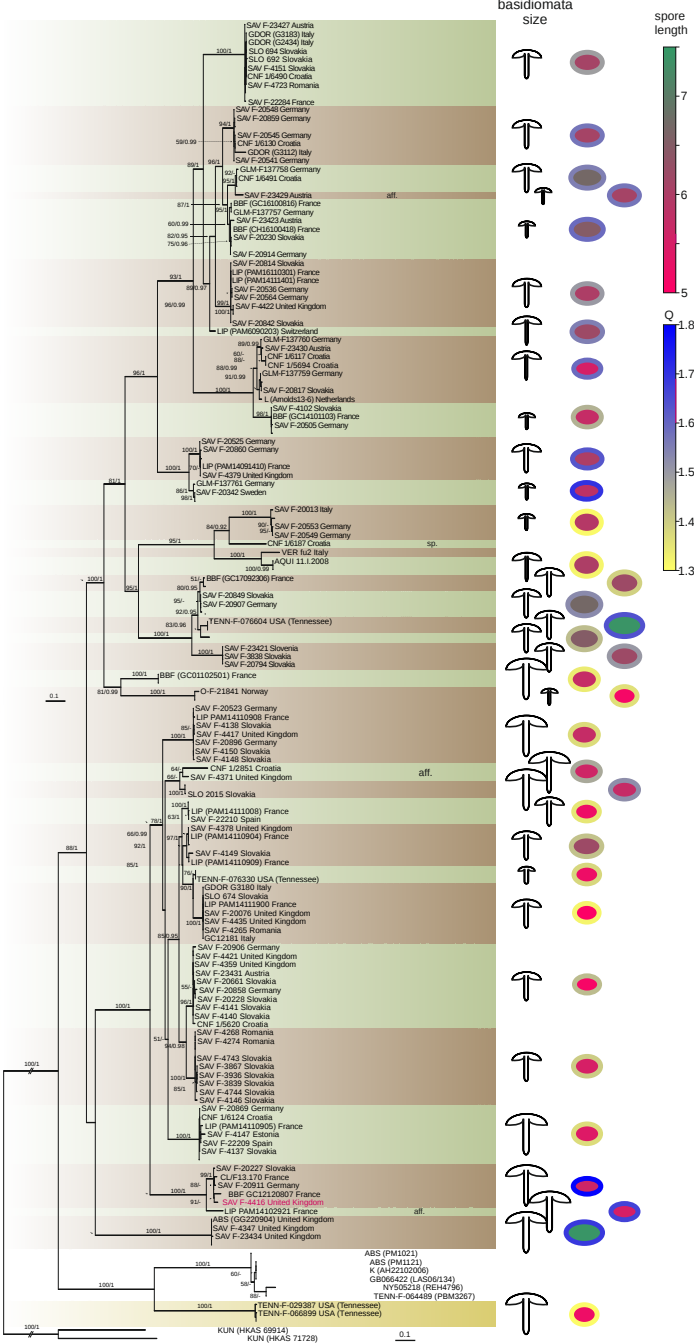
Nomenclatural review of names published in the fungal genus *Dermoloma* (Basidiomycota, Agaricales, Tricholomataceae) based on morphological analyses of type specimens

Michaela Caboňová[‡], Marisol Sanchez-García[§], Miroslav Caboň[‡], Katarína Adamčíková[‡], Pierre-Arthur Moreau[¶], Alfredo Vizzini[‡], Slavomir Adamčík[‡], Soňa Jančovičová[‡]

Basidiomata chromatograms



Phylogram generated by Maximum Likelihood with additional Bayes Inference analysis based on combined sequence data of ITS, LSU, rpb1, rpb2, mcm7 and tef1a



Morphology based hypothesis

Plant Systematics and Evolution (2018) 304:747–756
https://doi.org/10.1007/s00606-018-1506-3

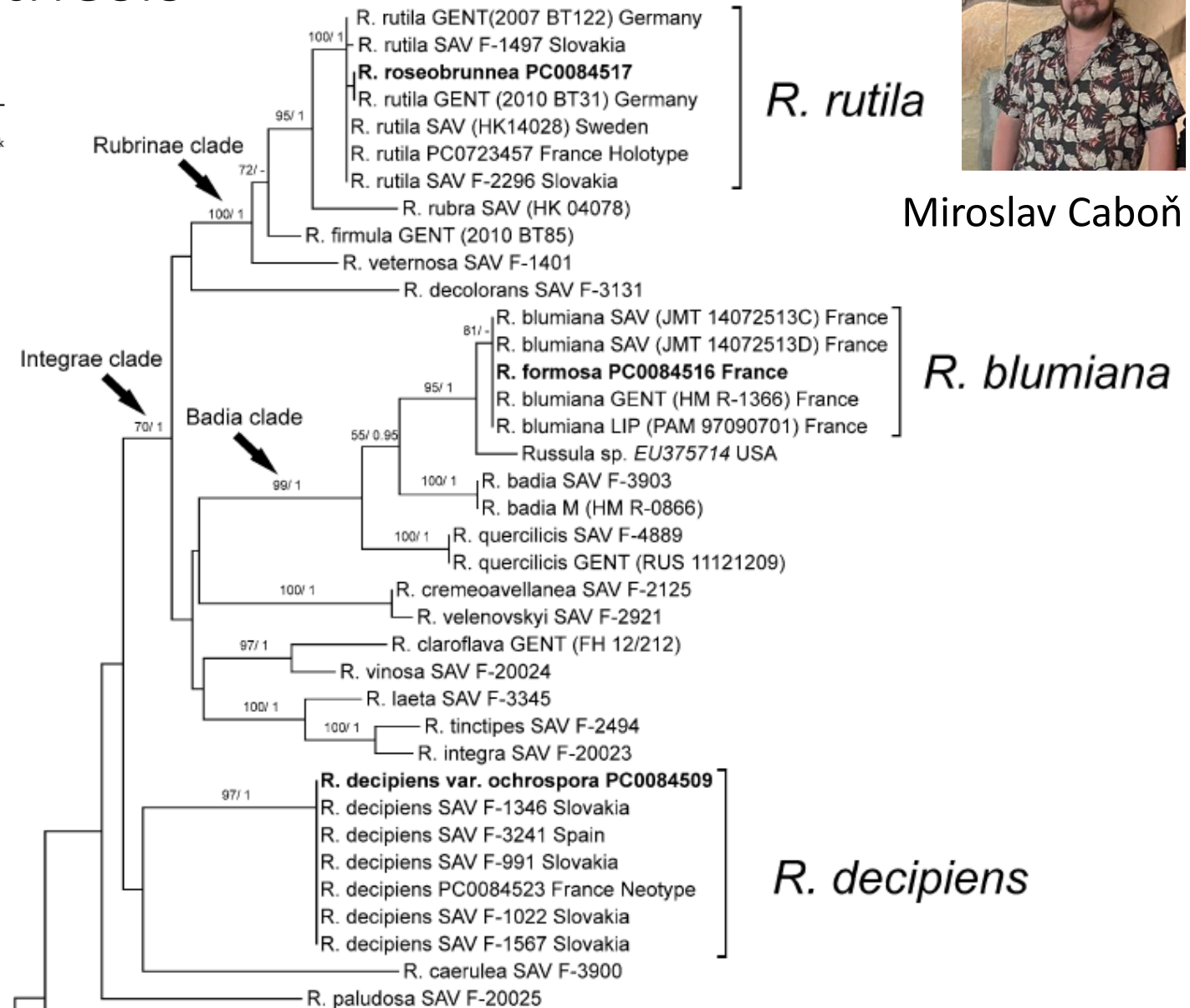
ORIGINAL ARTICLE



Blum versus Romagnesi: testing possible synonymies of some European russulas (Russulaceae, Basidiomycota)

Miroslav Caboň¹ · Soňa Jančovičová² · Jean M. Trendel³ · Pierre-Arthur Moreau⁴ · Felix Hampe⁵ · Miroslav Kolařík⁶ · Annemieke Verbeken⁵ · Slavomír Adamčík¹

J. Blum published 45 *Russula* taxa from France in 1951-1968, but only but only five were adopted by in a monograph of a conterporary autor H. Romagnesi (1967)

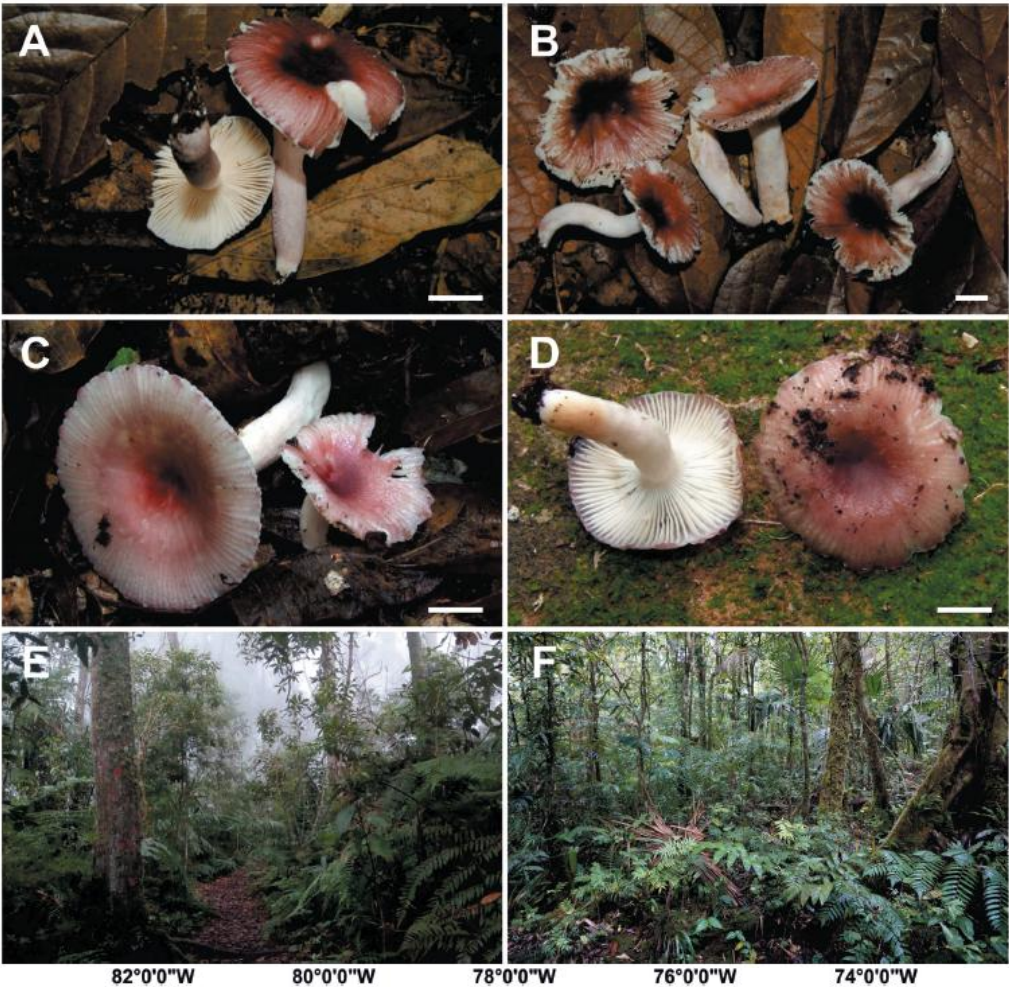


Miroslav Caboň

Fig. 2 Field appearance of *Russula blumiana*. a–b JMT 14072513 (SAV), photograph by J.M. Trendel.

Geography based hypothesis

two subspecies of *Russula floriformis* separated by Isthmus of Panama

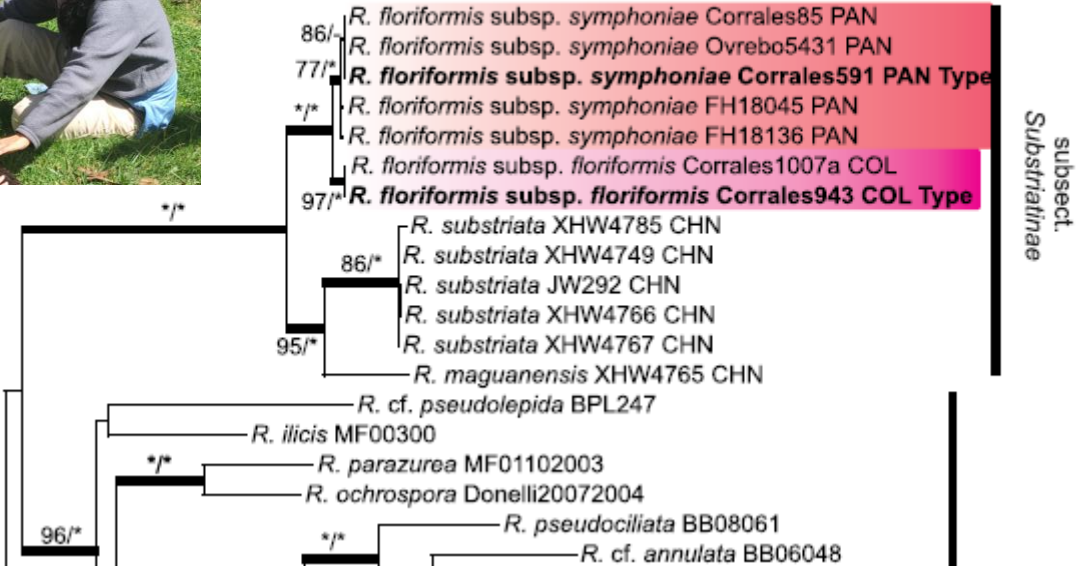


Russula subsp. and voucher no.	ITS		28S				rpb2				tef1						
	17	579	581	191	699	90	142	160	205	343	391	727	174	859	941		
Rf_Corrales911	T	C	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Rf_Corrales1007	Y	C	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Rf_Corrales952	Y	C	A	G	G	-	-	-	-	-	-	-	-	-	-	-	-
Rf_Corrales904	C	C	A	-	G	-	-	-	-	-	-	-	-	-	-	-	-
Rf_Corrales1007a	Y	C	A	G	G	T	C	C	T	G	G	T	A	C	T	-	-
Rf_Corrales943	C	C	A	G	G	T	C	C	T	G	G	T	R	C	T	-	-
Rs_Corrales591	C	T	G	A	A	A	T	S	Y	A	T	C	G	T	C	-	-
Rs_Ovrebo5431	C	T	G	-	-	A	T	C	Y	A	T	C	G	T	C	-	-
Rs_FH-18-136	C	Y	G	R	A	T	T	S	Y	A	K	C	-	Y	C	-	-
Rs_FH-18-045	C	T	G	A	A	T	T	S	T	A	K	C	-	C	C	-	-
Rs_Corrales85	-	-	-	R	A	A	T	S	Y	-	-	-	-	-	-	-	-

Figure 4. Nucleotide differences of *Russula floriformis* subsp. *floriformis* (Rf) and subsp. *symphoniae* (Rs) across ITS, 28S, *rpb2*, and *tef1*. The numbers at the top indicate the positions of the polymorphic sites in each fragment. The dashes indicate the lack of data for the respective positions.

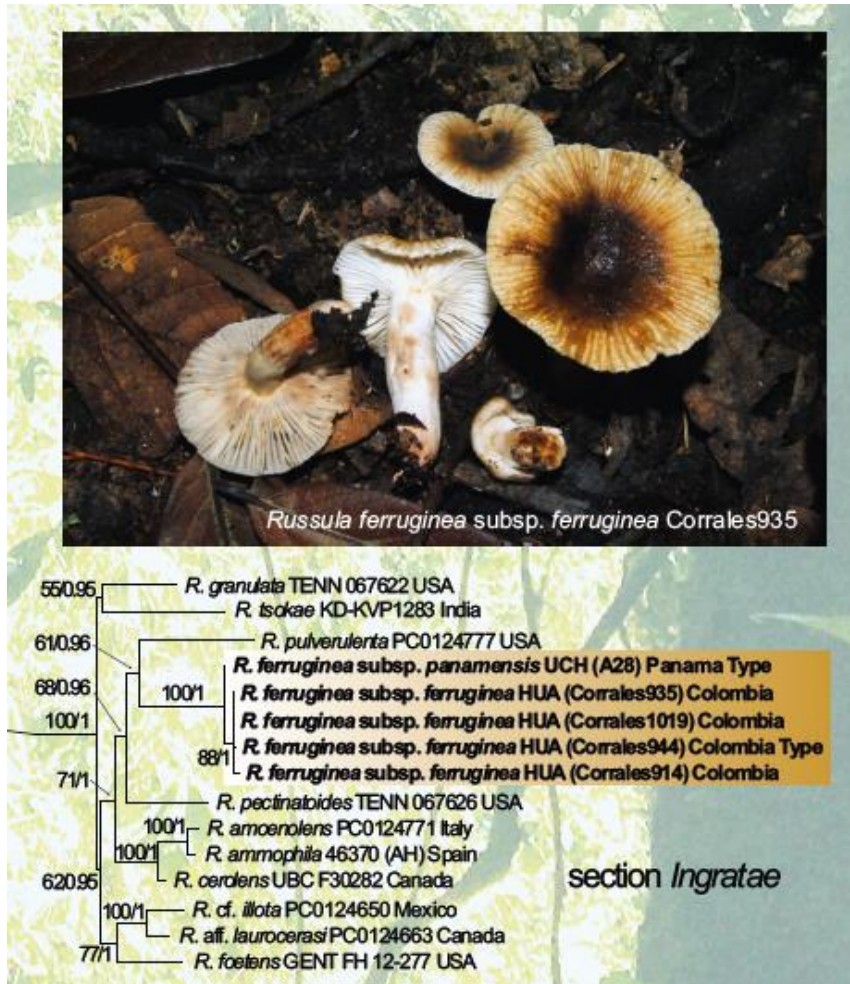


Adriana Corrales



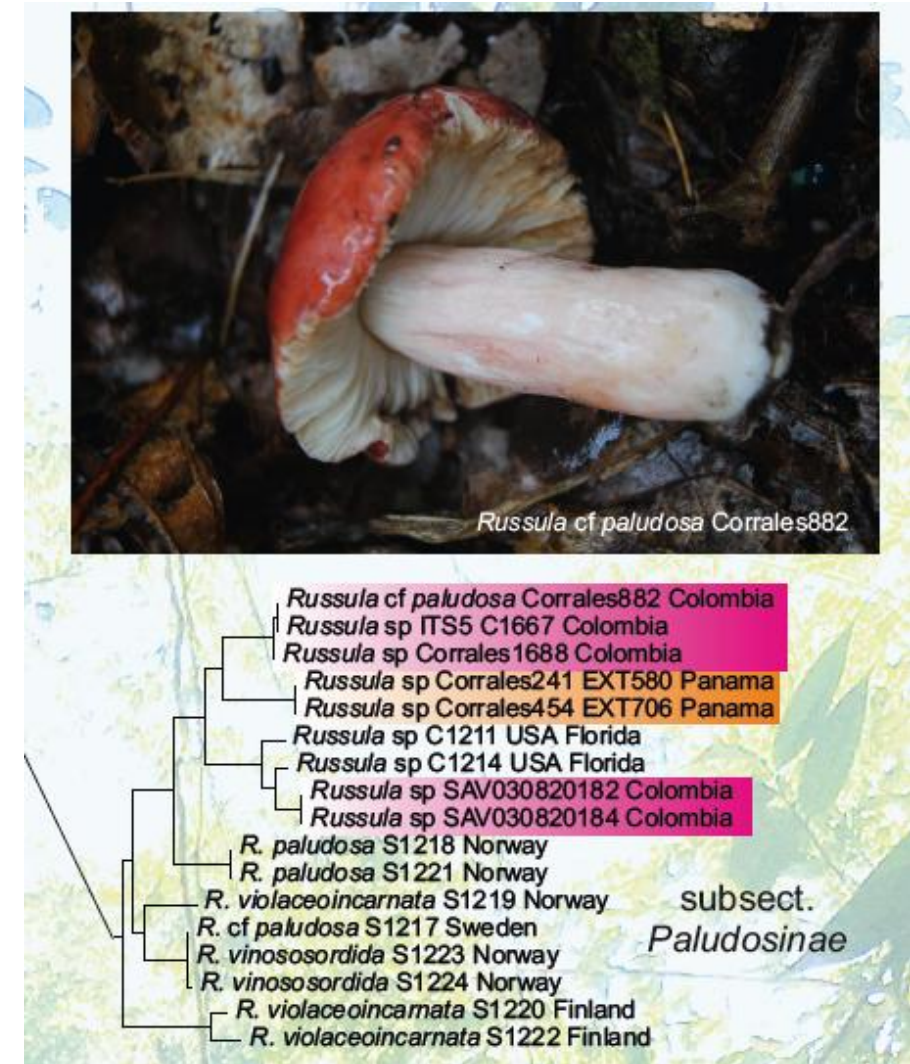
Geography based hypothesis

two subspecies of *Russula ferruginea*
separated by Isthmus of Panama



Adriana
Corrales

three distinct and well supported
species in *Russula paludosa* complex

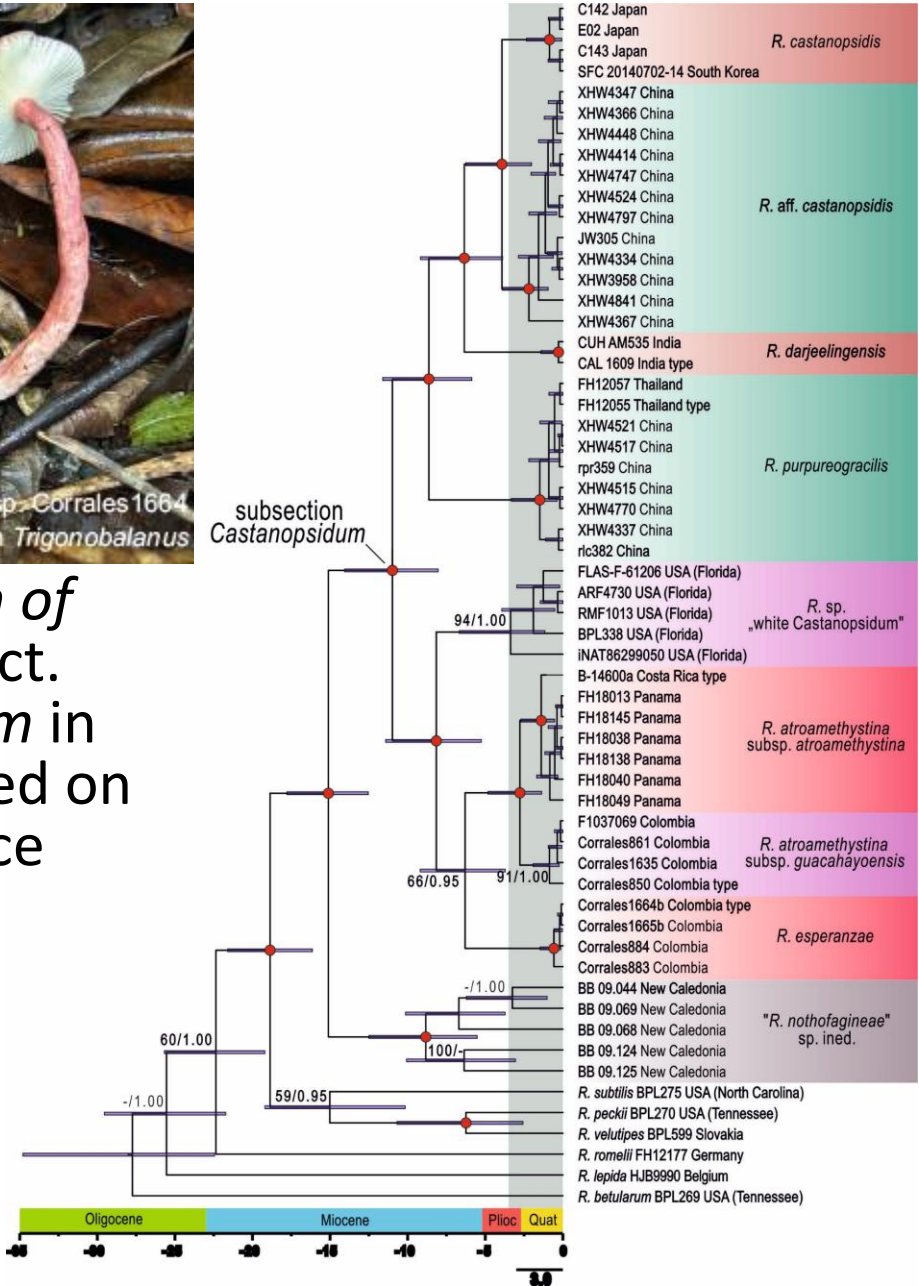


Ecology based hypothesis



Diversification of *Russula* subsect. *Castanopsidum* in Colombia based on host preference

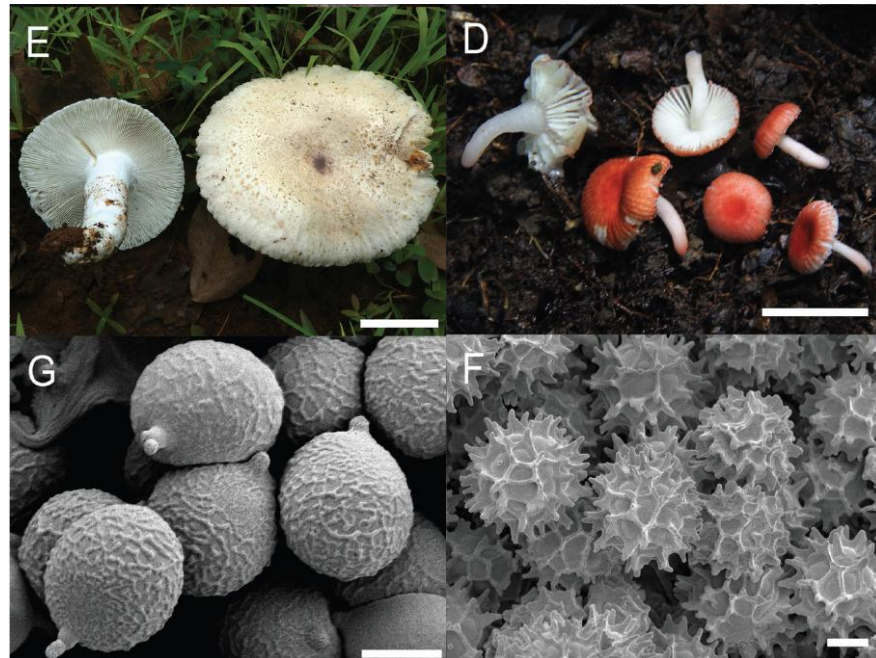
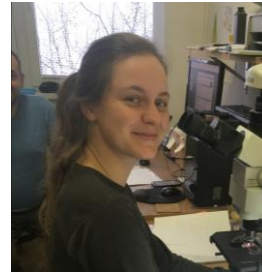
Colombian Andean ectotrophic forests



Evolutionary based hypothesis

Members of *Russula* “Afrovirescentinae” are morphologically adapted to a specific environmental conditions

Cathrin Manz

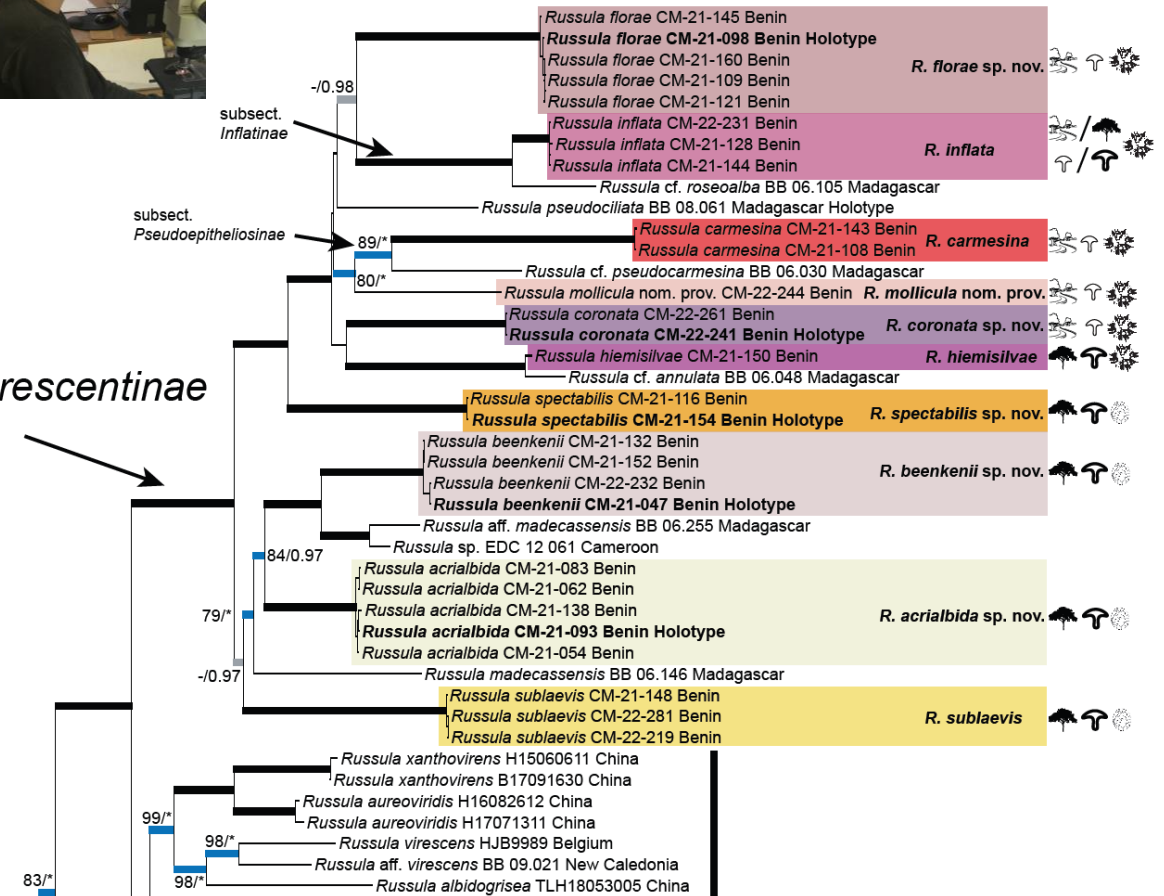


- = small, thin-fleshed basidiomata
- = big, thick-fleshed basidiomata
- = gallery forest
- = Sudanian savannah woodland
- = spore ornamentation $\geq 1 \mu\text{m}$
- = spore ornamentation $\leq 0.5 \mu\text{m}$

IMA
Fungus

Cathrin Manz et al.: African *Russula* species with habitat adaptatio

Afrovirescentinae
clade



eDNA and new species discoveries

Fungal Diversity (2022) 114:327–386
<https://doi.org/10.1007/s13225-022-00502-3>



The numbers of fungi: contributions from traditional taxonomic studies and challenges of metabarcoding

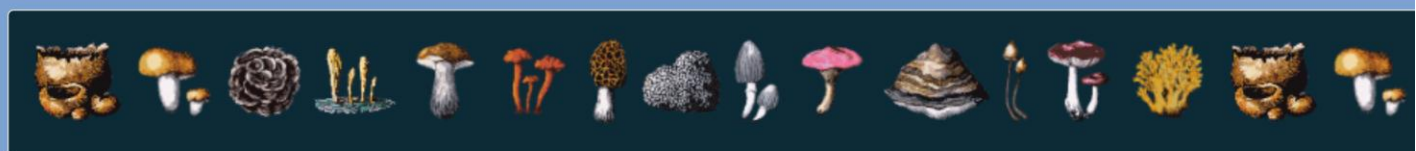
Chayanard Phukhamsakda^{1,2} · Rolf Henrik Nilsson^{3,4} · Chitrabhanu S. Bhunjun^{5,6} · Antonio Roberto Gomes de Farias⁵ · Ya-Ru Sun^{5,6,7} · Subodini N. Wijesinghe^{5,6} · Mubashar Raza⁸ · Dan-Feng Bao^{5,9,10} · Li Lu^{5,11,12} · Saowaluck Tibpromma^{11,12} · Wei Dong¹³ · Danushka S. Tennakoon^{5,6,14} · Xing-Guo Tian^{5,6,11,12,15,16} · Yin-Ru Xiong^{5,13} · Samantha C. Karunarathna^{11,12} · Lei Cai⁸ · Zong-Long Luo⁹ · Yong Wang⁷ · Ishara S. Manawasinghe¹³ · Erio Camporesi^{17,18,19} · Paul M. Kirk²⁰ · Itthayakorn Promputtha^{21,22,23} · Chang-Hsin Kuo¹⁴ · Hong-Yan Su⁹ · Mingkwan Doilom¹³ · Yu Li^{1,2} · Yong-Ping Fu^{1,2} · Kevin D. Hyde^{1,2,5,13}



Current version: **10.0**; Last updated: 2025-02-25 ([read more](#))

Number of ITS sequences (UNITE+INSD): **3 846 536**; Number of UNITE fungal Species Hypotheses with DOIs at 1.0% threshold: **239 180** ([more statistics](#))

„Metabarcoding has revealed a much larger diversity of fungi than traditional methods.“



Welcome to GlobalFungi!

GlobalFungi dataset release 5.0 (16.11.2023). Taxonomy based on UNITE version 10.0 (4.4.2024).

Actual number of samples in the database: 84972; actual number of studies included: 846.

Number of ITS sequence variants: 593 399 355; number of ITS1 sequences 1 233 820 630; number of ITS2 sequences 3 474 636 588.

eDNA and metabarcoding

Ecology and Evolution

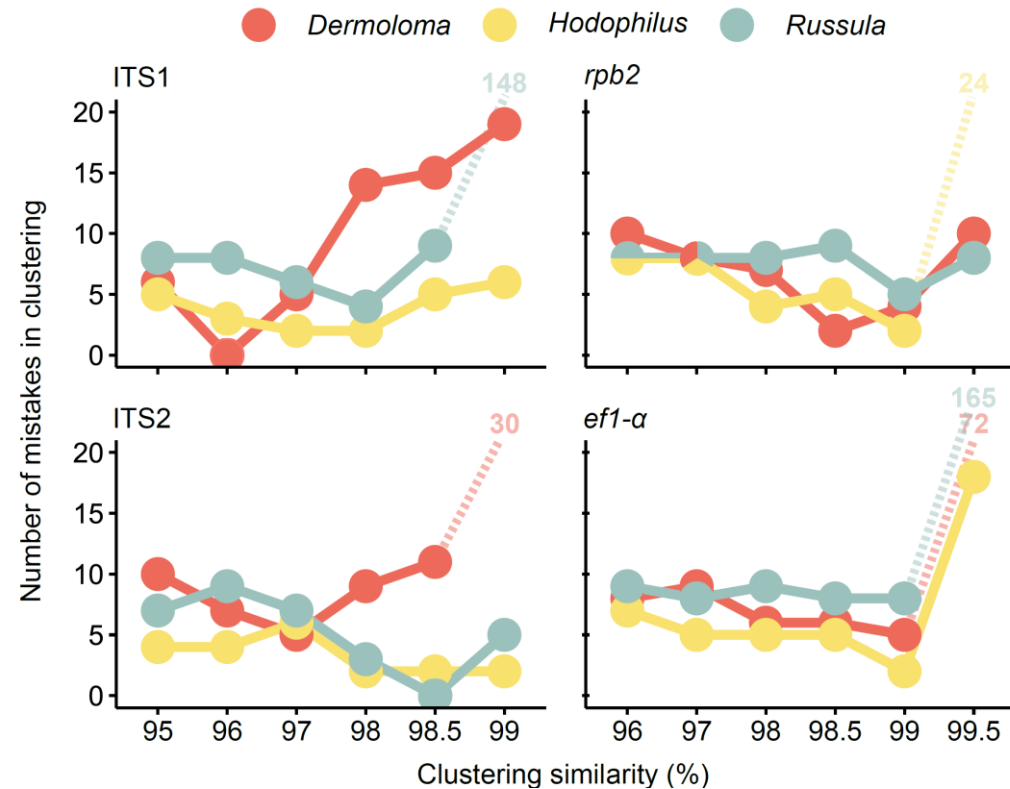
WILEY

Ecology and Evolution

RESEARCH ARTICLE OPEN ACCESS

Protein Coding Low-Copy *rpb2* and *ef1-α* Regions Are Viable Fungal Metabarcoding DNA Markers Which Can Supplement ITS for Better Accuracy

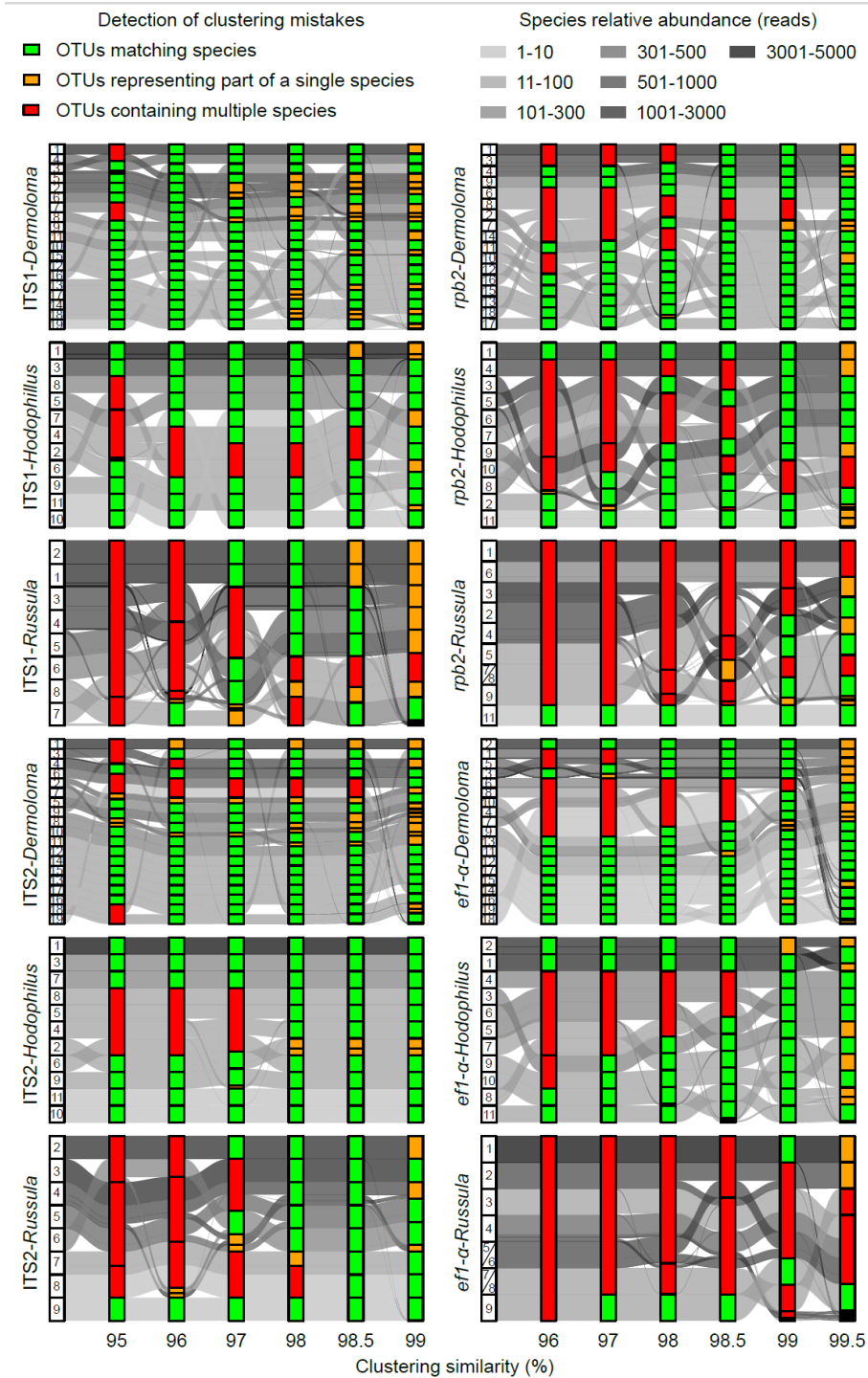
Vasilii Shapkin¹ | Miroslav Caboň^{1,2} | Miroslav Kolařík^{3,4} | Katarína Adamčíková⁵ | Petr Baldrian³ | Tereza Michalková³ | Tomáš Větrovský³ | Slavomír Adamčík^{1,6}



Mock community analysis revealed contrasting best clustering thresholds for different agaric genera



Vasilii Shapkin and Miroslav Caboň



Estimation of species distribution using eDNA metadata

MYCOLOGIA
<https://doi.org/10.1080/00275514.2023.2295957>



Three new species in *Russula* subsection *Xerampelinae* supported by genealogical and phenotypic coherence

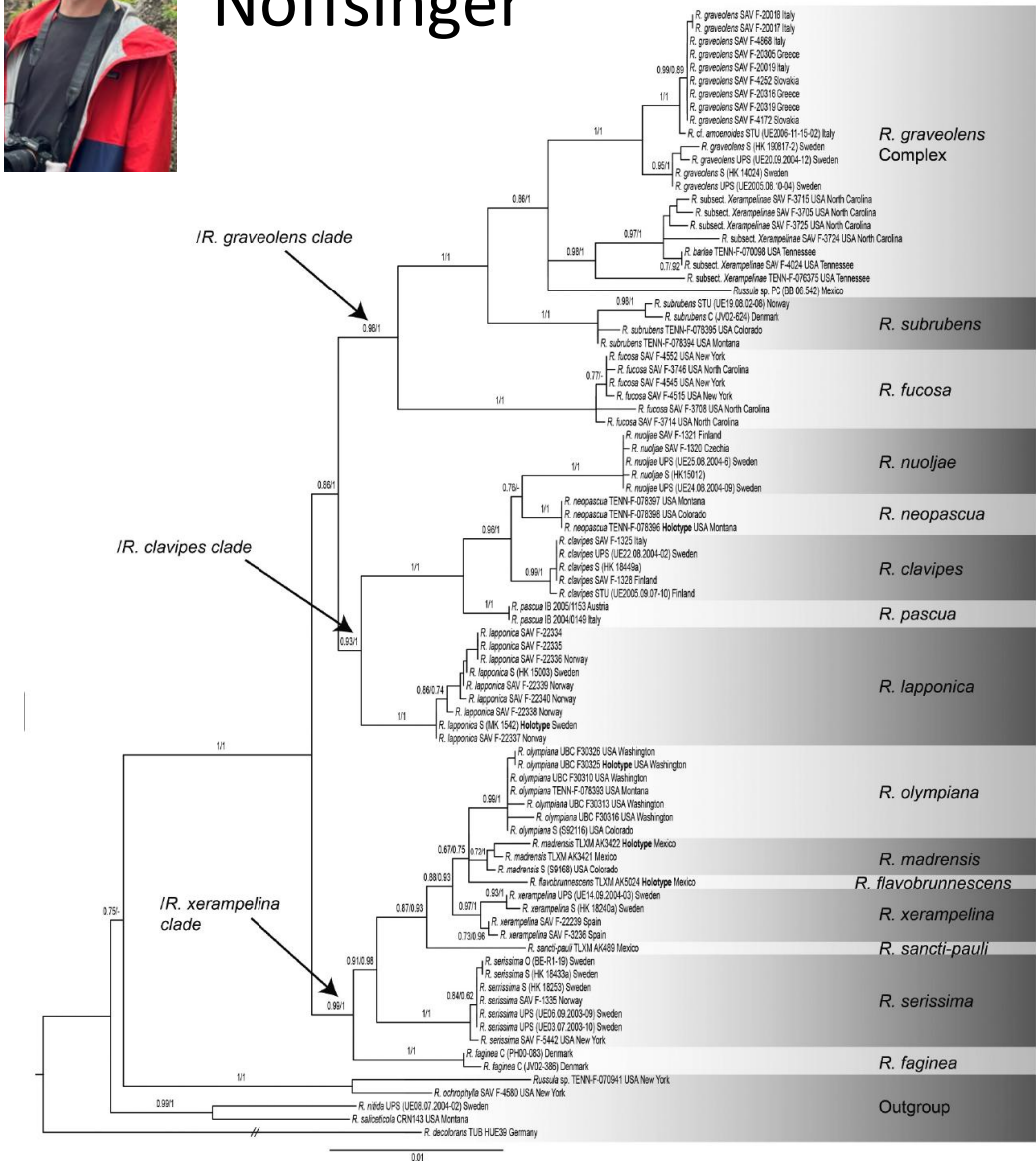
Chance R. Noffsinger^a, Katarina Adamčíková^b, Ursula Eberhardt^c, Miroslav Caboň^d, Anna Bazzicalupo^e, Bart Buyck^f, Herbert Kaufmann^g, Øyvind Weholt^h, Brian P. Looneyⁱ, P. Brandon Matheny^j, Mary L. Berbee^k, Daniel Tausan^l, and Slavomír Adamčík^{d,k}

reference sequence data about
boreal and arctic *Russula* subsect.
Xerampelinae species



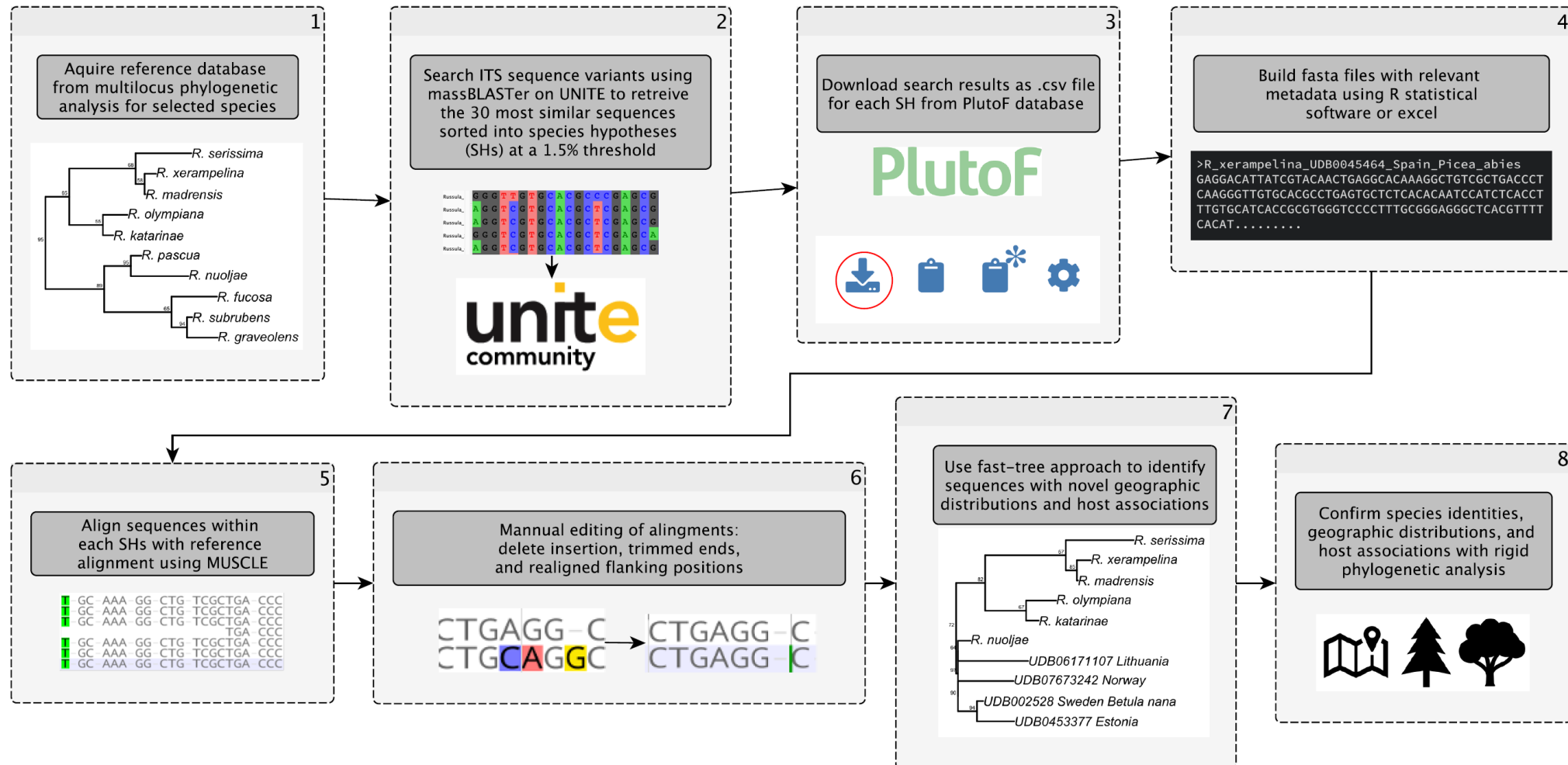
Chance Noffsinger

MYCOLOGIA 7



Estimation of species distribution using eDNA metadata

workflow for data mining and data processing

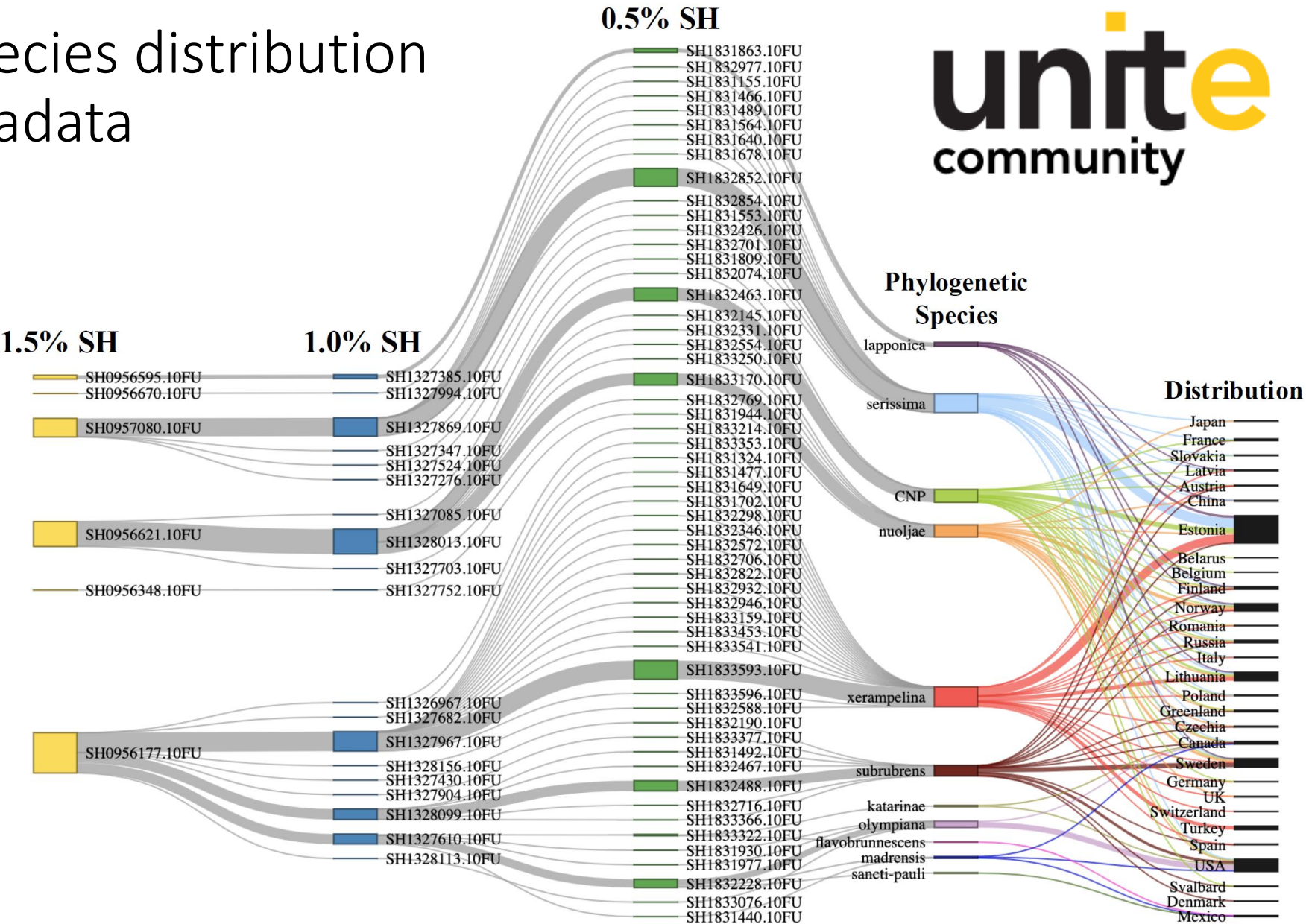


Chance
Noffsinger

Estimation of species distribution using eDNA metadata

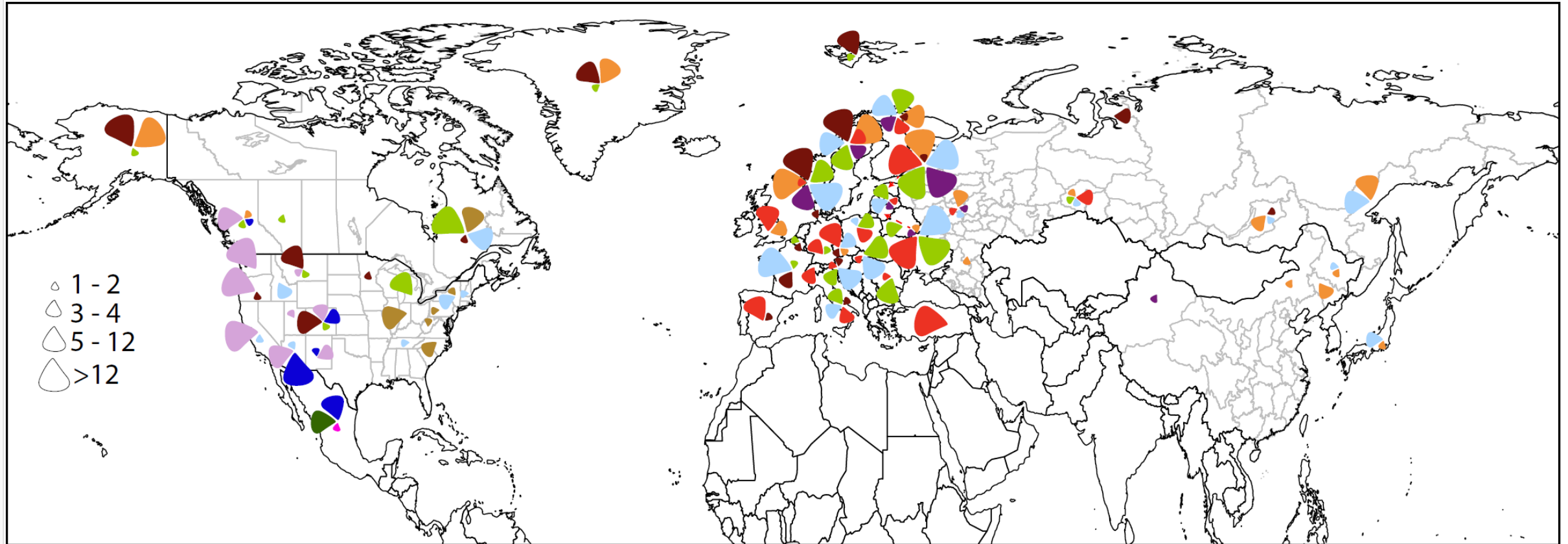


sorting of Unite sequences by phylogenetic algorithm



Estimation of species distribution using eDNA metadata

distribution estimation
for 13 boreal and arctic
Russula species



● CNP ● *R. flavobrunnescens* ● *R. katarinae* ● *R. lapponica* ● *R. madrensis* ● *R. nuoljae*
● *R. olympiana* ● *R. sancti-pauli* ● *R. serissima* ● *R. subrubens* ● *R. xerampelina*



my MEM lab team

