

High-Coverage ITS Primers for the DNA-Based Identification of Basidiomycetes in Environmental Samples

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Modelling the global distribution of fungal species: new insights into microbial cosmopolitanism. <i>Molecular Ecology</i> , 2012, 21, 5599-5612.	2.0	61
2	Global ITS diversity in the <i>Sporothrix schenckii</i> complex. <i>Fungal Diversity</i> , 2014, 66, 153.	4.7	63
3	Improved Selection of Internal Transcribed Spacer-Specific Primers Enables Quantitative, Ultra-High-Throughput Profiling of Fungal Communities. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2519-2526.	1.4	442
4	Utilizing ITS1 and ITS2 to study environmental fungal diversity using pyrosequencing. <i>FEMS Microbiology Ecology</i> , 2013, 84, 165-175.	1.3	76
5	Strong coupling of plant and fungal community structure across western Amazonian rainforests. <i>ISME Journal</i> , 2013, 7, 1852-1861.	4.4	333
6	Illumina metabarcoding of a soil fungal community. <i>Soil Biology and Biochemistry</i> , 2013, 65, 128-132.	4.2	409
7	Fungal community analysis by high-throughput sequencing of amplified markers – a user's guide. <i>New Phytologist</i> , 2013, 199, 288-299.	3.5	747
8	Comparison of ITS1 and ITS2 rDNA in 454 sequencing of hyperdiverse fungal communities. <i>Fungal Ecology</i> , 2013, 6, 102-109.	0.7	138
9	454 Pyrosequencing Analysis of Fungal Assemblages from Geographically Distant, Disparate Soils Reveals Spatial Patterning and a Core Mycobiome. <i>Diversity</i> , 2013, 5, 73-98.	0.7	82
10	How are plant and fungal communities linked to each other in belowground ecosystems? A massively parallel pyrosequencing analysis of the association specificity of root-associated fungi and their host plants. <i>Ecology and Evolution</i> , 2013, 3, 3112-3124.	0.8	71
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13	Spatial Segregation and Aggregation of Ectomycorrhizal and Root-Endophytic Fungi in the Seedlings of Two <i>Quercus</i> Species. <i>PLoS ONE</i> , 2014, 9, e96363.	1.1	32
14	Molecular Analysis of <i>Colletotrichum</i> Species in the Carposphere and Phyllosphere of Olive. <i>PLoS ONE</i> , 2014, 9, e114031.	1.1	42
15	A metagenomics-based approach to the top-down effect on the detritivore food web: a salamanders influence on fungal communities within a deciduous forest. <i>Ecology and Evolution</i> , 2014, 4, 4106-4116.	0.8	10
16	Detection of the horizontal spatial structure of soil fungal communities in a natural forest. <i>Population Ecology</i> , 2014, 56, 301-310.	0.7	29
17	Resilience of the Natural Phyllosphere Microbiota of the Grapevine to Chemical and Biological Pesticides. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3585-3596.	1.4	144
18	Fungal pathogen accumulation at the expense of plant-beneficial fungi as a consequence of consecutive peanut monoculturing. <i>Soil Biology and Biochemistry</i> , 2014, 72, 11-18.	4.2	216

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19	Changes within a single land-use category alter microbial diversity and community structure: Molecular evidence from wood-inhabiting fungi in forest ecosystems. <i>Journal of Environmental Management</i> , 2014, 139, 109-119.	3.8	61
20	Meta-analysis of deep-sequenced fungal communities indicates limited taxon sharing between studies and the presence of biogeographic patterns. <i>New Phytologist</i> , 2014, 201, 623-635.	3.5	106
21	Tissue storage and primer selection influence pyrosequencing-based inferences of diversity and community composition of endolichenic and endophytic fungi. <i>Molecular Ecology Resources</i> , 2014, 14, 1032-1048.	2.2	83
22	An Illumina metabarcoding pipeline for fungi. <i>Ecology and Evolution</i> , 2014, 4, 2642-2653.	0.8	107
23	Impact of primer choice on characterization of orchid mycorrhizal communities using 454 pyrosequencing. <i>Molecular Ecology Resources</i> , 2014, 14, 679-699.	2.2	105
24	Symptomless Endophytic Fungi Suppress Endogenous Levels of Salicylic Acid and Interact With the Jasmonate-Dependent Indirect Defense Traits of Their Host, Lima Bean (<i>Phaseolus lunatus</i>). <i>Journal of Chemical Ecology</i> , 2014, 40, 816-825.	0.9	46
25	Molecular sequence data from populations of <i>Bryoria fuscescens</i> s. lat. in the mountains of central Spain indicates a mismatch between haplotypes and chemotypes. <i>Lichenologist</i> , 2015, 47, 279-286.	0.5	8
26	Molecular studies reveal a new species of <i>Bryoria</i> in Chile. <i>Lichenologist</i> , 2015, 47, 387-394.	0.5	5
27	A Comprehensive, Automatically Updated Fungal ITS Sequence Dataset for Reference-Based Chimera Control in Environmental Sequencing Efforts. <i>Microbes and Environments</i> , 2015, 30, 145-150.	0.7	231
28	Bringing Laboulbeniales into the 21st century: enhanced techniques for extraction and PCR amplification of DNA from minute ectoparasitic fungi. <i>IMA Fungus</i> , 2015, 6, 363-372.	1.7	45
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31	Metagenomic Insights into the Bioaerosols in the Indoor and Outdoor Environments of Childcare Facilities. <i>PLoS ONE</i> , 2015, 10, e0126960.	1.1	75
32	Metabarcoding Analysis of Fungal Diversity in the Phyllosphere and Carposphere of Olive (<i>Olea</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.1	123
33	Elevated Genetic Diversity in the Emerging Blueberry Pathogen <i>Exobasidium maculosum</i> . <i>PLoS ONE</i> , 2015, 10, e0132545.	1.1	9
34	Accuracy of the high-throughput amplicon sequencing to identify species within the genus <i>Aspergillus</i> . <i>Fungal Biology</i> , 2015, 119, 1311-1321.	1.1	12
35	Analysis of the community compositions of rhizosphere fungi in soybeans continuous cropping fields. <i>Microbiological Research</i> , 2015, 180, 49-56.	2.5	126
36	Rare biosphere exploration using high-throughput sequencing: research progress and perspectives. <i>Conservation Genetics</i> , 2015, 16, 513-522.	0.8	62

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37	High-throughput DNA barcoding for ecological network studies. <i>Population Ecology</i> , 2015, 57, 37-51.	0.7	26
38	Comparison of ITS and 18S rDNA for estimating fungal diversity using PCR-DGGE. <i>World Journal of Microbiology and Biotechnology</i> , 2015, 31, 1387-1395.	1.7	44
39	Fungal Communities Respond to Long-Term CO ₂ Elevation by Community Reassembly. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2445-2454.	1.4	48
40	Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. <i>MycoKeys</i> , 0, 10, 1-43.	0.8	409
41	Systemic canine histoplasmosis: A case report from Ecuador. <i>Medical Mycology Case Reports</i> , 2015, 9, 18-21.	0.7	1
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45	Comparison of the Diversity of Basidiomycetes from Dead Wood of the Manchurian fir (<i>Abies</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 <i>Microbial Ecology</i> , 2015, 70, 634-645.	1.4	13
46	Diversity of Fungi on Decomposing Leaf Litter in a Sugarcane Plantation and Their Response to Tillage Practice and Bagasse Mulching: Implications for Management Effects on Litter Decomposition. <i>Microbial Ecology</i> , 2015, 70, 646-658.	1.4	22
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56	Detection of Invertebrate Suppressing Soils, and Identification of a Possible Biological Control Agent for Meloidogyne Nematodes Using High Resolution Rhizosphere Microbial Community Analysis. <i>Frontiers in Plant Science</i> , 2016, 7, 1946.	1.7	27
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65	Advance Detection Techniques of Phytopathogenic Fungi: Current Trends and Future Perspectives. <i>Fungal Biology</i> , 2016, , 265-298.	0.3	9
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74	Molecular variation analysis of <i>Aspergillus flavus</i> using polymerase chain reaction-restriction fragment length polymorphism of the internal transcribed spacer rDNA region. <i>Experimental and Therapeutic Medicine</i> , 2016, 12, 1628-1632.	0.8	8
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107	Critical Issues in Mycobiota Analysis. <i>Frontiers in Microbiology</i> , 2017, 8, 180.	1.5	83
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