

Cross-biome metagenomic analyses of soil microbial community attributes

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Interspecific bacterial sensing through airborne signals modulates locomotion and drug resistance. <i>Nature Communications</i> , 2013, 4, 1809.	5.8	102
2	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	9.4	8,049
3	Global marine bacterial diversity peaks at high latitudes in winter. <i>ISME Journal</i> , 2013, 7, 1669-1677.	4.4	195
4	Culture-Independent Molecular Tools for Soil and Rhizosphere Microbiology. <i>Diversity</i> , 2013, 5, 581-612.	0.7	88
5	Reconstructing the Microbial Diversity and Function of Pre-Agricultural Tallgrass Prairie Soils in the United States. <i>Science</i> , 2013, 342, 621-624.	6.0	480
6	Structural Basis for flg22-Induced Activation of the <i>Arabidopsis</i> FLS2-BAK1 Immune Complex. <i>Science</i> , 2013, 342, 624-628.	6.0	604
7	Cell Size Distributions of Soil Bacterial and Archaeal Taxa. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7610-7617.	1.4	98
8	Soil bacterial communities shaped by geochemical factors and land use in a less-explored area, Tibetan Plateau. <i>BMC Genomics</i> , 2013, 14, 820.	1.2	51
9	Lessons Learned from the Microbial Analysis of the Herschel Spacecraft during Assembly, Integration, and Test Operations. <i>Astrobiology</i> , 2013, 13, 1125-1139.	1.5	25
10	Changes induced by <i>Trichoderma harzianum</i> in suppressive compost controlling <i>Fusarium</i> wilt. <i>Pesticide Biochemistry and Physiology</i> , 2013, 107, 112-119.	1.6	45
11	Forensic analysis of soils using single arbitrarily primed amplification and high throughput sequencing. <i>Forensic Science International: Genetics Supplement Series</i> , 2013, 4, e39-e40.	0.1	5
12	Phylogenetic beta diversity in bacterial assemblages across ecosystems: deterministic versus stochastic processes. <i>ISME Journal</i> , 2013, 7, 1310-1321.	4.4	515
13	Evidence for successional development in Antarctic hypolithic bacterial communities. <i>ISME Journal</i> , 2013, 7, 2080-2090.	4.4	93
14	From molecules to dynamic biological communities. <i>Biology and Philosophy</i> , 2013, 28, 241-259.	0.7	12
15	Microbial modulators of soil carbon storage: integrating genomic and metabolic knowledge for global prediction. <i>Trends in Microbiology</i> , 2013, 21, 641-651.	3.5	429
16	Analytical Tools and Databases for Metagenomics in the Next-Generation Sequencing Era. <i>Genomics and Informatics</i> , 2013, 11, 102.	0.4	117
17	A metagenomic snapshot of taxonomic and functional diversity in an alpine glacier cryoconite ecosystem. <i>Environmental Research Letters</i> , 2013, 8, 035003.	2.2	88
18	Functional ecology of an Antarctic Dry Valley. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8990-8995.	3.3	224

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19	Different bacterial communities in ectomycorrhizae and surrounding soil. <i>Scientific Reports</i> , 2013, 3, 3471.	1.6	77
20	Metagenomic analysis reveals significant changes of microbial compositions and protective functions during drinking water treatment. <i>Scientific Reports</i> , 2013, 3, 3550.	1.6	116
21	Assessment of Fungal Diversity in the Environment using Metagenomics:a Decade in Review. <i>Fungal Genomics & Biology</i> , 2013, 03, .	0.4	36
22	Home Life: Factors Structuring the Bacterial Diversity Found within and between Homes. <i>PLoS ONE</i> , 2013, 8, e64133.	1.1	277
23	Changes in Bacterial and Fungal Communities across Compost Recipes, Preparation Methods, and Composting Times. <i>PLoS ONE</i> , 2013, 8, e79512.	1.1	258
24	Coupled high-throughput functional screening and next generation sequencing for identification of plant polymer decomposing enzymes in metagenomic libraries. <i>Frontiers in Microbiology</i> , 2013, 4, 282.	1.5	44
25	Structure, Composition and Metagenomic Profile of Soil Microbiomes Associated to Agricultural Land Use and Tillage Systems in Argentine Pampas. <i>PLoS ONE</i> , 2014, 9, e99949.	1.1	191
26	Bioinformatic Approaches Reveal Metagenomic Characterization of Soil Microbial Community. <i>PLoS ONE</i> , 2014, 9, e93445.	1.1	56
27	Random Whole Metagenomic Sequencing for Forensic Discrimination of Soils. <i>PLoS ONE</i> , 2014, 9, e104996.	1.1	40
28	Differences in the Activities of Eight Enzymes from Ten Soil Fungi and Their Possible Influences on the Surface Structure, Functional Groups, and Element Composition of Soil Colloids. <i>PLoS ONE</i> , 2014, 9, e111740.	1.1	16
29	Soil fauna and soil functions: a jigsaw puzzle. <i>Frontiers in Environmental Science</i> , 2014, 2, .	1.5	153
30	Seeing the forest for the genes: using metagenomics to infer the aggregated traits of microbial communities. <i>Frontiers in Microbiology</i> , 2014, 5, 614.	1.5	107
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35	Metagenomic evidence for metabolism of trace atmospheric gases by high-elevation desert Actinobacteria. <i>Frontiers in Microbiology</i> , 2014, 5, 698.	1.5	62
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38	Belowground biodiversity and ecosystem functioning. <i>Nature</i> , 2014, 515, 505-511.	13.7	2,371
39	Measuring fluxes of trace gases and energy between ecosystems and the atmosphere – the state and future of the eddy covariance method. <i>Global Change Biology</i> , 2014, 20, 3600-3609.	4.2	377
40	Census-based rapid and accurate metagenome taxonomic profiling. <i>BMC Genomics</i> , 2014, 15, 918.	1.2	18
41	Diversity and relative abundance of the bacterial pathogen, <i>Flavobacterium</i> spp., infecting reproductive ecotypes of kokanee salmon. <i>BMC Research Notes</i> , 2014, 7, 778.	0.6	0
42	Human and Environmental Impacts on River Sediment Microbial Communities. <i>PLoS ONE</i> , 2014, 9, e97435.	1.1	115
43	The Potential of Metagenomic Approaches for Understanding Soil Microbial Processes. <i>Soil Science Society of America Journal</i> , 2014, 78, 3-10.	1.2	105
44	Similar Processes but Different Environmental Filters for Soil Bacterial and Fungal Community Composition Turnover on a Broad Spatial Scale. <i>PLoS ONE</i> , 2014, 9, e111667.	1.1	35
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46	Responses of soil microbial community to different concentration of fomesafen. <i>Journal of Hazardous Materials</i> , 2014, 273, 155-164.	6.5	71
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48	Predicting the responsiveness of soil biodiversity to deforestation: a cross-biome study. <i>Global Change Biology</i> , 2014, 20, 2983-2994.	4.2	101
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51	Microbial community development and unseen diversity recovery in inoculated sterile soil. <i>Biology and Fertility of Soils</i> , 2014, 50, 1069-1076.	2.3	53
52	Endemism and functional convergence across the North American soil mycobiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6341-6346.	3.3	482
53	Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1777-1786.	1.4	131
54	Habitat-specific type I polyketide synthases in soils and street sediments. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 75-85.	1.4	21

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56	Biogeographic patterns in below-ground diversity in New York City's Central Park are similar to those observed globally. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20141988.	1.2	295
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61	Molecular ecology of microbial mats. <i>FEMS Microbiology Ecology</i> , 2014, 90, 335-50.	1.3	154
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63	Niche partitioning of bacterial communities in biological crusts and soils under grasses, shrubs and trees in the Kalahari. <i>Biodiversity and Conservation</i> , 2014, 23, 1709-1733.	1.2	47
64	The unseen world: environmental microbial sequencing and identification methods for ecologists. <i>Frontiers in Ecology and the Environment</i> , 2014, 12, 224-231.	1.9	27
65	Wastewater Irrigation Increases the Abundance of Potentially Harmful Gammaproteobacteria in Soils in Mezquital Valley, Mexico. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5282-5291.	1.4	80
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72	Pros and cons of methylation-based enrichment methods for ancient DNA. <i>Scientific Reports</i> , 2015, 5, 11826.	1.6	61

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74	Evaluation of shotgun metagenomics sequence classification methods using in silico and in vitro simulated communities. <i>BMC Bioinformatics</i> , 2015, 16, 363.	1.2	145
75	Maternal fucosyltransferase 2 status affects the gut bifidobacterial communities of breastfed infants. <i>Microbiome</i> , 2015, 3, 13.	4.9	319
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80	Microbial Ecology in the Era of Next Generation Sequencing. <i>Journal of Next Generation Sequencing & Applications</i> , 2015, 01, .	0.3	9
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84	Namib Desert dune/interdune transects exhibit habitat-specific edaphic bacterial communities. <i>Frontiers in Microbiology</i> , 2015, 6, 845.	1.5	46
85	Relations of microbiome characteristics to edaphic properties of tropical soils from Trinidad. <i>Frontiers in Microbiology</i> , 2015, 6, 1045.	1.5	28
86	Emerging spatial patterns in Antarctic prokaryotes. <i>Frontiers in Microbiology</i> , 2015, 6, 1058.	1.5	58
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88	Pyrosequencing Reveals Changes in Soil Bacterial Communities after Conversion of Yungas Forests to Agriculture. <i>PLoS ONE</i> , 2015, 10, e0119426.	1.1	48
89	CoMeta: Classification of Metagenomes Using k-mers. <i>PLoS ONE</i> , 2015, 10, e0121453.	1.1	28
90	Genus-Wide Comparative Genomics of <i>Malassezia</i> Delineates Its Phylogeny, Physiology, and Niche Adaptation on Human Skin. <i>PLoS Genetics</i> , 2015, 11, e1005614.	1.5	198

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104	Cyanobacteria drive community composition and functionality in rock-soil interface communities. <i>Molecular Ecology</i> , 2015, 24, 812-821.	2.0	63
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106	Functional congruence of rhizosphere microbial communities associated to leguminous tree from Brazilian semiarid region. <i>Environmental Microbiology Reports</i> , 2015, 7, 95-101.	1.0	20
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111	Microbiomes of Streptophyte Algae and Bryophytes Suggest That a Functional Suite of Microbiota Fostered Plant Colonization of Land. <i>International Journal of Plant Sciences</i> , 2015, 176, 405-420.	0.6	88
112	The changing form of Antarctic biodiversity. <i>Nature</i> , 2015, 522, 431-438.	13.7	277
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119	Thermophiles in the genomic era: Biodiversity, science, and applications. <i>Biotechnology Advances</i> , 2015, 33, 633-647.	6.0	125
120	Continental-scale distributions of dust-associated bacteria and fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5756-5761.	3.3	372
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124	Bacterial diversity in native habitats of the medicinal fungus <i>Ophiocordyceps sinensis</i> on Tibetan Plateau as determined using Illumina sequencing data. <i>FEMS Microbiology Letters</i> , 2015, 362, .	0.7	24
125	Tax4Fun: predicting functional profiles from metagenomic 16S rRNA data. <i>Bioinformatics</i> , 2015, 31, 2882-2884.	1.8	1,283
126	A metagenome for lacustrine <i>Cladophora</i> (Cladophorales) reveals remarkable diversity of eukaryotic epibionts and genes relevant to materials cycling. <i>Journal of Phycology</i> , 2015, 51, 408-418.	1.0	15
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129	Scale-dependent effects of climate and geographic distance on bacterial diversity patterns across northern China's grasslands. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv133.	1.3	87
130	Available nitrogen is the key factor influencing soil microbial functional gene diversity in tropical rainforest. <i>BMC Microbiology</i> , 2015, 15, 167.	1.3	41
131	Assembly independent functional annotation of short-read data using SOFA: Short-ORF functional annotation. , 2015, , .		2
132	Rapid comparison and correlation analysis among massive number of microbial community samples based on MDV data model. <i>Scientific Reports</i> , 2015, 4, 6393.	1.6	4
133	Direct and indirect effects of climate change on soil microbial and soil microbial-plant interactions: What lies ahead?. <i>Ecosphere</i> , 2015, 6, 1-21.	1.0	433
134	Genomics in a changing arctic: critical questions await the molecular ecologist. <i>Molecular Ecology</i> , 2015, 24, 2301-2309.	2.0	10
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136	Nitrogen Cycling Potential of a Grassland Litter Microbial Community. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7012-7022.	1.4	51
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142	Combined Flux Chamber and Genomics Approach Links Nitrous Acid Emissions to Ammonia Oxidizing Bacteria and Archaea in Urban and Agricultural Soil. <i>Environmental Science & Technology</i> , 2015, 49, 13825-13834.	4.6	56
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144	Microbial diversity - exploration of natural ecosystems and microbiomes. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 66-72.	1.5	105
145	Relationships between protein-encoding gene abundance and corresponding process are commonly assumed yet rarely observed. <i>ISME Journal</i> , 2015, 9, 1693-1699.	4.4	276

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147	Forest Health in a Changing World. <i>Microbial Ecology</i> , 2015, 69, 826-842.	1.4	92
148	Ancient and modern environmental DNA. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130383.	1.8	292
149	The functional and taxonomic richness of wastewater treatment plant microbial communities are associated with each other and with ambient nitrogen and carbon availability. <i>Environmental Microbiology</i> , 2015, 17, 4851-4860.	1.8	59
150	The genus <i>Nonomuraea</i> : A review of a rare actinomycete taxon for novel metabolites. <i>Journal of Basic Microbiology</i> , 2015, 55, 554-565.	1.8	44
151	Soil biodiversity and DNA barcodes: opportunities and challenges. <i>Soil Biology and Biochemistry</i> , 2015, 80, 244-250.	4.2	137
152	Metagenomic analysis reveals microbial functional redundancies and specificities in a soil under different tillage and crop-management regimes. <i>Applied Soil Ecology</i> , 2015, 86, 106-112.	2.1	76
153	Responses of Soil Fungi to Logging and Oil Palm Agriculture in Southeast Asian Tropical Forests. <i>Microbial Ecology</i> , 2015, 69, 733-747.	1.4	87
154	Taxonomic and Functional Metagenomic Signature of Turfs in the Abrolhos Reef System (Brazil). <i>PLoS ONE</i> , 2016, 11, e0161168.	1.1	21
155	Metagenomic analyses of the late Pleistocene permafrost – additional tools for reconstruction of environmental conditions. <i>Biogeosciences</i> , 2016, 13, 2207-2219.	1.3	59
156	Comparison of Fungal Community in Black Pepper-Vanilla and Vanilla Monoculture Systems Associated with Vanilla Fusarium Wilt Disease. <i>Frontiers in Microbiology</i> , 2016, 7, 117.	1.5	78
157	Microbes as Engines of Ecosystem Function: When Does Community Structure Enhance Predictions of Ecosystem Processes?. <i>Frontiers in Microbiology</i> , 2016, 7, 214.	1.5	479
158	Metagenomics Reveals Pervasive Bacterial Populations and Reduced Community Diversity across the Alaska Tundra Ecosystem. <i>Frontiers in Microbiology</i> , 2016, 7, 579.	1.5	66
159	Metagenomic Reconstruction of Key Anaerobic Digestion Pathways in Municipal Sludge and Industrial Wastewater Biogas-Producing Systems. <i>Frontiers in Microbiology</i> , 2016, 7, 778.	1.5	103
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