

Richard C Hamelin

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

171
papers

7,898
citations

36
h-index

85
g-index

188
ext. papers

9,555
ext. citations

4.2
avg, IF

5.35
L-index

#	Paper	IF	Citations
171	Genomic biosurveillance detects a sexual hybrid in the sudden oak death pathogen.. <i>Communications Biology</i> , 2022 , 5, 477	6.7	0
170	Rust diseases of forest trees 2022 , 201-213		
169	Development of a Rapid Loop-Mediated Isothermal Amplification Assay for the Detection of <i>Dothistroma septosporum</i> . <i>Forests</i> , 2021 , 12, 362	2.8	4
168	Comparative Gene Expression Analysis Reveals Mechanism of Response to the Fungal Pathogen. <i>Molecular Plant-Microbe Interactions</i> , 2021 , 34, 397-409	3.6	4
167	Transcriptional profile of oil palm pathogen, <i>Ganoderma boninense</i> , reveals activation of lignin degradation machinery and possible evasion of host immune response. <i>BMC Genomics</i> , 2021 , 22, 326	4.5	2
166	Oh the places they go: improving species distribution modelling for invasive forest pests in an uncertain world. <i>Biological Invasions</i> , 2021 , 23, 297-349	2.7	10
165	Evolution and Adaptation of Forest and Crop Pathogens in the Anthropocene. <i>Phytopathology</i> , 2021 , 111, 49-67	3.8	9
164	DNA-barcoding identification of <i>Dothistroma septosporum</i> on <i>Pinus contorta</i> var. <i>latifolia</i> , <i>P. banksiana</i> and their hybrid in northern Alberta, Canada. <i>Canadian Journal of Plant Pathology</i> , 2021 , 43, 472-479	1.6	5
163	Swiss needle cast tolerance in British Columbia coastal Douglas-fir breeding population. <i>Forestry</i> , 2021 , 94, 193-203	2.2	3
162	Potential Differences and Methods of Determining Gypsy Moth Female Flight Capabilities: Implications for the Establishment and Spread in Novel Habitats. <i>Forests</i> , 2021 , 12, 103	2.8	1
161	Worldwide Genetic Structure Elucidates the Eurasian Origin and Invasion Pathways of , Causal Agent of <i>Dothistroma</i> Needle Blight. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	10
160	Signatures of Post-Glacial Genetic Isolation and Human-Driven Migration in the <i>Dothistroma</i> Needle Blight Pathogen in Western Canada. <i>Phytopathology</i> , 2021 , 111, 116-127	3.8	12
159	An Applied Empirical Framework for Invasion Science: Confronting Biological Invasion Through Collaborative Research Aimed at Tool Production. <i>Annals of the Entomological Society of America</i> , 2020 , 113, 230-245	2	8
158	Molecular assays to detect the presence and viability of <i>Phytophthora ramorum</i> and <i>Grosmannia clavigera</i> . <i>PLoS ONE</i> , 2020 , 15, e0221742	3.7	3
157	Hybridization and introgression drive genome evolution of Dutch elm disease pathogens. <i>Nature Ecology and Evolution</i> , 2020 , 4, 626-638	12.3	23
156	Long-term effects of stump removal and tree species composition on the diversity and structure of soil fungal communities. <i>FEMS Microbiology Ecology</i> , 2020 , 96,	4.3	4
155	Supervised learning on phylogenetically distributed data. <i>Bioinformatics</i> , 2020 , 36, i895-i902	7.2	1

154	Genomic biosurveillance of forest invasive alien enemies: A story written in code. <i>Evolutionary Applications</i> , 2020 , 13, 95-115	4.8	31
153	Population Genomic Analyses Reveal Connectivity via Human-Mediated Transport across Plantations in North America and an Undescribed Subpopulation of. <i>Molecular Plant-Microbe Interactions</i> , 2020 , 33, 189-199	3.6	6
152	Reassessment of the status of <i>Lymantria albescens</i> and <i>Lymantria postalba</i> (Lepidoptera: Erebidae: Lymantriinae) as distinct Asian gypsy moth species, using both mitochondrial and nuclear sequence data. <i>Systematic Entomology</i> , 2020 , 45, 493-504	3.4	1
151	Assessing Niche Shifts and Conservatism by Comparing the Native and Post-Invasion Niches of Major Forest Invasive Species. <i>Insects</i> , 2020 , 11,	2.8	2
150	CRISPR/Cas9 Gene Editing: An Unexplored Frontier for Forest Pathology. <i>Frontiers in Plant Science</i> , 2020 , 11, 1126	6.2	11
149	Stump removal and tree species composition promote a bacterial microbiome that may be beneficial in the suppression of root disease. <i>FEMS Microbiology Ecology</i> , 2020 , 97,	4.3	1
148	Mycorrhiza: genotype assignment using phylogenetic networks. <i>Bioinformatics</i> , 2020 , 36, 212-220	7.2	1
147	In Situ Processing and Efficient Environmental Detection (iSPEED) of tree pests and pathogens using point-of-use real-time PCR. <i>PLoS ONE</i> , 2020 , 15, e0226863	3.7	10
146	In Situ Processing and Efficient Environmental Detection (iSPEED) of tree pests and pathogens using point-of-use real-time PCR 2020 , 15, e0226863		
145	In Situ Processing and Efficient Environmental Detection (iSPEED) of tree pests and pathogens using point-of-use real-time PCR 2020 , 15, e0226863		
144	In Situ Processing and Efficient Environmental Detection (iSPEED) of tree pests and pathogens using point-of-use real-time PCR 2020 , 15, e0226863		
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142	In Situ Processing and Efficient Environmental Detection (iSPEED) of tree pests and pathogens using point-of-use real-time PCR 2020 , 15, e0226863		
141	Molecular assays to detect the presence and viability of <i>Phytophthora ramorum</i> and <i>Grosmannia clavigera</i> 2020 , 15, e0221742		
140	Molecular assays to detect the presence and viability of <i>Phytophthora ramorum</i> and <i>Grosmannia clavigera</i> 2020 , 15, e0221742		
139	Molecular assays to detect the presence and viability of <i>Phytophthora ramorum</i> and <i>Grosmannia clavigera</i> 2020 , 15, e0221742		
138	Molecular assays to detect the presence and viability of <i>Phytophthora ramorum</i> and <i>Grosmannia clavigera</i> 2020 , 15, e0221742		
137	Fine-scale genetic diversity and relatedness in fungi associated with the mountain pine beetle. <i>Canadian Journal of Forest Research</i> , 2019 , 49, 933-941	1.9	4

136	Ecology and Evolution of the Sudden Oak Death Pathogen. <i>Annual Review of Phytopathology</i> , 2019 , 57, 301-321	10.8	36
135	A needle in a haystack: a multigene TaqMan assay for the detection of Asian gypsy moths in bulk pheromone trap samples. <i>Biological Invasions</i> , 2019 , 21, 1843-1856	2.7	6
134	Improved detection and identification of the sudden oak death pathogen <i>Phytophthora ramorum</i> and the Port Orford cedar root pathogen <i>Phytophthora lateralis</i> . <i>Plant Pathology</i> , 2019 , 68, 878-888	2.8	4
133	Mitotic Recombination and Rapid Genome Evolution in the Invasive Forest Pathogen. <i>MBio</i> , 2019 , 10,	7.8	34
132	Genome-enhanced detection and identification of fungal pathogens responsible for pine and poplar rust diseases. <i>PLoS ONE</i> , 2019 , 14, e0210952	3.7	7
131	Biosurveillance of forest insects: part I Integration and application of genomic tools to the surveillance of non-native forest insects. <i>Journal of Pest Science</i> , 2019 , 92, 51-70	5.5	22
130	Cryptic Speciation in Western North America and Eastern Eurasia of the Pathogens Responsible for Laminated Root Rot. <i>Phytopathology</i> , 2019 , 109, 456-468	3.8	4
129	Biosurveillance of forest insects: part II Adoption of genomic tools by end user communities and barriers to integration. <i>Journal of Pest Science</i> , 2019 , 92, 71-82	5.5	11
128	The contribution of genetics and genomics to understanding the ecology of the mountain pine beetle system. <i>Canadian Journal of Forest Research</i> , 2019 , 49, 721-730	1.9	9
127	Variable genome evolution in fungi after transposon-mediated amplification of a housekeeping gene. <i>Mobile DNA</i> , 2019 , 10, 37	4.4	1
126	Expansion of LINEs and species-specific DNA repeats drives genome expansion in Asian Gypsy Moths. <i>Scientific Reports</i> , 2019 , 9, 16413	4.9	1
125	Assessing the potential of genotyping-by-sequencing-derived single nucleotide polymorphisms to identify the geographic origins of intercepted gypsy moth (<i>Lymantria dispar</i>) specimens: A proof-of-concept study. <i>Evolutionary Applications</i> , 2018 , 11, 325-339	4.8	19
124	Overexpression of AtGolS3 and CsRFS in poplar enhances ROS tolerance and represses defense response to leaf rust disease. <i>Tree Physiology</i> , 2018 , 38, 457-470	4.2	11
123	Genome-Enhanced Detection and Identification (GEDI) of plant pathogens. <i>PeerJ</i> , 2018 , 6, e4392	3.1	15
122	Genetic diversity of <i>Phytophthora pluvialis</i> , a pathogen of conifers, in New Zealand and the west coast of the United States of America. <i>Plant Pathology</i> , 2018 , 67, 1131-1139	2.8	13
121	An Overview of Canadian Research Activities on Diseases Caused by <i>Phytophthora ramorum</i> : Results, Progress, and Challenges. <i>Plant Disease</i> , 2018 , 102, 1218-1233	1.5	5
120	Genetic and genomic evidence of niche partitioning and adaptive radiation in mountain pine beetle fungal symbionts. <i>Molecular Ecology</i> , 2017 , 26, 2077-2091	5.7	26
119	Development and Validation of Polymorphic Microsatellite Loci for the NA2 Lineage of <i>Phytophthora ramorum</i> from Whole Genome Sequence Data. <i>Plant Disease</i> , 2017 , 101, 666-673	1.5	10

118	Sexual homomorphism in dioecious trees: extensive tests fail to detect sexual dimorphism in <i>Populus</i> . <i>Scientific Reports</i> , 2017 , 7, 1831	4.9	36
117	Real-time PCR assays for the detection of <i>Heterobasidion irregulare</i> , <i>H. occidentale</i> , <i>H. annosum sensu stricto</i> and the <i>Heterobasidion annosum</i> complex. <i>Forest Pathology</i> , 2017 , 47, e12321	1.2	12
116	Comparative analysis of mitochondrial genomes of geographic variants of the gypsy moth, <i>Lymantria dispar</i> , reveals a previously undescribed genotypic entity. <i>Scientific Reports</i> , 2017 , 7, 14245	4.9	21
115	Say hello to my little friends: how microbiota can modulate tree health. <i>New Phytologist</i> , 2017 , 215, 508-518	5.80	11
114	Anthropogenic signature in the incidence and distribution of an emerging pathogen of poplars. <i>Biological Invasions</i> , 2016 , 18, 1147-1161	2.7	9
113	<i>Neofusicoccum arbuti</i> : a hidden threat to <i>Arbutus menziesii</i> characterized by widespread latent infections and a broad host range. <i>Canadian Journal of Plant Pathology</i> , 2016 , 38, 70-81	1.6	1
112	Combating a Global Threat to a Clonal Crop: Banana Black Sigatoka Pathogen <i>Pseudocercospora fijiensis</i> (Synonym <i>Mycosphaerella fijiensis</i>) Genomes Reveal Clues for Disease Control. <i>PLoS Genetics</i> , 2016 , 12, e1005876	6	44
111	A Multi-Species TaqMan PCR Assay for the Identification of Asian Gypsy Moths (<i>Lymantria</i> spp.) and Other Invasive <i>Lymantriines</i> of Biosecurity Concern to North America. <i>PLoS ONE</i> , 2016 , 11, e0160878	3.7	21
110	Simultaneous monitoring and quantification of <i>Melampsora allii-populina</i> and <i>Melampsora larici-populina</i> on infected poplar leaves using a duplex real-time PCR assay. <i>Plant Pathology</i> , 2016 , 65, 380-391	2.8	7
109	Genetic patterns reveal historical and contemporary dispersal of a tree pathogen. <i>Biological Invasions</i> , 2016 , 18, 1781-1799	2.7	12
108	Genome sequences of six species threatening forest ecosystems. <i>Genomics Data</i> , 2016 , 10, 85-88		20
107	Horizontal gene transfer and gene dosage drives adaptation to wood colonization in a tree pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 3451-6	11.5	47
106	Asexual propagation of a virulent clone complex in a human and feline outbreak of sporotrichosis. <i>Eukaryotic Cell</i> , 2015 , 14, 158-69		32
105	The MAT1-1:MAT1-2 ratio of <i>Sporothrix globosa</i> isolates in Japan. <i>Mycopathologia</i> , 2015 , 179, 81-6	2.9	9
104	Colonization history, host distribution, anthropogenic influence and landscape features shape populations of white pine blister rust, an invasive alien tree pathogen. <i>PLoS ONE</i> , 2015 , 10, e0127916	3.7	17
103	Molecular Detection of 10 of the Most Unwanted Alien Forest Pathogens in Canada Using Real-Time PCR. <i>PLoS ONE</i> , 2015 , 10, e0134265	3.7	41
102	Evolutionary Quantitative Genomics of <i>Populus trichocarpa</i> . <i>PLoS ONE</i> , 2015 , 10, e0142864	3.7	20
101	Real-time PCR assay to distinguish <i>Phytophthora ramorum</i> lineages using the cellulose binding elicitor lectin (CBEL) locus. <i>Canadian Journal of Plant Pathology</i> , 2014 , 36, 367-376	1.6	12

100	Real-time PCR detection and discrimination of the <i>Ceratocystis coerulea</i> complex and of the fungal species from the <i>Ceratocystis polonica</i> complex validated on pure cultures and bark beetle vectors. <i>Canadian Journal of Forest Research</i> , 2014 , 44, 1103-1111	1.9	7
99	Finding needles in haystacks: linking scientific names, reference specimens and molecular data for Fungi. <i>Database: the Journal of Biological Databases and Curation</i> , 2014 , 2014,	5	199
98	Genetic Resistance to Fusiform Rust in Southern Pines and White Pine Blister Rust in White Pines: A Contrasting Tale of Two Rust Pathosystems: Current Status and Future Prospects. <i>Forests</i> , 2014 , 5, 2050-2083	2.8	61
97	Duplications and losses in gene families of rust pathogens highlight putative effectors. <i>Frontiers in Plant Science</i> , 2014 , 5, 299	6.2	32
96	The landscape of transposable elements in the finished genome of the fungal wheat pathogen <i>Mycosphaerella graminicola</i> . <i>BMC Genomics</i> , 2014 , 15, 1132	4.5	49
95	Association genetics, geography and ecophysiology link stomatal patterning in <i>Populus trichocarpa</i> with carbon gain and disease resistance trade-offs. <i>Molecular Ecology</i> , 2014 , 23, 5771-90	5.7	67
94	Single-nucleotide polymorphism discovery in <i>Leptographium longiclavatum</i> , a mountain pine beetle-associated symbiotic fungus, using whole-genome resequencing. <i>Molecular Ecology Resources</i> , 2014 , 14, 401-10	8.4	13
93	Advancing Knowledge on Biology of Rust Fungi Through Genomics. <i>Advances in Botanical Research</i> , 2014 , 173-209	2.2	22
92	Extensive functional pleiotropy of REVOLUTA substantiated through forward genetics. <i>Plant Physiology</i> , 2014 , 164, 548-54	6.6	15
91	Population structure of mountain pine beetle symbiont <i>Leptographium longiclavatum</i> and the implication on the multipartite beetle-fungi relationships. <i>PLoS ONE</i> , 2014 , 9, e105455	3.7	10
90	Phylogenetic species recognition reveals host-specific lineages among poplar rust fungi. <i>Molecular Phylogenetics and Evolution</i> , 2013 , 66, 628-44	4.1	37
89	Rapid Identification and Detection of Pathogenic Fungi by Padlock Probes 2013 , 505-517		
88	A sensitive real-time PCR assay for the detection of the two <i>Melampsora medusae</i> formae speciales on infected poplar leaves. <i>European Journal of Plant Pathology</i> , 2013 , 136, 433-441	2.1	6
87	Optimization of a real-time PCR assay for the detection of the quarantine pathogen <i>Melampsora medusae</i> f. sp. <i>deltoidea</i> . <i>Fungal Biology</i> , 2013 , 117, 389-98	2.8	8
86	Unequal recombination and evolution of the mating-type (MAT) loci in the pathogenic fungus <i>Grosmannia clavigera</i> and relatives. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 465-80	3.2	34
85	The effects of high-tannin leaf litter from transgenic poplars on microbial communities in microcosm soils. <i>Frontiers in Microbiology</i> , 2013 , 4, 290	5.7	20
84	Association analysis identifies <i>Melampsora columbiana</i> poplar leaf rust resistance SNPs. <i>PLoS ONE</i> , 2013 , 8, e78423	3.7	26
83	A comprehensive analysis of genes encoding small secreted proteins identifies candidate effectors in <i>Melampsora larici-populina</i> (poplar leaf rust). <i>Molecular Plant-Microbe Interactions</i> , 2012 , 25, 279-93	3.6	109

82	Contributions of genomics to forest pathology. <i>Canadian Journal of Plant Pathology</i> , 2012 , 34, 20-28	1.6	6
81	Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 6241-6	11.5	2981
80	Population structure and migration pattern of a conifer pathogen, <i>Grosmannia clavigera</i> , as influenced by its symbiont, the mountain pine beetle. <i>Molecular Ecology</i> , 2012 , 21, 71-86	5.7	40
79	The genomes of the fungal plant pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> reveal adaptation to different hosts and lifestyles but also signatures of common ancestry. <i>PLoS Genetics</i> , 2012 , 8, e1003088	6	189
78	Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen Dothideomycetes fungi. <i>PLoS Pathogens</i> , 2012 , 8, e1003037	7.6	387
77	DNA barcoding in the rust genus <i>Chrysomyxa</i> and its implications for the phylogeny of the genus. <i>Mycologia</i> , 2011 , 103, 1250-66	2.4	37
76	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 9166-71	11.5	479
75	Putative origin of clonal lineages of <i>Amylostereum areolatum</i> , the fungal symbiont associated with <i>Sirex noctilio</i> , retrieved from <i>Pinus sylvestris</i> , in eastern Canada. <i>Fungal Biology</i> , 2011 , 115, 750-8	2.8	28
74	Spatial genetic structure of a symbiotic beetle-fungal system: toward multi-taxa integrated landscape genetics. <i>PLoS ONE</i> , 2011 , 6, e25359	3.7	47
73	Gene genealogies reveal cryptic species and host preferences for the pine fungal pathogen <i>Grosmannia clavigera</i> . <i>Molecular Ecology</i> , 2011 , 20, 2581-602	5.7	47
72	Impact of endochitinase-transformed white spruce on soil fungal communities under greenhouse conditions. <i>FEMS Microbiology Ecology</i> , 2011 , 76, 199-208	4.3	14
71	Functional categorization of unique expressed sequence tags obtained from the yeast-like growth phase of the elm pathogen <i>Ophiostoma novo-ulmi</i> . <i>BMC Genomics</i> , 2011 , 12, 431	4.5	9
70	Poplar rust systematics and refinement of <i>Melampsora</i> species delineation. <i>Fungal Diversity</i> , 2011 , 50, 227-248	17.6	30
69	Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont <i>Grosmannia clavigera</i> , a lodgepole pine pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 2504-9	11.5	161
68	<i>Morchella tomentosa</i> : a unique belowground structure and a new clade of morels. <i>Mycologia</i> , 2010 , 102, 1082-8	2.4	14
67	Impact of endochitinase-transformed white spruce on soil fungal biomass and ectendomycorrhizal symbiosis. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 2607-14	4.8	19
66	Recent advances related to poplar leaf spot and canker caused by <i>Septoria musiva</i> . <i>Canadian Journal of Plant Pathology</i> , 2010 , 32, 122-134	1.6	26
65	Current state of genetically modified plant impact on target and non-target fungi. <i>Environmental Reviews</i> , 2010 , 18, 441-475	4.5	18

64	Rapid identification and detection of pine pathogenic fungi associated with mountain pine beetles by padlock probes. <i>Journal of Microbiological Methods</i> , 2010 , 83, 26-33	2.8	21
63	Target-specific PCR primers can detect and differentiate ophiostomatoid fungi from microbial communities associated with the mountain pine beetle <i>Dendroctonus ponderosae</i> . <i>Fungal Biology</i> , 2010 , 114, 825-33	2.8	12
62	Comparative analysis of secreted protein evolution using expressed sequence tags from four poplar leaf rusts (<i>Melampsora</i> spp.). <i>BMC Genomics</i> , 2010 , 11, 422	4.5	55
61	Impact of an 8-year-old transgenic poplar plantation on the ectomycorrhizal fungal community. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 7527-36	4.8	30
60	Fungal pathogen (mis-) identifications: a case study with DNA barcodes on <i>Melampsora</i> rusts of aspen and white poplar. <i>Mycological Research</i> , 2009 , 113, 713-24		42
59	Patterns of colonization and spread in the fungal spruce pathogen <i>Onnia tomentosa</i> . <i>Molecular Ecology</i> , 2009 , 18, 4422-33	5.7	3
58	De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. <i>Genome Biology</i> , 2009 , 10, R94	18.3	119
57	Multiplex real-time polymerase chain reaction (PCR) for detection of <i>Phytophthora ramorum</i> , the causal agent of sudden oak death. <i>Canadian Journal of Plant Pathology</i> , 2009 , 31, 195-210	1.6	23
56	Evaluation of mitochondrial genes as DNA barcode for Basidiomycota. <i>Molecular Ecology Resources</i> , 2009 , 9 Suppl s1, 99-113	8.4	77
55	Characterization of microsatellite loci in the fungus, <i>Grosmannia clavigera</i> , a pine pathogen associated with the mountain pine beetle. <i>Molecular Ecology Resources</i> , 2009 , 9, 1500-3	8.4	9
54	Standardizing the nomenclature for clonal lineages of the sudden oak death pathogen, <i>Phytophthora ramorum</i> . <i>Phytopathology</i> , 2009 , 99, 792-5	3.8	83
53	Evaluation of molecular markers for <i>Phytophthora ramorum</i> detection and identification: testing for specificity using a standardized library of isolates. <i>Phytopathology</i> , 2009 , 99, 390-403	3.8	28
52	Effects of transgenic hybrid aspen overexpressing polyphenol oxidase on rhizosphere diversity. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 5340-8	4.8	23
51	Differentiation of European and North American genotypes of <i>Phytophthora ramorum</i> by real-time polymerase chain reaction primer extension. <i>Canadian Journal of Plant Pathology</i> , 2007 , 29, 408-420	1.6	15
50	Molecular Detection of <i>Phytophthora ramorum</i> by Real-Time Polymerase Chain Reaction Using TaqMan, SYBR Green, and Molecular Beacons. <i>Phytopathology</i> , 2007 , 97, 632-42	3.8	80
49	Detection and validation of EST-derived SNPs for poplar leaf rust <i>Melampsora medusae</i> f. sp. <i>deltoidae</i> . <i>Molecular Ecology Notes</i> , 2007 , 7, 1222-1228		13
48	Variability of nuclear SSU-rDNA group introns within <i>Septoria</i> species: incongruence with host sequence phylogenies. <i>Journal of Molecular Evolution</i> , 2007 , 64, 489-99	3.1	15
47	Fungal diversity, dominance, and community structure in the rhizosphere of clonal <i>Picea mariana</i> plants throughout nursery production chronosequences. <i>Microbial Ecology</i> , 2007 , 54, 672-84	4.4	29

46	Alteration of soil rhizosphere communities following genetic transformation of white spruce. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 4128-34	4.8	26
45	No evidence of an impact on the rhizosphere diazotroph community by the expression of <i>Bacillus thuringiensis</i> Cry1Ab toxin by Bt white spruce. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 6577-83	4.8	33
44	Genetic Diversity and the Presence of Two Distinct Groups in <i>Ophiostoma clavigerum</i> Associated with <i>Dendroctonus ponderosae</i> in British Columbia and the Northern Rocky Mountains. <i>Phytopathology</i> , 2007 , 97, 1177-85	3.8	17
43	Genetic Diversity in Poplar Leaf Rust (<i>Melampsora medusae</i> f. sp. <i>deltoidae</i>) in the Zones of Host Sympatry and Allopatry. <i>Phytopathology</i> , 2007 , 97, 603-10	3.8	10
42	Poplar leaf rusts: model pathogens for a model tree This minireview is one of a selection of papers published in the Special Issue on Poplar Research in Canada.. <i>Canadian Journal of Botany</i> , 2007 , 85, 1127-1135		24
41	Identification of mycobacteria in peat moss processing plants: application of molecular biology approaches. <i>Canadian Journal of Microbiology</i> , 2007 , 53, 92-9	3.2	24
40	Molecular epidemiology of forest pathogens: from genes to landscape. <i>Canadian Journal of Plant Pathology</i> , 2006 , 28, 167-181	1.6	8
39	Screening of ESTs from <i>Septoria musiva</i> (teleomorph <i>Mycosphaerella populorum</i>) for detection of SSR and PCR-BFLP markers. <i>Molecular Ecology Notes</i> , 2006 , 6, 356-358		4
38	Attributes and congruence of three molecular data sets: inferring phylogenies among <i>Septoria</i> -related species from woody perennial plants. <i>Molecular Phylogenetics and Evolution</i> , 2006 , 40, 808-29	4.1	21
37	Genetic Structure of <i>Mycosphaerella populorum</i> (Anamorph <i>Septoria musiva</i>) Populations in North-Central and Northeastern North America. <i>Phytopathology</i> , 2005 , 95, 608-16	3.8	25
36	Fingerprinting techniques as tools towards molecular quality control of <i>Pseudozyma flocculosa</i> . <i>Mycological Research</i> , 2005 , 109, 335-41		0
35	In vivo monitoring of obligate biotrophic pathogen growth by kinetic PCR. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 1546-52	4.8	39
34	Molecular epidemiology of white pine blister rust: recombination and spatial distribution. <i>Phytopathology</i> , 2005 , 95, 793-9	3.8	11
33	Molecular profiling of rhizosphere microbial communities associated with healthy and diseased black spruce (<i>Picea mariana</i>) seedlings grown in a nursery. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 3541-51	4.8	72
32	A spruce defensin showing strong antifungal activity and increased transcript accumulation after wounding and jasmonate treatments. <i>Physiological and Molecular Plant Pathology</i> , 2004 , 64, 331-341	2.6	32
31	A comparative study of genetic diversity of populations of <i>Nectria galligena</i> and <i>N. coccinea</i> var. <i>faginata</i> in North America. <i>Mycological Research</i> , 2002 , 106, 183-193		11
30	DNA polymorphism and molecular diagnosis in <i>Inonotus</i> spp.. <i>Canadian Journal of Plant Pathology</i> , 2002 , 24, 194-199	1.6	12
29	Nucleotide polymorphisms in three genes support host and geographic speciation in tree pathogens belonging to <i>Gremmeniella</i> spp.. <i>Canadian Journal of Botany</i> , 2002 , 80, 1151-1159		9

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27	Approaches to molecular characterization of fungal biocontrol agents: some case studies. <i>Canadian Journal of Plant Pathology</i> , 2001 , 23, 8-12	1.6	27
26	Phylogenetics of Helotiales and Rhytismatales based on partial small subunit nuclear ribosomal DNA sequences. <i>Mycologia</i> , 2001 , 93, 915-933	2.4	50
25	Molecular and Physiological Analysis of the Powdery Mildew Antagonist <i>Pseudozyma flocculosa</i> and Related Fungi. <i>Phytopathology</i> , 2001 , 91, 249-54	3.8	37
24	Genetic Variability of Canadian Populations of the Sapstain Fungus <i>Ophiostoma piceae</i> . <i>Phytopathology</i> , 2001 , 91, 369-76	3.8	11
23	Barrier to Gene Flow Between Eastern and Western Populations of <i>Cronartium ribicola</i> in North America. <i>Phytopathology</i> , 2000 , 90, 1073-8	3.8	37
22	PCR detection of <i>Gremmeniella abietina</i> , the causal agent of Scleroderris canker of pine. <i>Mycological Research</i> , 2000 , 104, 527-532		43
21	Molecular Epidemiology of Tree Pathogens. <i>Forestry Sciences</i> , 2000 , 375-393		1
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19	Genetic Structure of <i>Cronartium ribicola</i> Populations in Eastern Canada. <i>Phytopathology</i> , 1999 , 89, 915-938	3.8	30
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16	Sequence-tagged sites (STS) for studies of molecular epidemiology of scleroderris canker of conifers. <i>Theoretical and Applied Genetics</i> , 1998 , 97, 789-796	6	13
15	Molecular Evidence of Distinct Introductions of the European Race of <i>Gremmeniella abietina</i> into North America. <i>Phytopathology</i> , 1998 , 88, 582-8	3.8	29
14	Fine-level genetic structure of white pine blister rust populations. <i>Phytopathology</i> , 1998 , 88, 1187-91	3.8	15
13	Phylogeny of <i>Gremmeniella</i> spp. based on sequences of the 5.8S rDNA and internal transcribed spacer region. <i>Canadian Journal of Botany</i> , 1997 , 75, 693-698		20
12	Comparison of RAPD technique and somatic incompatibility tests for the identification of <i>Phlebiopsis gigantea</i> strains. <i>Canadian Journal of Botany</i> , 1997 , 75, 2097-2104		8
11	Genetic differentiation within the European race of <i>Gremmeniella abietina</i> . <i>Mycological Research</i> , 1996 , 100, 49-56		48

10	Genetic Diversity Between and Within Cankers of the White Pine Blister Rust. <i>Phytopathology</i> , 1996 , 86, 875	3.8	28
9	Genetic diversity in populations of <i>Cronartium ribicola</i> in plantations and natural stands of <i>Pinus strobus</i> . <i>Theoretical and Applied Genetics</i> , 1995 , 91, 1214-21	6	35
8	Discrimination between alfalfa and potato isolates of <i>Verticillium albo-atrum</i> using RAPD markers. <i>Mycological Research</i> , 1995 , 99, 1507-1512		22
7	Prediction of poplar leaf rust epidemics from a leaf-disk assay. <i>Canadian Journal of Forest Research</i> , 1994 , 24, 2085-2088	1.9	14
6	Genetic diversity in <i>Cronartium quercuum</i> f.sp. <i>fusiforme</i> on loblolly pines in southern U.S. <i>Current Genetics</i> , 1994 , 26, 359-63	2.9	31
5	Identification of <i>Gremmeniella abietina</i> Races with Random Amplified Polymorphic DNA Markers. <i>Applied and Environmental Microbiology</i> , 1993 , 59, 1752-5	4.8	59
4	Quantification of Disease Progress and Defoliation in the Poplar Leaf Rust-Eastern Cottonwood Pathosystem. <i>Phytopathology</i> , 1993 , 83, 140	3.8	10
3	Influence of leaf wetness, temperature, and rain on poplar leaf rust epidemics. <i>Canadian Journal of Forest Research</i> , 1992 , 22, 1249-1254	1.9	8
2	Adaptation of poplar leaf rust to Eastern cottonwood. <i>Euphytica</i> , 1992 , 62, 69-75	2.1	9
1	<i>Phytophthora</i> species associated with red alder dieback in British Columbia, Canada. <i>Canadian Journal of Plant Pathology</i> , 1-10	1.6	0