

# Bruce Alan McDonald

## List of Publications by Year in descending order

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190  
papers

17,872  
citations

12322

69  
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18115

120  
g-index

224  
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224  
docs citations

224  
times ranked

9009  
citing authors

#	ARTICLE	IF	CITATIONS
1	PATHOGEN POPULATION GENETICS, EVOLUTIONARY POTENTIAL, AND DURABLE RESISTANCE. Annual Review of Phytopathology, 2002, 40, 349-379.	3.5	1,785
2	Emergence of a new disease as a result of interspecific virulence gene transfer. Nature Genetics, 2006, 38, 953-956.	9.4	667
3	The Origins of Plant Pathogens in Agro-Ecosystems. Annual Review of Phytopathology, 2008, 46, 75-100.	3.5	514
4	Gene Flow in Plant Pathosystems. Annual Review of Phytopathology, 1993, 31, 353-373.	3.5	498
5	The population genetics of plant pathogens and breeding strategies for durable resistance. Euphytica, 2002, 124, 163-180.	0.6	437
6	Emergence of wheat blast in Bangladesh was caused by a South American lineage of <i>Magnaporthe oryzae</i> . BMC Biology, 2016, 14, 84.	1.7	355
7	The Population Genetics of Fungi: Tools and Techniques. Phytopathology, 1997, 87, 448-453.	1.1	351
8	Population Structure of <i>Mycosphaerella graminicola</i> : From Lesions to Continents. Phytopathology, 2002, 92, 946-955.	1.1	278
9	The global genetic structure of the wheat pathogen <i>Mycosphaerella graminicola</i> is characterized by high nuclear diversity, low mitochondrial diversity, regular recombination, and gene flow. Fungal Genetics and Biology, 2003, 38, 286-297.	0.9	262
10	Rapid emergence of pathogens in agro-ecosystems: global threats to agricultural sustainability and food security. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20160026.	1.8	240
11	Dothideomycete "Plant Interactions Illuminated by Genome Sequencing and EST Analysis of the Wheat Pathogen <i>Stagonospora nodorum</i> . Plant Cell, 2007, 19, 3347-3368.	3.1	235
12	The Cysteine Rich Necrotrophic Effector SnTox1 Produced by <i>Stagonospora nodorum</i> Triggers Susceptibility of Wheat Lines Harboring Snn1. PLoS Pathogens, 2012, 8, e1002467.	2.1	233
13	The Accessory Genome as a Cradle for Adaptive Evolution in Pathogens. PLoS Pathogens, 2012, 8, e1002608.	2.1	227
14	A small secreted protein in <i>Zymoseptoria tritici</i> is responsible for avirulence on wheat cultivars carrying the <i>Stb6</i> resistance gene. New Phytologist, 2017, 214, 619-631.	3.5	218
15	Origin and Domestication of the Fungal Wheat Pathogen <i>Mycosphaerella graminicola</i> via Sympatric Speciation. Molecular Biology and Evolution, 2006, 24, 398-411.	3.5	216
16	Sexual Reproduction Plays a Major Role in the Genetic Structure of Populations of the Fungus <i>Mycosphaerella graminicola</i> . Genetics, 1996, 142, 1119-1127.	1.2	197
17	The making of a new pathogen: Insights from comparative population genomics of the domesticated wheat pathogen <i>Mycosphaerella graminicola</i> and its wild sister species. Genome Research, 2011, 21, 2157-2166.	2.4	191
18	An Analysis of the Durability of Resistance to Plant Viruses. Phytopathology, 2003, 93, 941-952.	1.1	190

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19	Comparative Pathogenomics Reveals Horizontally Acquired Novel Virulence Genes in Fungi Infecting Cereal Hosts. <i>PLoS Pathogens</i> , 2012, 8, e1002952.	2.1	176
20	SnTox3 Acts in Effector Triggered Susceptibility to Induce Disease on Wheat Carrying the Snn3 Gene. <i>PLoS Pathogens</i> , 2009, 5, e1000581.	2.1	175
21	Qol resistance emerged independently at least 4 times in European populations of <i>Mycosphaerella graminicola</i> . <i>Pest Management Science</i> , 2009, 65, 155-162.	1.7	168
22	Population Genetics of Plant Pathogenic Fungi. <i>BioScience</i> , 1993, 43, 311-319.	2.2	167
23	Breakage-fusion-bridge Cycles and Large Insertions Contribute to the Rapid Evolution of Accessory Chromosomes in a Fungal Pathogen. <i>PLoS Genetics</i> , 2013, 9, e1003567.	1.5	166
24	A fungal wheat pathogen evolved host specialization by extensive chromosomal rearrangements. <i>ISME Journal</i> , 2017, 11, 1189-1204.	4.4	166
25	Evolution of Linked Avirulence Effectors in <i>Leptosphaeria maculans</i> Is Affected by Genomic Environment and Exposure to Resistance Genes in Host Plants. <i>PLoS Pathogens</i> , 2010, 6, e1001180.	2.1	158
26	Global migration patterns in the fungal wheat pathogen <i>Phaeosphaeria nodorum</i> . <i>Molecular Ecology</i> , 2006, 15, 2895-2904.	2.0	154
27	DNA Restriction Fragment Length Polymorphisms Among <i>Mycosphaerella graminicola</i> (Anamorph <i>Septoria tritici</i> ) Isolates Collected from a Single Wheat Field. <i>Phytopathology</i> , 1990, 80, 1368.	1.1	150
28	Local adaptation and effect of host genotype on the rate of pathogen evolution: an experimental test in a plant pathosystem. <i>Journal of Evolutionary Biology</i> , 2002, 15, 634-647.	0.8	147
29	Variation for neutral markers is correlated with variation for quantitative traits in the plant pathogenic fungus <i>Mycosphaerella graminicola</i> . <i>Molecular Ecology</i> , 2005, 14, 2683-2693.	2.0	146
30	Population Structure and Pathotype Diversity of the Wheat Blast Pathogen <i>Magnaporthe oryzae</i> 25 Years After Its Emergence in Brazil. <i>Phytopathology</i> , 2014, 104, 95-107.	1.1	144
31	Genetic Variability in Nuclear DNA in Field Populations of <i>Stagonospora nodorum</i> . <i>Phytopathology</i> , 1994, 84, 250.	1.1	143
32	Whole-Genome and Chromosome Evolution Associated with Host Adaptation and Speciation of the Wheat Pathogen <i>Mycosphaerella graminicola</i> . <i>PLoS Genetics</i> , 2010, 6, e1001189.	1.5	142
33	Genetic Structure of <i>Rhynchosporium secalis</i> in Australia. <i>Phytopathology</i> , 1999, 89, 639-645.	1.1	136
34	Population Genetics of Fungal and Oomycete Effectors Involved in Gene-for-Gene Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 371-380.	1.4	134
35	Distribution of mating type alleles in the wheat pathogen <i>Mycosphaerella graminicola</i> over spatial scales from lesions to continents. <i>Fungal Genetics and Biology</i> , 2002, 36, 128-136.	0.9	131
36	Molecular Population Genetic Analysis Differentiates Two Virulence Mechanisms of the Fungal Avirulence Gene NIP1. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 1114-1125.	1.4	129

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37	Comparative Transcriptome Analyses in <i>Zymoseptoria tritici</i> Reveal Significant Differences in Gene Expression Among Strains During Plant Infection. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 231-244.	1.4	129
38	The Impact of Recombination Hotspots on Genome Evolution of a Fungal Plant Pathogen. <i>Genetics</i> , 2015, 201, 1213-1228.	1.2	123
39	Resistance to QoI Fungicides Is Widespread in Brazilian Populations of the Wheat Blast Pathogen <i>Magnaporthe oryzae</i> . <i>Phytopathology</i> , 2015, 105, 284-294.	1.1	121
40	Gene Flow Between Geographic Populations of <i>Mycosphaerella graminicola</i> (Anamorph <i>Septoria tritici</i> ) Detected with Restriction Fragment Length Polymorphism Markers. <i>Phytopathology</i> , 1993, 83, 1148.	1.1	121
41	Experimental Measures of Pathogen Competition and Relative Fitness. <i>Annual Review of Phytopathology</i> , 2013, 51, 131-153.	3.5	117
42	Genetic stability in a population of a plant pathogenic fungus over time. <i>Molecular Ecology</i> , 1994, 3, 209-218.	2.0	114
43	Measuring Immigration and Sexual Reproduction in Field Populations of <i>Mycosphaerella graminicola</i> . <i>Phytopathology</i> , 1998, 88, 1330-1337.	1.1	114
44	How Knowledge of Pathogen Population Biology Informs Management of <i>Septoria Tritici</i> Blotch. <i>Phytopathology</i> , 2016, 106, 948-955.	1.1	112
45	Further evidence for sexual reproduction in <i>Rhynchosporium secalis</i> based on distribution and frequency of mating-type alleles. <i>Fungal Genetics and Biology</i> , 2003, 40, 115-125.	0.9	106
46	Gene Flow and Sexual Reproduction in the Wheat Glume Blotch Pathogen <i>Phaeosphaeria nodorum</i> (Anamorph <i>Stagonospora nodorum</i> ). <i>Phytopathology</i> , 1997, 87, 353-358.	1.1	103
47	A fungal avirulence factor encoded in a highly plastic genomic region triggers partial resistance to <i>septoria tritici</i> blotch. <i>New Phytologist</i> , 2018, 219, 1048-1061.	3.5	103
48	The Genetic Structure of Field Populations of <i>Rhynchosporium secalis</i> from Three Continents Suggests Moderate Gene Flow and Regular Recombination. <i>Phytopathology</i> , 2000, 90, 901-908.	1.1	102
49	Measuring Quantitative Virulence in the Wheat Pathogen <i>Zymoseptoria tritici</i> Using High-Throughput Automated Image Analysis. <i>Phytopathology</i> , 2014, 104, 985-992.	1.1	102
50	Global diversity and distribution of three necrotrophic effectors in <i>Phaeosphaeria nodorum</i> and related species. <i>New Phytologist</i> , 2013, 199, 241-251.	3.5	101
51	Restriction fragment length polymorphisms in <i>Septoria tritici</i> occur at a high frequency. <i>Current Genetics</i> , 1990, 17, 133-138.	0.8	100
52	Thermal adaptation in the fungal pathogen <i>Mycosphaerella graminicola</i> . <i>Molecular Ecology</i> , 2011, 20, 1689-1701.	2.0	98
53	RAPID SPECIATION FOLLOWING RECENT HOST SHIFTS IN THE PLANT PATHOGENIC FUNGUS <i>RHYNCHOSPORIUM</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 1418-1436.	1.1	97
54	Chromosome length polymorphisms in a <i>Septoria tritici</i> population. <i>Current Genetics</i> , 1991, 19, 265-271.	0.8	96

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55	Population Genomics of Fungal and Oomycete Pathogens. Annual Review of Phytopathology, 2016, 54, 323-346.	3.5	96
56	Is <i>Zymoseptoria tritici</i> a hemibiotroph?. Fungal Genetics and Biology, 2015, 79, 29-32.	0.9	95
57	A 19-isolate reference-quality global pangenome for the fungal wheat pathogen <i>Zymoseptoria tritici</i> . BMC Biology, 2020, 18, 12.	1.7	95
58	Evolution of the <i>CYP51</i> gene in <i>Mycosphaerella graminicola</i> : evidence for intragenic recombination and selective replacement. Molecular Plant Pathology, 2008, 9, 305-316.	2.0	94
59	Geographical variation and positive diversifying selection in the host-specific toxin SnToxA. Molecular Plant Pathology, 2007, 8, 321-332.	2.0	92
60	Genetic Structure of Populations of the Rice-Infecting Pathogen <i>Rhizoctonia solani</i> AG-1 IA from China. Phytopathology, 2009, 99, 1090-1099.	1.1	90
61	An Improved Method for Measuring Quantitative Resistance to the Wheat Pathogen <i>Zymoseptoria tritici</i> Using High-Throughput Automated Image Analysis. Phytopathology, 2016, 106, 782-788.	1.1	90
62	Genome-Wide Association Study Identifies Novel Candidate Genes for Aggressiveness, Deoxynivalenol Production, and Azole Sensitivity in Natural Field Populations of <i>Fusarium graminearum</i> . Molecular Plant-Microbe Interactions, 2016, 29, 417-430.	1.4	89
63	Molecular evidence for recent founder populations and human-mediated migration in the barley scald pathogen <i>Rhynchosporium secalis</i> . Molecular Phylogenetics and Evolution, 2009, 51, 454-464.	1.2	88
64	Ranking Quantitative Resistance to <i>Septoria tritici</i> Blotch in Elite Wheat Cultivars Using Automated Image Analysis. Phytopathology, 2018, 108, 568-581.	1.1	88
65	Wheat blast: from its origins in South America to its emergence as a global threat. Molecular Plant Pathology, 2019, 20, 155-172.	2.0	88
66	Quantitative Trait Locus Mapping of Melanization in the Plant Pathogenic Fungus <i>Zymoseptoria tritici</i> . G3: Genes, Genomes, Genetics, 2014, 4, 2519-2533.	0.8	86
67	Evidence for subdivision of the root-endophyte <i>Phialocephala fortinii</i> into cryptic species and recombination within species. Fungal Genetics and Biology, 2004, 41, 676-687.	0.9	85
68	Differential Selection on <i>Rhynchosporium secalis</i> During Parasitic and Saprophytic Phases in the Barley Scald Disease Cycle. Phytopathology, 2006, 96, 1214-1222.	1.1	85
69	Comparative transcriptomic analyses of <i>Zymoseptoria tritici</i> strains show complex lifestyle transitions and intraspecific variability in transcription profiles. Molecular Plant Pathology, 2016, 17, 845-859.	2.0	82
70	Emergence and early evolution of fungicide resistance in North American populations of <i>Zymoseptoria tritici</i> . Plant Pathology, 2015, 64, 961-971.	1.2	79
71	Intraspecific comparison and annotation of two complete mitochondrial genome sequences from the plant pathogenic fungus <i>Mycosphaerella graminicola</i> . Fungal Genetics and Biology, 2008, 45, 628-637.	0.9	78
72	Coevolution and Life Cycle Specialization of Plant Cell Wall Degrading Enzymes in a Hemibiotrophic Pathogen. Molecular Biology and Evolution, 2013, 30, 1337-1347.	3.5	77

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73	Selection for increased cyproconazole tolerance in <i>Mycosphaerella graminicola</i> through local adaptation and in response to host resistance. <i>Molecular Plant Pathology</i> , 2006, 7, 259-268.	2.0	76
74	Quantitative trait locus mapping reveals complex genetic architecture of quantitative virulence in the wheat pathogen <i>Zymoseptoria tritici</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 201-216.	2.0	76
75	High Levels of Gene Flow and Heterozygote Excess Characterize <i>Rhizoctonia solani</i> AG-1 IA ( <i>Thanatephorus cucumeris</i> ) from Texas. <i>Fungal Genetics and Biology</i> , 1999, 28, 148-159.	0.9	75
76	No biogeographical pattern for a root-associated fungal species complex. <i>Global Ecology and Biogeography</i> , 2011, 20, 160-169.	2.7	74
77	Comparative analysis of mitochondrial genomes from closely related <i>Rhynchosporium</i> species reveals extensive intron invasion. <i>Fungal Genetics and Biology</i> , 2014, 62, 34-42.	0.9	74
78	Validation of Genome-Wide Association Studies as a Tool to Identify Virulence Factors in <i>Parastagonospora nodorum</i> . <i>Phytopathology</i> , 2016, 106, 1177-1185.	1.1	74
79	Genome-wide evidence for divergent selection between populations of a major agricultural pathogen. <i>Molecular Ecology</i> , 2018, 27, 2725-2741.	2.0	74
80	The interaction among evolutionary forces in the pathogenic fungus <i>Mycosphaerella graminicola</i> . <i>Fungal Genetics and Biology</i> , 2004, 41, 590-599.	0.9	73
81	The genetic basis of local adaptation for pathogenic fungi in agricultural ecosystems. <i>Molecular Ecology</i> , 2017, 26, 2027-2040.	2.0	73
82	Morphological changes in response to environmental stresses in the fungal plant pathogen <i>Zymoseptoria tritici</i> . <i>Scientific Reports</i> , 2019, 9, 9642.	1.6	73
83	Migration patterns among global populations of the pathogenic fungus <i>Mycosphaerella graminicola</i> . <i>Molecular Ecology</i> , 2005, 14, 1881-1896.	2.0	71
84	Global Hierarchical Gene Diversity Analysis Suggests the Fertile Crescent Is Not the Center of Origin of the Barley Scald Pathogen <i>Rhynchosporium secalis</i> . <i>Phytopathology</i> , 2006, 96, 941-950.	1.1	71
85	<i>Zymoseptoria ardabiliae</i> and <i>Z. pseudotritici</i> , two progenitor species of the septoria tritici leaf blotch fungus <i>Z. tritici</i> (synonym: <i>Mycosphaerella graminicola</i> ). <i>Mycologia</i> , 2012, 104, 1397-1407.	0.8	71
86	Quantitative Variation in Effector Activity of ToxA Isoforms from <i>Stagonospora nodorum</i> and <i>Pyrenophora tritici-repentis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 515-522.	1.4	70
87	Transposable element insertions shape gene regulation and melanin production in a fungal pathogen of wheat. <i>BMC Biology</i> , 2018, 16, 78.	1.7	70
88	QTL mapping of temperature sensitivity reveals candidate genes for thermal adaptation and growth morphology in the plant pathogenic fungus <i>Zymoseptoria tritici</i> . <i>Heredity</i> , 2016, 116, 384-394.	1.2	68
89	Intra- and intersporal diversity of ITS rDNA sequences in <i>Glomus intraradices</i> assessed by cloning and sequencing, and by SSCP analysis. <i>Mycological Research</i> , 2002, 106, 670-681.	2.5	66
90	<i>Pyricularia graminis-tritici</i> , a new <i>Pyricularia</i> species causing wheat blast. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2016, 37, 199-216.	1.6	66

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91	Genome-wide analysis of <i>Fusarium graminearum</i> field populations reveals hotspots of recombination. <i>BMC Genomics</i> , 2015, 16, 996.	1.2	65
92	QTL mapping of fungicide sensitivity reveals novel genes and pleiotropy with melanization in the pathogen <i>Zymoseptoria tritici</i> . <i>Fungal Genetics and Biology</i> , 2015, 80, 53-67.	0.9	65
93	Two new species of <i>Rhynchosporium</i> . <i>Mycologia</i> , 2011, 103, 195-202.	0.8	62
94	The Population Biology of Host-Pathogen Interactions. <i>Annual Review of Phytopathology</i> , 1989, 27, 77-94.	3.5	61
95	Hyperspectral Canopy Sensing of Wheat <i>Septoria Tritici</i> Blotch Disease. <i>Frontiers in Plant Science</i> , 2018, 9, 1195.	1.7	61
96	Responses of Two-, Three-, and Four-Component Barley Mixtures to a Variable Pathogen Population. <i>Crop Science</i> , 1988, 28, 447-452.	0.8	60
97	Genetic Structure and Temporal Dynamics of a <i>Colletotrichum graminicola</i> Population in a Sorghum Disease Nursery. <i>Phytopathology</i> , 1998, 88, 1087-1093.	1.1	60
98	Multilocus resistance evolution to azole fungicides in fungal plant pathogen populations. <i>Molecular Ecology</i> , 2016, 25, 6124-6142.	2.0	60
99	High Genetic Similarity Among Populations of <i>Phaeosphaeria nodorum</i> Across Wheat Cultivars and Regions in Switzerland. <i>Phytopathology</i> , 1997, 87, 1134-1139.	1.1	59
100	The Frequencies and Spatial Distribution of Mating Types in <i>Stagonospora nodorum</i> Are Consistent with Recurring Sexual Reproduction. <i>Phytopathology</i> , 2006, 96, 234-239.	1.1	57
101	Evidence for Extensive Recent Intron Transposition in Closely Related Fungi. <i>Current Biology</i> , 2011, 21, 2017-2022.	1.8	57
102	Genetic Structure of Populations of <i>Rhizoctonia solani</i> Anastomosis Group-1 IA from Soybean in Brazil. <i>Phytopathology</i> , 2008, 98, 932-941.	1.1	55
103	Using Restriction Fragment Length Polymorphisms to Assess Temporal Variation and Estimate the Number of Ascospores that Initiate Epidemics in Field Populations of <i>Mycosphaerella graminicola</i> . <i>Phytopathology</i> , 2001, 91, 1011-1017.	1.1	54
104	Divergence Between Sympatric Rice- and Maize-Infecting Populations of <i>Rhizoctonia solani</i> AG-1 IA from Latin America. <i>Phytopathology</i> , 2010, 100, 172-182.	1.1	54
105	Using dynamic diversity to achieve durable disease resistance in agricultural ecosystems. <i>Tropical Plant Pathology</i> , 2014, 39, 191-196.	0.8	54
106	When resistance gene pyramids are not durable—the role of pathogen diversity. <i>Molecular Plant Pathology</i> , 2018, 19, 521-524.	2.0	53
107	DNA fingerprinting of the plant pathogenic fungus <i>Mycosphaerella graminicola</i> (anamorph <i>Septoria</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	1.8	51
108	How can research on pathogen population biology suggest disease management strategies? The example of barley scald ( <i>Rhynchosporium commune</i> ). <i>Plant Pathology</i> , 2015, 64, 1005-1013.	1.2	51

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109	Phylogenetic analysis of globally distributed <i>Mycosphaerella graminicola</i> populations based on three DNA sequence loci. <i>Fungal Genetics and Biology</i> , 2004, 41, 226-238.	0.9	50
110	Local adaptation and evolutionary potential along a temperature gradient in the fungal pathogen <i>Rhynchosporium commune</i> . <i>Evolutionary Applications</i> , 2013, 6, 524-534.	1.5	50
111	How can we achieve durable disease resistance in agricultural ecosystems?. <i>New Phytologist</i> , 2010, 185, 3-5.	3.5	49
112	A population-level invasion by transposable elements triggers genome expansion in a fungal pathogen. <i>ELife</i> , 2021, 10, .	2.8	49
113	Significant variation in sensitivity to a DMI fungicide in field populations of <i>Fusarium graminearum</i> . <i>Plant Pathology</i> , 2015, 64, 664-670.	1.2	48
114	The origin and colonization history of the barley scald pathogen <i>Rhynchosporium secalis</i> . <i>Journal of Evolutionary Biology</i> , 2007, 20, 1311-1321.	0.8	46
115	Phylogenetic and population genetic analyses of <i>Phaeosphaeria nodorum</i> and its close relatives indicate cryptic species and an origin in the Fertile Crescent. <i>Fungal Genetics and Biology</i> , 2012, 49, 882-895.	0.9	46
116	The role of selection on the genetic structure of pathogen populations: Evidence from field experiments with <i>Mycosphaerella graminicola</i> on wheat. <i>Euphytica</i> , 1996, 92, 73-80.	0.6	45
117	Significant difference in pathogenicity between MAT1-1 and MAT1-2 isolates in the wheat pathogen <i>Mycosphaerella graminicola</i> . <i>Fungal Genetics and Biology</i> , 2007, 44, 339-346.	0.9	45
118	Population structure of the rice sheath blight pathogen <i>Rhizoctonia solani</i> AG-1 IA from India. <i>European Journal of Plant Pathology</i> , 2005, 112, 113-121.	0.8	44
119	Can High-Risk Fungicides be Used in Mixtures Without Selecting for Fungicide Resistance?. <i>Phytopathology</i> , 2014, 104, 324-331.	1.1	44
120	Developing smarter host mixtures to control plant disease. <i>Plant Pathology</i> , 2015, 64, 996-1004.	1.2	44
121	Phylogeographical analyses reveal global migration patterns of the barley scald pathogen <i>Rhynchosporium secalis</i> . <i>Molecular Ecology</i> , 2009, 18, 279-293.	2.0	43
122	Pan-Parastagonospora Comparative Genome Analysis—Effector Prediction and Genome Evolution. <i>Genome Biology and Evolution</i> , 2018, 10, 2443-2457.	1.1	43
123	Mutations in the <i>CYP51</i> gene reduce DMI sensitivity in <i>Parastagonospora nodorum</i> populations in Europe and China. <i>Pest Management Science</i> , 2017, 73, 1503-1510.	1.7	42
124	Sexual reproduction facilitates the adaptation of parasites to antagonistic host environments: Evidence from empirical study in the wheat- <i>Mycosphaerella graminicola</i> system. <i>International Journal for Parasitology</i> , 2007, 37, 861-870.	1.3	40
125	Frequency of mutations associated with fungicide resistance and population structure of <i>Mycosphaerella graminicola</i> in Tunisia. <i>European Journal of Plant Pathology</i> , 2012, 132, 111-122.	0.8	38
126	Effect of hosts on competition among clones and evidence of differential selection between pathogenic and saprophytic phases in experimental populations of the wheat pathogen <i>Phaeosphaeria nodorum</i> . <i>BMC Evolutionary Biology</i> , 2011, 11, 188.	3.2	37



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127	Comparative Transcriptomics Reveals How Wheat Responds to Infection by <i>Zymoseptoria tritici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 420-431.	1.4	37
128	Precision Phenotyping Reveals Novel Loci for Quantitative Resistance to Septoria Tritici Blotch. <i>Plant Phenomics</i> , 2019, 2019, 3285904.	2.5	37
129	A Global Analysis of <i>CYP51</i> Diversity and Azole Sensitivity in <i>Rhynchosporium commune</i> . <i>Phytopathology</i> , 2016, 106, 355-361.	1.1	35
130	Estimation of Rates of Recombination and Migration in Populations of Plant Pathogens—A Reply. <i>Phytopathology</i> , 2000, 90, 324-326.	1.1	34
131	Sexual Recombinants Make a Significant Contribution to Epidemics Caused by the Wheat Pathogen <i>Phaeosphaeria nodorum</i> . <i>Phytopathology</i> , 2010, 100, 855-862.	1.1	34
132	Divergence Between Sympatric Rice- and Soybean-Infecting Populations of <i>Rhizoctonia solani</i> Anastomosis Group-1 IA. <i>Phytopathology</i> , 2008, 98, 1326-1333.	1.1	33
133	Frequency of Sexual Reproduction by <i>Mycosphaerella graminicola</i> on Partially Resistant Wheat Cultivars. <i>Phytopathology</i> , 2002, 92, 1175-1181.	1.1	31
134	Association between Virulence and Triazole Tolerance in the Phytopathogenic Fungus <i>Mycosphaerella graminicola</i> . <i>PLoS ONE</i> , 2013, 8, e59568.	1.1	31
135	An assay for quantitative virulence in <i>Rhynchosporium commune</i> reveals an association between effector genotype and virulence. <i>Plant Pathology</i> , 2014, 63, 405-414.	1.2	30
136	Evolutionary analyses of the avirulence effector AvrStb6 in global populations of <i>Zymoseptoria tritici</i> identify candidate amino acids involved in recognition. <i>Molecular Plant Pathology</i> , 2018, 19, 1836-1846.	2.0	30
137	Chromatin Dynamics Contribute to the Spatiotemporal Expression Pattern of Virulence Genes in a Fungal Plant Pathogen. <i>MBio</i> , 2020, 11, .	1.8	29
138	The Genetic Architecture of Emerging Fungicide Resistance in Populations of a Global Wheat Pathogen. <i>Genome Biology and Evolution</i> , 2020, 12, 2231-2244.	1.1	29
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