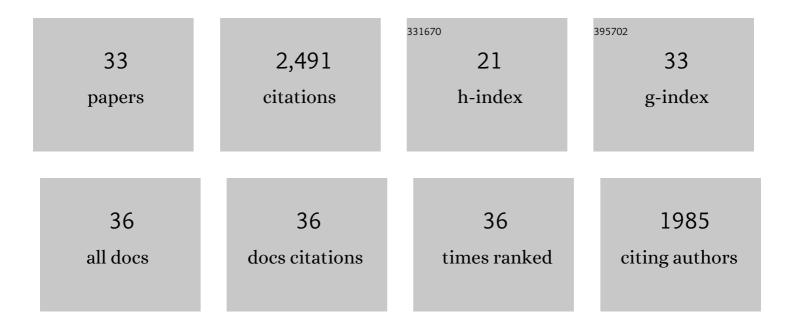
Michael G Milgroom

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genetic Differentiation of <i>Verticillium dahliae</i> Populations Recovered from Symptomatic and Asymptomatic Hosts. Phytopathology, 2021, 111, 149-159.	2.2	9
2	Microevolution in the pansecondary metabolome of <i>Aspergillus flavus</i> and its potential macroevolutionary implications for filamentous fungi. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	34
3	The Frequency of Sex: Population Genomics Reveals Differences in Recombination and Population Structure of the Aflatoxin-Producing Fungus Aspergillus flavus. MBio, 2020, 11, .	4.1	27
4	Genome Sequence of the Chestnut Blight Fungus <i>Cryphonectria parasitica</i> EP155: A Fundamental Resource for an Archetypical Invasive Plant Pathogen. Phytopathology, 2020, 110, 1180-1188.	2.2	34
5	Fitness Cost of Aflatoxin Production in Aspergillus flavus When Competing with Soil Microbes Could Maintain Balancing Selection. MBio, 2019, 10, .	4.1	21
6	Population Subdivision and the Frequency of Aflatoxigenic Isolates in Aspergillus flavus in the United States. Phytopathology, 2019, 109, 878-886.	2.2	8
7	Population Genetics of <i>Verticillium dahliae</i> in Iran Based on Microsatellite and Single Nucleotide Polymorphism Markers. Phytopathology, 2018, 108, 780-788.	2.2	9
8	Balancing selection at nonself recognition loci in the chestnut blight fungus, Cryphonectria parasitica, demonstrated by trans-species polymorphisms, positive selection, and even allele frequencies. Heredity, 2018, 121, 511-523.	2.6	14
9	Balancing selection for aflatoxin in <i>Aspergillus flavus</i> is maintained through interference competition with, and fungivory by insects. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20172408.	2.6	54
10	Clonal Expansion and Migration of a Highly Virulent, Defoliating Lineage of <i>Verticillium dahliae</i> . Phytopathology, 2016, 106, 1038-1046.	2.2	34
11	Population Genomics of Fungal and Oomycete Pathogens. Annual Review of Phytopathology, 2016, 54, 323-346.	7.8	96
12	Aphid vector population density determines the emergence of necrogenic satellite RNAs in populations of cucumber mosaic virus. Journal of General Virology, 2016, 97, 1453-1457.	2.9	6
13	Vertical Transmission Selects for Reduced Virulence in a Plant Virus and for Increased Resistance in the Host. PLoS Pathogens, 2014, 10, e1004293.	4.7	65
14	Recombination between Clonal Lineages of the Asexual Fungus Verticillium dahliae Detected by Genotyping by Sequencing. PLoS ONE, 2014, 9, e106740.	2.5	95
15	Clonal population structure and introductions of the chestnut blight fungus, Cryphonectria parasitica, in Asturias, northern Spain. European Journal of Plant Pathology, 2011, 131, 67-79.	1.7	20
16	Heterokaryons and parasexual recombinants of Cryphonectria parasitica in two clonal populations in southeastern Europe. Fungal Genetics and Biology, 2009, 46, 849-854.	2.1	36
17	Clonal population structure of the chestnut blight fungus in expanding ranges in southeastern Europe. Molecular Ecology, 2008, 17, 4446-4458.	3.9	87
18	High diversity of vegetative compatibility types inCryphonectria parasiticain Japan and China. Mycologia, 2007, 99, 279-284.	1.9	47

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#	Article	IF	CITATIONS
19	Markers linked to vegetative incompatibility (vic) genes and a region of high heterogeneity and reduced recombination near the mating type locus (MAT) in Cryphonectria parasitica. Fungal Genetics and Biology, 2006, 43, 453-463.	2.1	32
20	Heterokaryon incompatibility function of barrage-associated vegetative incompatibility genes (vic) inCryphonectria parasitica. Mycologia, 2006, 98, 43-50.	1.9	14
21	Heterokaryon incompatibility function of barrage-associated vegetative incompatibility genes (vic) in Cryphonectria parasitica. Mycologia, 2006, 98, 43-50.	1.9	26
22	BIOLOGICAL CONTROL OF CHESTNUT BLIGHT WITH HYPOVIRULENCE: A Critical Analysis. Annual Review of Phytopathology, 2004, 42, 311-338.	7.8	409
23	Recombination and Migration of <i>Cryphonectria hypovirus 1</i> as Inferred From Gene Genealogies and the Coalescent. Genetics, 2004, 166, 1611-1629.	2.9	14
24	Persistence of Cryphonectria hypoviruses after their release for biological control of chestnut blight in West Virginia forests. Forest Pathology, 2002, 32, 345-356.	1.1	14
25	The mating system of the fungus Cryphonectria parasitica: selfing and self-incompatibility. Heredity, 2001, 86, 134-143.	2.6	61
26	Genetic Control of Horizontal Virus Transmission in the Chestnut Blight Fungus, <i>Cryphonectria parasitica</i> . Genetics, 2001, 159, 107-118.	2.9	188
27	Variation in Tolerance and Virulence in the Chestnut Blight Fungus-Hypovirus Interaction. Applied and Environmental Microbiology, 2000, 66, 4863-4869.	3.1	91
28	Origin, genetic diversity, and population structure of <i>Nectria coccinea</i> var. <i>faginata</i> in North America. Mycologia, 1999, 91, 583-592.	1.9	20
29	Genetics of Vegetative Incompatibility in <i>Cryphonectria parasitica</i> . Applied and Environmental Microbiology, 1998, 64, 2988-2994.	3.1	176
30	Potential diversity in vegetative compatibility types of Ophiostoma novo-ulmi in North America. Mycologia, 1997, 89, 722-726.	1.9	17
31	RECOMBINATION AND THE MULTILOCUS STRUCTURE OF FUNGAL POPULATIONS. Annual Review of Phytopathology, 1996, 34, 457-477.	7.8	496
32	Intercontinental population structure of the chestnut blight fungus, <i>Cryphonectria parasitica</i> . Mycologia, 1996, 88, 179-190.	1.9	109
33	Estimation of the outcrossing rate in the chestnut blight fungus, Cryphonectria parasitica. Heredity, 1993, 70, 385-392.	2.6	54