Pierre Gladieux

List of Publications by Year
in descending order

71 papers	4,481 citations	117625 34 h-index	118850 62 g-index
81 all docs	81 docs citations	81 times ranked	4922 citing authors

#	Article	IF	Citations
1	Means, motive and opportunity for biological invasions: Genetic introgression in a fungal pathogen. Molecular Ecology, 2023, 32, 2428-2442.	3.9	10
2	Hybridizations between formae speciales of Venturia inaequalis pave the way for a new biocontrol strategy to manage fungal plant pathogens. Phytopathology, 2022, , .	2.2	2
3	Tracing the Origin and Evolutionary History ofPyricularia oryzaeInfecting Maize and Barnyard Grass. Phytopathology, 2021, 111, 128-136.	2.2	14
4	Population Genomic- and Phylogenomic-Enabled Advances to Increase Insight Into Pathogen Biology and Epidemiology. Phytopathology, 2021, 111, 8-11.	2.2	4
5	Population Genomics Reveals Molecular Determinants of Specialization to Tomato in the Polyphagous Fungal Pathogen Botrytis cinerea in France. Phytopathology, 2021, 111, 2355-2366.	2.2	11
6	A Genomic Approach to Develop a New qPCR Test Enabling Detection of the Pyricularia oryzae Lineage Causing Wheat Blast. Plant Disease, 2020, 104, 60-70.	1.4	20
7	Higher Gene Flow in Sex-Related Chromosomes than in Autosomes during Fungal Divergence. Molecular Biology and Evolution, 2020, 37, 668-682.	8.9	19
8	Heterogeneity of the rice microbial community of the Chinese centuriesâ€old Honghe Hani rice terraces system. Environmental Microbiology, 2020, 22, 3429-3445.	3.8	8
9	Neurospora from Natural Populations: Population Genomics Insights into the Life History of a Model Microbial Eukaryote. Methods in Molecular Biology, 2020, 2090, 313-336.	0.9	16
10	The taxonomy of the model filamentous fungus Podospora anserina. MycoKeys, 2020, 75, 51-69.	1.9	6
11	Understanding Adaptation, Coevolution, Host Specialization, and Mating System in Castrating Anther-Smut Fungi by Combining Population and Comparative Genomics. Annual Review of Phytopathology, 2019, 57, 431-457.	7.8	23
12	The polyphagous plant pathogenic fungus Botrytis cinerea encompasses hostâ€specialized and generalist populations. Environmental Microbiology, 2019, 21, 4808-4821.	3.8	30
13	Origin of the Aromatic Group of Cultivated Rice (Oryza sativa L.) Traced to the Indian Subcontinent. Genome Biology and Evolution, 2019, 11, 832-843.	2.5	40
14	Emergence of Southern Rice Black-Streaked Dwarf Virus in the Centuries-Old Chinese Yuanyang Agrosystem of Rice Landraces. Viruses, 2019, 11, 985.	3.3	7
15	Programmed Cell Death inNeurospora crassaIs Controlled by the Allorecognition Determinantrcd-1. Genetics, 2019, 213, 1387-1400.	2.9	32
16	Multiple Introductions Without Admixture of Colletotrichum truncatum Associated with Soybean Anthracnose in Brazil. Phytopathology, 2019, 109, 681-689.	2.2	19
17	Pyricularia graminisâ€tritici is not the correct species name for the wheat blast fungus: response to Ceresini etÂal. (MPP 20:2). Molecular Plant Pathology, 2019, 20, 173-179.	4.2	42
18	NLR surveillance of essential SEC-9 SNARE proteins induces programmed cell death upon allorecognition in filamentous fungi. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2292-E2301.	7.1	69

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19	Gene Flow between Divergent Cereal- and Grass-Specific Lineages of the Rice Blast Fungus Magnaporthe oryzae. MBio, 2018, 9, .	4.1	163
20	Coexistence of Multiple Endemic and Pandemic Lineages of the Rice Blast Pathogen. MBio, 2018, 9, .	4.1	59
21	Genome wide analysis of the transition to pathogenic lifestyles in Magnaporthales fungi. Scientific Reports, 2018, 8, 5862.	3.3	28
22	What makes a specialized endophyte special?. Molecular Ecology, 2018, 27, 3037-3039.	3.9	11
23	Coâ€occurrence among three divergent plantâ€castrating fungi in the same Silene host species. Molecular Ecology, 2018, 27, 3357-3370.	3.9	17
24	Updates in the Language of Histoplasma Biodiversity. MBio, 2018, 9, .	4.1	1
25	Coâ€occurrence and hybridization of antherâ€smut pathogens specialized on Dianthus hosts. Molecular Ecology, 2017, 26, 1877-1890.	3.9	28
26	Genomic signatures of adaptation to wine biological ageing conditions in biofilmâ€forming flor yeasts. Molecular Ecology, 2017, 26, 2150-2166.	3.9	68
27	Widespread selective sweeps throughout the genome of model plant pathogenic fungi and identification of effector candidates. Molecular Ecology, 2017, 26, 2041-2062.	3.9	71
28	Sources of Fungal Genetic Variation and Associating It with Phenotypic Diversity. Microbiology Spectrum, 2017, 5, .	3.0	33
29	Continentalâ€level population differentiation and environmental adaptation in the mushroom <scp>S</scp>uillus brevipes. Molecular Ecology, 2017, 26, 2063-2076.	3.9	55
30	Pathogen effectors and plant immunity determine specialization of the blast fungus to rice subspecies. ELife, 2016, 5, .	6.0	67
31	Distribution and population structure of the anther smut <scp>M</scp>icrobotryum silenesâ€acaulis parasitizing an arcticâ€“alpine plant. Molecular Ecology, 2016, 25, 811-824.	3.9	17
32	Emergence of wheat blast in Bangladesh was caused by a South American lineage of Magnaporthe oryzae. BMC Biology, 2016, 14, 84.	3.8	355
33	Strong phylogeographic coâ€structure between the antherâ€smut fungus and its white campion host. New Phytologist, 2016, 212, 668-679.	7.3	36
34	<scp>cloncase</scp>: Estimation of sex frequency and effective population size by clonemate resampling in partially clonal organisms. Molecular Ecology Resources, 2016, 16, 845-861.	4.8	25
35	Emergence of new virulent populations of apple scab from nonagricultural disease reservoirs. New Phytologist, 2016, 209, 1220-1229.	7.3	42
36	Characterization of Greenbeard Genes Involved in Long-Distance Kind Discrimination in a Microbial Eukaryote. PLoS Biology, 2016, 14, e1002431.	5.6	49

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37	Genomic sequencing reveals historical, demographic and selective factors associated with the diversification of the fireâ€associated fungus Neurospora discreta. Molecular Ecology, 2015, 24, 5657-5675.	3.9	32
38	Globally invading populations of the fungal plant pathogen <scp>V</scp>erticillium dahliae are dominated by multiple divergent lineages. Environmental Microbiology, 2015, 17, 2824-2840.	3.8	42
39	Degeneration of the Nonrecombining Regions in the Mating-Type Chromosomes of the Anther-Smut Fungi. Molecular Biology and Evolution, 2015, 32, 928-943.	8.9	49
40	Population structure and temporal maintenance of the multihost fungal pathogen <scp>B</scp>otrytis cinerea: causes and implications for disease management. Environmental Microbiology, 2015, 17, 1261-1274.	3.8	44
41	Genetic isolation between two recently diverged populations of a symbiotic fungus. Molecular Ecology, 2015, 24, 2747-2758.	3.9	100
42	Anthropogenic and natural drivers of gene flow in a temperate wild fruit tree: a basis for conservation and breeding programs in apples. Evolutionary Applications, 2015, 8, 373-384.	3.1	59
43	Identification of Allorecognition Loci inNeurospora crassaby Genomics and Evolutionary Approaches. Molecular Biology and Evolution, 2015, 32, 2417-2432.	8.9	52
44	The population biology of fungal invasions. Molecular Ecology, 2015, 24, 1969-1986.	3.9	173
45	Origin, Migration Routes and Worldwide Population Genetic Structure of the Wheat Yellow Rust Pathogen Puccinia striiformis f.sp. tritici. PLoS Pathogens, 2014, 10, e1003903.	4.7	241
46	Fungal evolutionary genomics provides insight into the mechanisms of adaptive divergence in eukaryotes. Molecular Ecology, 2014, 23, 753-773.	3.9	203
47	The domestication and evolutionary ecology of apples. Trends in Genetics, 2014, 30, 57-65.	6.7	261
48	Inferring the contribution of sexual reproduction, migration and offâ€season survival to the temporal maintenance of microbial populations: a case study on the wheat fungal pathogen <scp>P</scp>uccinia striiformis f.sp. tritici. Molecular Ecology, 2014, 23, 603-617.	3.9	87
49	A high virulence and pathotype diversity of Puccinia striiformis f.sp. tritici at its centre of diversity, the Himalayan region of Pakistan. European Journal of Plant Pathology, 2014, 140, 275-290.	1.7	31
50	History of the invasion of the anther smut pathogen on S ilene latifolia in N orth A merica. New Phytologist, 2013, 198, 946-956.	7.3	33
51	Postglacial recolonization history of the <scp>E</scp>uropean crabapple (Malus sylvestris) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 2249-2263.	3.9	86
52	Purifying selection after episodes of recurrent adaptive diversification in fungal pathogens. Infection, Genetics and Evolution, 2013, 17, 123-131.	2.3	15
53	The â€˜<scp>D</scp>r <scp>J</scp>ekyll and <scp>M</scp>r <scp>H</scp>yde fungusâ€™: noble rot versus gray mold symptoms of <scp>B</scp>otrytis cinerea on grapes. Evolutionary Applications, 2013, 6, 960-969.	3.1	40
54	Cropâ€toâ€wild gene flow and spatial genetic structure in the closest wild relatives of the cultivated apple. Evolutionary Applications, 2013, 6, 737-748.	3.1	54

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55	New Insight into the History of Domesticated Apple: Secondary Contribution of the European Wild Apple to the Genome of Cultivated Varieties. PLoS Genetics, 2012, 8, e1002703.	3.5	334
56	Evolution of pathogenicity traits in the apple scab fungal pathogen in response to the domestication of its host. Evolutionary Applications, 2012, 5, 694-704.	3.1	28
57	Migration patterns and changes in population biology associated with the worldwide spread of the oilseed rape pathogen Leptosphaeria maculans. Molecular Ecology, 2012, 21, 2519-2533.	3.9	34
58	Epidemiology and Evolution of Fungal Pathogens in Plants and Animals. , 2011, , 59-132.		17
59	The genetic structure of the plant pathogenic fungus Melampsora larici-populina on its wild host is extensively impacted by host domestication. Molecular Ecology, 2011, 20, 2739-2755.	3.9	40
60	Emergence of novel fungal pathogens by ecological speciation: importance of the reduced viability of immigrants. Molecular Ecology, 2011, 20, 4521-4532.	3.9	60
61	Distinct invasion sources of common ragweed (Ambrosia artemisiifolia) in Eastern and Western Europe. Biological Invasions, 2011, 13, 933-944.	2.4	69
62	Maintenance of Fungal Pathogen Species That Are Specialized to Different Hosts: Allopatric Divergence and Introgression through Secondary Contact. Molecular Biology and Evolution, 2011, 28, 459-471.	8.9	79
63	Genetic polymorphism of Microbotryum violaceum s. l. Isolates collected from different plant species on the territory of Russia. Russian Journal of Genetics, 2010, 46, 1395-1398.	0.6	0
64	Distribution of the antherâ€smut pathogen Microbotryum on species of the Caryophyllaceae. New Phytologist, 2010, 187, 217-229.	7.3	73
65	Evolution of the population structure ofVenturia inaequalis, the apple scab fungus, associated with the domestication of its host. Molecular Ecology, 2010, 19, 658-674.	3.9	79
66	Glacial Refugia in Pathogens: European Genetic Structure of Anther Smut Pathogens on Silene latifolia and Silene dioica. PLoS Pathogens, 2010, 6, e1001229.	4.7	70
67	Host-specific differentiation among populations of Venturia inaequalis causing scab on apple, pyracantha and loquat. Fungal Genetics and Biology, 2010, 47, 511-521.	2.1	34
68	Linking the emergence of fungal plant diseases with ecological speciation. Trends in Ecology and Evolution, 2010, 25, 387-395.	8.7	281
69	On the Origin and Spread of the Scab Disease of Apple: Out of Central Asia. PLoS ONE, 2008, 3, e1455.	2.5	111
70	Origin and colonization history of newly virulent strains of the phytopathogenic fungus Venturia inaequalis. Fungal Genetics and Biology, 2007, 44, 284-292.	2.1	49
71	Sources of Fungal Genetic Variation and Associating It with Phenotypic Diversity. , 0, , 635-655.		3