

Harold Corby Kistler

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116
papers

12,876
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57
h-index

113
g-index

120
ext. papers

15,353
ext. citations

5.3
avg, IF

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L-index

#	Paper	IF	Citations
116	Multiple evolutionary origins of the fungus causing Panama disease of banana: concordant evidence from nuclear and mitochondrial gene genealogies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 2044-9	11.5	1252
115	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010 , 464, 367-73	50.4	1085
114	Heading for disaster: <i>Fusarium graminearum</i> on cereal crops. <i>Molecular Plant Pathology</i> , 2004 , 5, 515-25	5.7	841
113	The <i>Fusarium graminearum</i> genome reveals a link between localized polymorphism and pathogen specialization. <i>Science</i> , 2007 , 317, 1400-2	33.3	668
112	Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of <i>Fusarium graminearum</i> , the fungus causing wheat scab. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 7905-10	11.5	662
111	Genealogical concordance between the mating type locus and seven other nuclear genes supports formal recognition of nine phylogenetically distinct species within the <i>Fusarium graminearum</i> clade. <i>Fungal Genetics and Biology</i> , 2004 , 41, 600-23	3.9	577
110	Ancestral polymorphism and adaptive evolution in the trichothecene mycotoxin gene cluster of phytopathogenic <i>Fusarium</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 9278-83	11.5	414
109	A mitogen-activated protein kinase gene (MGV1) in <i>Fusarium graminearum</i> is required for female fertility, heterokaryon formation, and plant infection. <i>Molecular Plant-Microbe Interactions</i> , 2002 , 15, 1119-27	3.6	342
108	Global molecular surveillance reveals novel <i>Fusarium</i> head blight species and trichothecene toxin diversity. <i>Fungal Genetics and Biology</i> , 2007 , 44, 1191-204	3.9	341
107	Role of Horizontal Gene Transfer in the Evolution of Fungi. <i>Annual Review of Phytopathology</i> , 2000 , 38, 325-363	10.8	216
106	A two-locus DNA sequence database for typing plant and human pathogens within the <i>Fusarium oxysporum</i> species complex. <i>Fungal Genetics and Biology</i> , 2009 , 46, 936-48	3.9	207
105	Functional analysis of the kinome of the wheat scab fungus <i>Fusarium graminearum</i> . <i>PLoS Pathogens</i> , 2011 , 7, e1002460	7.6	202
104	Global gene regulation by <i>Fusarium</i> transcription factors Tri6 and Tri10 reveals adaptations for toxin biosynthesis. <i>Molecular Microbiology</i> , 2009 , 72, 354-67	4.1	191
103	New modes of genetic change in filamentous fungi. <i>Annual Review of Phytopathology</i> , 1992 , 30, 131-53	10.8	174
102	Pathogenicity and In Planta Mycotoxin Accumulation Among Members of the <i>Fusarium graminearum</i> Species Complex on Wheat and Rice. <i>Phytopathology</i> , 2005 , 95, 1397-404	3.8	170
101	Multilocus genotyping and molecular phylogenetics resolve a novel head blight pathogen within the <i>Fusarium graminearum</i> species complex from Ethiopia. <i>Fungal Genetics and Biology</i> , 2008 , 45, 1514-22	3.9	164
100	Population Analysis of <i>Fusarium graminearum</i> from Wheat Fields in Eastern China. <i>Phytopathology</i> , 2002 , 92, 1315-22	3.8	164

99	One fungus, one name: defining the genus <i>Fusarium</i> in a scientifically robust way that preserves longstanding use. <i>Phytopathology</i> , 2013 , 103, 400-8	3.8	155
98	Genetic Diversity in the Plant-Pathogenic Fungus <i>Fusarium oxysporum</i> . <i>Phytopathology</i> , 1997 , 87, 474-9	3.8	154
97	Novel <i>Fusarium</i> head blight pathogens from Nepal and Louisiana revealed by multilocus genealogical concordance. <i>Fungal Genetics and Biology</i> , 2011 , 48, 1096-107	3.9	153
96	Development of a <i>Fusarium graminearum</i> Affymetrix GeneChip for profiling fungal gene expression in vitro and in planta. <i>Fungal Genetics and Biology</i> , 2006 , 43, 316-25	3.9	150
95	Genes determining pathogenicity to pea are clustered on a supernumerary chromosome in the fungal plant pathogen <i>Nectria haematococca</i> . <i>Plant Journal</i> , 2001 , 25, 305-14	6.9	146
94	A novel Asian clade within the <i>Fusarium graminearum</i> species complex includes a newly discovered cereal head blight pathogen from the Russian Far East. <i>Mycologia</i> , 2009 , 101, 841-52	2.4	141
93	Conidial germination in the filamentous fungus <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2008 , 45, 389-99	3.9	136
92	Nivalenol-type populations of <i>Fusarium graminearum</i> and <i>F. asiaticum</i> are prevalent on wheat in southern Louisiana. <i>Phytopathology</i> , 2011 , 101, 124-34	3.8	133
91	Population Subdivision of <i>Fusarium graminearum</i> Sensu Stricto in the Upper Midwestern United States. <i>Phytopathology</i> , 2007 , 97, 1434-9	3.8	127
90	<i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Consists of a Small Number of Divergent and Globally Distributed Clonal Lineages. <i>Phytopathology</i> , 1997 , 87, 915-23	3.8	125
89	Random Insertional Mutagenesis Identifies Genes Associated with Virulence in the Wheat Scab Fungus <i>Fusarium graminearum</i> . <i>Phytopathology</i> , 2005 , 95, 744-50	3.8	124
88	The genomic organization of plant pathogenicity in <i>Fusarium</i> species. <i>Current Opinion in Plant Biology</i> , 2010 , 13, 420-6	9.9	121
87	New tricks of an old enemy: isolates of <i>Fusarium graminearum</i> produce a type A trichothecene mycotoxin. <i>Environmental Microbiology</i> , 2015 , 17, 2588-600	5.2	111
86	Analysis of expressed sequence tags from <i>Gibberella zeae</i> (anamorph <i>Fusarium graminearum</i>). <i>Fungal Genetics and Biology</i> , 2003 , 38, 187-97	3.9	111
85	In vivo rearrangement of foreign DNA by <i>Fusarium oxysporum</i> produces linear self-replicating plasmids. <i>Journal of Bacteriology</i> , 1990 , 172, 3163-71	3.5	109
84	Genetic transformation of the fungal plant wilt pathogen, <i>Fusarium oxysporum</i> . <i>Current Genetics</i> , 1988 , 13, 145-149	2.9	99
83	The transcriptome of <i>Fusarium graminearum</i> during the infection of wheat. <i>Molecular Plant-Microbe Interactions</i> , 2011 , 24, 995-1000	3.6	95
82	Effector profiles distinguish formae speciales of <i>Fusarium oxysporum</i> . <i>Environmental Microbiology</i> , 2016 , 18, 4087-4102	5.2	94

81	Chromosome complement of the fungal plant pathogen <i>Fusarium graminearum</i> based on genetic and physical mapping and cytological observations. <i>Genetics</i> , 2005 , 171, 985-1001	4	91
80	The Wor1-like protein Fgp1 regulates pathogenicity, toxin synthesis and reproduction in the phytopathogenic fungus <i>Fusarium graminearum</i> . <i>PLoS Pathogens</i> , 2012 , 8, e1002724	7.6	87
79	Trichothecene Mycotoxins: Biosynthesis, Regulation, and Management. <i>Annual Review of Phytopathology</i> , 2019 , 57, 15-39	10.8	84
78	Cellular compartmentalization of secondary metabolism. <i>Frontiers in Microbiology</i> , 2015 , 6, 68	5.7	82
77	Relatedness of Strains of <i>Fusarium oxysporum</i> from Crucifers Measured by Examination of Mitochondrial and Ribosomal DNA. <i>Phytopathology</i> , 1987 , 77, 1289	3.8	82
76	<i>Fusarium graminearum</i> : pathogen or endophyte of North American grasses?. <i>New Phytologist</i> , 2018 , 217, 1203-1212	9.8	81
75	Statistical Analysis of Electrophoretic Karyotype Variation Among Vegetative Compatibility Groups of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> . <i>Molecular Plant-Microbe Interactions</i> , 1994 , 7, 196	3.6	73
74	Diversity of <i>Fusarium</i> head blight populations and trichothecene toxin types reveals regional differences in pathogen composition and temporal dynamics. <i>Fungal Genetics and Biology</i> , 2015 , 82, 22-31 ⁹	3.9	72
73	Systematics, Phylogeny and Trichothecene Mycotoxin Potential of <i>Fusarium</i> Head Blight Cereal Pathogens. <i>Mycotoxins</i> , 2012 , 62, 91-102	0.2	72
72	Transducin beta-like gene FTL1 is essential for pathogenesis in <i>Fusarium graminearum</i> . <i>Eukaryotic Cell</i> , 2009 , 8, 867-76		72
71	The transcription factor FgStuAp influences spore development, pathogenicity, and secondary metabolism in <i>Fusarium graminearum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2011 , 24, 54-67	3.6	71
70	Cellular development associated with induced mycotoxin synthesis in the filamentous fungus <i>Fusarium graminearum</i> . <i>PLoS ONE</i> , 2013 , 8, e63077	3.7	70
69	Origin of Race 3 of <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> at a Single Site in California. <i>Phytopathology</i> , 2003 , 93, 1014-22	3.8	69
68	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, 148-59	3.9	69
67	Comparative genomics and prediction of conditionally dispensable sequences in legume-infecting <i>Fusarium oxysporum</i> formae speciales facilitates identification of candidate effectors. <i>BMC Genomics</i> , 2016 , 17, 191	4.5	68
66	<i>Fusarium graminearum</i> Tri12p influences virulence to wheat and trichothecene accumulation. <i>Molecular Plant-Microbe Interactions</i> , 2012 , 25, 1408-18	3.6	67
65	Linear plasmidlike DNA in the plant pathogenic fungus <i>Fusarium oxysporum</i> f. sp. <i>conglutinans</i> . <i>Journal of Bacteriology</i> , 1986 , 167, 587-93	3.5	67
64	Species-specific banding patterns of restriction endonuclease-digested mitochondrial DNA from the genus <i>Pythium</i> . <i>Experimental Mycology</i> , 1990 , 14, 32-46		65

63	Soil fungal communities respond to grassland plant community richness and soil edaphics. <i>Microbial Ecology</i> , 2015 , 70, 188-95	4.4	64
62	The HDF1 histone deacetylase gene is important for conidiation, sexual reproduction, and pathogenesis in <i>Fusarium graminearum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2011 , 24, 487-96	3.6	62
61	Systematic Numbering of Vegetative Compatibility Groups in the Plant Pathogenic Fungus <i>Fusarium oxysporum</i> . <i>Phytopathology</i> , 1998 , 88, 30-2	3.8	61
60	Temporal dynamics and population genetic structure of <i>Fusarium graminearum</i> in the upper Midwestern United States. <i>Fungal Genetics and Biology</i> , 2014 , 73, 83-92	3.9	58
59	Development of VNTR markers for two <i>Fusarium graminearum</i> clade species. <i>Molecular Ecology Notes</i> , 2004 , 4, 468-470		57
58	Interactions between <i>Fusarium verticillioides</i> , <i>Ustilago maydis</i> , and <i>Zea mays</i> : an endophyte, a pathogen, and their shared plant host. <i>Fungal Genetics and Biology</i> , 2012 , 49, 578-87	3.9	56
57	The fungal myosin I is essential for <i>Fusarium</i> toxosome formation. <i>PLoS Pathogens</i> , 2018 , 14, e1006827	7.6	54
56	Autonomously replicating plasmids and chromosome rearrangement during transformation of <i>Nectria haematococca</i> . <i>Gene</i> , 1992 , 117, 81-9	3.8	53
55	The genome of the generalist plant pathogen <i>Fusarium avenaceum</i> is enriched with genes involved in redox, signaling and secondary metabolism. <i>PLoS ONE</i> , 2014 , 9, e112703	3.7	51
54	A novel transcriptional factor important for pathogenesis and ascosporeogenesis in <i>Fusarium graminearum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2011 , 24, 118-28	3.6	49
53	Structural reorganization of the fungal endoplasmic reticulum upon induction of mycotoxin biosynthesis. <i>Scientific Reports</i> , 2017 , 7, 44296	4.9	46
52	Population Genetic Analysis Corroborates Dispersal of <i>Fusarium oxysporum</i> f. sp. <i>radicis-lycopersici</i> from Florida to Europe. <i>Phytopathology</i> , 1999 , 89, 623-30	3.8	45
51	In vitro interactions between <i>Fusarium verticillioides</i> and <i>Ustilago maydis</i> through real-time PCR and metabolic profiling. <i>Fungal Genetics and Biology</i> , 2011 , 48, 874-85	3.9	44
50	Metabolome and transcriptome of the interaction between <i>Ustilago maydis</i> and <i>Fusarium verticillioides</i> in vitro. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 3656-67	4.8	44
49	Genomic analysis of host-pathogen interaction between <i>Fusarium graminearum</i> and wheat during early stages of disease development. <i>Microbiology (United Kingdom)</i> , 2006 , 152, 1877-1890	2.9	44
48	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic that Includes the Species Complex. <i>Phytopathology</i> , 2021 , 111, 1064-1079	3.8	39
47	Cryptic promoter activity in the coding region of the HMG-CoA reductase gene in <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2006 , 43, 34-41	3.9	34
46	Genetic duplication in <i>Fusarium oxysporum</i> . <i>Current Genetics</i> , 1995 , 28, 173-6	2.9	33

45	No to : Phylogenomic and Practical Reasons for Continued Inclusion of the <i>Fusarium solani</i> Species Complex in the Genus. <i>MSphere</i> , 2020 , 5,	5	32
44	The Probable Center of Origin of <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> VCG 0033. <i>Plant Disease</i> , 2003 , 87, 1433-1438	1.5	31
43	Plant Community Richness Mediates Inhibitory Interactions and Resource Competition between <i>Streptomyces</i> and <i>Fusarium</i> Populations in the Rhizosphere. <i>Microbial Ecology</i> , 2017 , 74, 157-167	4.4	27
42	Compartmentalized gene regulatory network of the pathogenic fungus <i>Fusarium graminearum</i> . <i>New Phytologist</i> , 2016 , 211, 527-41	9.8	27
41	Examining the Transcriptional Response in Wheat Near-Isogenic Lines to Infection and Deoxynivalenol Treatment. <i>Plant Genome</i> , 2016 , 9, plantgenome2015.05.0032	4.4	27
40	The genome of opportunistic fungal pathogen <i>Fusarium oxysporum</i> carries a unique set of lineage-specific chromosomes. <i>Communications Biology</i> , 2020 , 3, 50	6.7	26
39	Rapid Detection of the <i>Fusarium oxysporum</i> Lineage Containing the Canary Island Date Palm Wilt Pathogen. <i>Phytopathology</i> , 1999 , 89, 407-13	3.8	25
38	A SIX1 homolog in <i>Fusarium oxysporum</i> f.sp. <i>cubense</i> tropical race 4 contributes to virulence towards Cavendish banana. <i>PLoS ONE</i> , 2018 , 13, e0205896	3.7	25
37	A molecular characterization of <i>Cercospora</i> species pathogenic to water hyacinth and emendation of <i>C. piaropi</i> . <i>Mycologia</i> , 2001 , 93, 323-334	2.4	24
36	Effort versus Reward: Preparing Samples for Fungal Community Characterization in High-Throughput Sequencing Surveys of Soils. <i>PLoS ONE</i> , 2015 , 10, e0127234	3.7	23
35	Genome Sequence of <i>Fusarium oxysporum</i> f. sp. <i>melonis</i> Strain NRRL 26406, a Fungus Causing Wilt Disease on Melon. <i>Genome Announcements</i> , 2014 , 2,		22
34	A high proportion of NX-2 genotype strains are found among <i>Fusarium graminearum</i> isolates from northeastern New York State. <i>European Journal of Plant Pathology</i> , 2018 , 150, 791-796	2.1	22
33	A phosphorylated transcription factor regulates sterol biosynthesis in <i>Fusarium graminearum</i> . <i>Nature Communications</i> , 2019 , 10, 1228	17.4	21
32	EBR1 genomic expansion and its role in virulence of <i>Fusarium</i> species. <i>Environmental Microbiology</i> , 2014 , 16, 1982-2003	5.2	21
31	Fungal Innate Immunity Induced by Bacterial Microbe-Associated Molecular Patterns (MAMPs). <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 1585-95	3.2	20
30	A Molecular Characterization of <i>Cercospora</i> Species Pathogenic to Water Hyacinth and Emendation of <i>C. piaropi</i> . <i>Mycologia</i> , 2001 , 93, 323	2.4	20
29	The mitochondrial genome of <i>Fusarium oxysporum</i> . <i>Plasmid</i> , 1989 , 22, 86-9	3.3	20
28	Kinome Expansion in the <i>Fusarium oxysporum</i> Species Complex Driven by Accessory Chromosomes. <i>MSphere</i> , 2018 , 3,	5	20

27	Effector Gene Suites in Some Soil Isolates of <i>Fusarium oxysporum</i> Are Not Sufficient Predictors of Vascular Wilt in Tomato. <i>Phytopathology</i> , 2017 , 107, 842-851	3.8	19
26	Nrs1, a repetitive element linked to pisatin demethylase genes on a dispensable chromosome of <i>Nectria haematococca</i> . <i>Molecular Plant-Microbe Interactions</i> , 1995 , 8, 524-31	3.6	19
25	Conservation and divergence of the cyclic adenosine monophosphate-protein kinase A (cAMP-PKA) pathway in two plant-pathogenic fungi: <i>Fusarium graminearum</i> and <i>F. verticillioides</i> . <i>Molecular Plant Pathology</i> , 2016 , 17, 196-209	5.7	19
24	Mitochondrial plasmids do not determine host range in crucifer-infecting strains of <i>Fusarium oxysporum</i> . <i>Plant Pathology</i> , 1992 , 41, 103-112	2.8	17
23	Nutrient use preferences among soil <i>Streptomyces</i> suggest greater resource competition in monoculture than polyculture plant communities. <i>Plant and Soil</i> , 2016 , 409, 329-343	4.2	17
22	Population Subdivision of <i>Fusarium graminearum</i> from Barley and Wheat in the Upper Midwestern United States at the Turn of the Century. <i>Phytopathology</i> , 2015 , 105, 1466-74	3.8	16
21	Expression of the <i>Fusarium graminearum</i> terpenome and involvement of the endoplasmic reticulum-derived toxosome. <i>Fungal Genetics and Biology</i> , 2019 , 124, 78-87	3.9	15
20	Systematic discovery of regulatory motifs in <i>Fusarium graminearum</i> by comparing four <i>Fusarium</i> genomes. <i>BMC Genomics</i> , 2010 , 11, 208	4.5	15
19	Plant diversity and plant identity influence <i>Fusarium</i> communities in soil. <i>Mycologia</i> , 2017 , 109, 128-139	2.4	14
18	Chromosome-Scale Genome Assembly of Strain Fo47, a Fungal Endophyte and Biocontrol Agent. <i>Molecular Plant-Microbe Interactions</i> , 2020 , 33, 1108-1111	3.6	13
17	Genetic diversity among isolates of <i>Fusarium oxysporum</i> f.sp. <i>canariensis</i> . <i>Plant Pathology</i> , 2000 , 49, 155-164	2.84	13
16	Npc1 is involved in sterol trafficking in the filamentous fungus <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2011 , 48, 725-30	3.9	12
15	A fungal ABC transporter FgAtm1 regulates iron homeostasis via the transcription factor cascade FgAreA-HapX. <i>PLoS Pathogens</i> , 2019 , 15, e1007791	7.6	11
14	Nanoscale enrichment of the cytosolic enzyme trichodiene synthase near reorganized endoplasmic reticulum in <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2019 , 124, 73-77	3.9	10
13	Genetic Manipulation of Plant Pathogenic Fungi 1991 , 152-170		9
12	Inhibitory and nutrient use phenotypes among coexisting <i>Fusarium</i> and <i>Streptomyces</i> populations suggest local coevolutionary interactions in soil. <i>Environmental Microbiology</i> , 2020 , 22, 976-985	5.2	8
11	Phylogeny, Plant Species, and Plant Diversity Influence Carbon Use Phenotypes Among <i>Fusarium</i> Populations in the Rhizosphere Microbiome. <i>Phytobiomes Journal</i> , 2017 , 1, 150-157	4.8	6
10	<i>Fusarium</i> BP1 is a reader of H3K27 methylation. <i>Nucleic Acids Research</i> , 2021 , 49, 10448-10464	20.1	5

9	The t-SNARE Is Involved in Growth, Defense, and DON Accumulation and Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2020 , 33, 888-901	3.6	4
8	Metatranscriptomic Comparison of Endophytic and Pathogenic -Arabidopsis Interactions Reveals Plant Transcriptional Plasticity. <i>Molecular Plant-Microbe Interactions</i> , 2021 , 34, 1071-1083	3.6	3
7	Targeted chromosome breakage in filamentous fungi. <i>Fungal Genetics and Biology</i> , 1997 , 22, 13-8	3.9	2
6	Bacterial artificial chromosome-based physical map of <i>Gibberella zeae</i> (<i>Fusarium graminearum</i>). <i>Genome</i> , 2007 , 50, 954-62	2.4	2
5	<i>Gibberella zeae</i> ascospore production and collection for microarray experiments. <i>Journal of Visualized Experiments</i> , 2006 , 115	1.6	2
4	Evolution of Plant Pathogenicity in <i>Fusarium</i> Species 2013 , 485-500		1
3	<i>Fusarium graminearum</i> species complex: A bibliographic analysis and web-accessible database for global mapping of species and trichothecene toxin chemotypes. <i>Phytopathology</i> , 2021 ,	3.8	1
2	First Report of <i>Sphaeropsis tumefaciens</i> on an Endangered St. John's-Wort in Florida. <i>Plant Disease</i> , 2002 , 86, 1177	1.5	0
1	Plant defense compound triggers mycotoxin synthesis by regulating H2B ub1 and H3K4 me2/3 deposition. <i>New Phytologist</i> , 2021 , 232, 2106-2123	9.8	0