

A Tale of Genome Compartmentalization: The Evolution of Fungi

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A complete toolset for the study of <i>Ustilago bromivora</i> and <i>Brachypodium</i> sp. as a fungal-temperate grass pathosystem. <i>ELife</i> , 2016, 5, .	6.0	49
2	Life cycle specialization of filamentous pathogens “ colonization and reproduction in plant tissues. <i>Current Opinion in Microbiology</i> , 2016, 32, 31-37.	5.1	21
3	Apoplastic fungal effectors in historic perspective; a personal view. <i>New Phytologist</i> , 2016, 212, 805-813.	7.3	32
4	The Evolution of Orphan Regions in Genomes of a Fungal Pathogen of Wheat. <i>MBio</i> , 2016, 7, .	4.1	132
5	Biology, dynamics, and applications of transposable elements in basidiomycete fungi. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1337-1350.	3.6	35
6	Putative orthologs of <i>Ustilago maydis</i> effectors screened from the genome of sugarcane smut fungus - <i>Sporisorium scitamineum</i> . <i>Australasian Plant Pathology</i> , 2017, 46, 147-156.	1.0	10
7	<i>Fusarium</i> in the age of genomics. <i>Tropical Plant Pathology</i> , 2017, 42, 184-189.	1.5	8
8	<i>Ustilago maydis</i> effectors and their impact on virulence. <i>Nature Reviews Microbiology</i> , 2017, 15, 409-421.	28.6	188
9	In vitro secretomic analysis identifies putative pathogenicity-related proteins of <i>Sporisorium scitamineum</i> “ The sugarcane smut fungus. <i>Fungal Biology</i> , 2017, 121, 199-211.	2.5	11
10	Evolution and genome architecture in fungal plant pathogens. <i>Nature Reviews Microbiology</i> , 2017, 15, 756-771.	28.6	378
11	Effector-Mediated Communication of Filamentous Plant Pathogens With Their Hosts. <i>Advances in Botanical Research</i> , 2017, , 161-185.	1.1	4
12	Small RNA sequencing reveals a role for sugarcane miRNAs and their targets in response to <i>Sporisorium scitamineum</i> infection. <i>BMC Genomics</i> , 2017, 18, 325.	2.8	34
13	Development of an efficient vector system for gene knock-out and near in-cis gene complementation in the sugarcane smut fungus. <i>Scientific Reports</i> , 2017, 7, 3113.	3.3	26
14	Using Population and Comparative Genomics to Understand the Genetic Basis of Effector-Driven Fungal Pathogen Evolution. <i>Frontiers in Plant Science</i> , 2017, 8, 119.	3.6	135
15	The Comparison of Expressed Candidate Secreted Proteins from Two Arbuscular Mycorrhizal Fungi Unravels Common and Specific Molecular Tools to Invade Different Host Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 124.	3.6	100
16	Insights into Host Cell Modulation and Induction of New Cells by the Corn Smut <i>Ustilago maydis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 899.	3.6	15
17	Plant jasmonate ZIM domain genes: shedding light on structure and expression patterns of JAZ gene family in sugarcane. <i>BMC Genomics</i> , 2017, 18, 771.	2.8	35
18	Cut-and-Paste Transposons in Fungi with Diverse Lifestyles. <i>Genome Biology and Evolution</i> , 2017, 9, 3463-3477.	2.5	77

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20	A Near-Complete Haplotype-Phased Genome of the Dikaryotic Wheat Stripe Rust Fungus <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Reveals High Interhaplotype Diversity. <i>MBio</i> , 2018, 9, .	4.1	112
21	Fine-Scale Recombination Maps of Fungal Plant Pathogens Reveal Dynamic Recombination Landscapes and Intragenic Hotspots. <i>Genetics</i> , 2018, 208, 1209-1229.	2.9	61
22	The birth and death of effectors in rapidly evolving filamentous pathogen genomes. <i>Current Opinion in Microbiology</i> , 2018, 46, 34-42.	5.1	106
23	Positively Selected Effector Genes and Their Contribution to Virulence in the Smut Fungus <i>Sporisorium reilianum</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 629-645.	2.5	48
24	How to make a tumour: cell type specific dissection of <i>Ustilago maydis</i> induced tumour development in maize leaves. <i>New Phytologist</i> , 2018, 217, 1681-1695.	7.3	55
25	Species Tree Estimation Using ASTRAL: How Many Genes Are Enough?. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1738-1747.	3.0	19
26	Comparative analyses of secreted proteins in plant pathogenic smut fungi and related basidiomycetes. <i>Fungal Genetics and Biology</i> , 2018, 112, 21-30.	2.1	86
27	Development of a Tandem Repeat-Based Polymerase Chain Displacement Reaction Method for Highly Sensitive Detection of <i>Candidatus Liberibacter asiaticus</i> . <i>Phytopathology</i> , 2018, 108, 292-298.	2.2	9
28	The Genome Biology of Effector Gene Evolution in Filamentous Plant Pathogens. <i>Annual Review of Phytopathology</i> , 2018, 56, 21-40.	7.8	195
29	Identification and evaluation of PCR reference genes for host and pathogen in sugarcane- <i>Sporisorium scitamineum</i> interaction system. <i>BMC Genomics</i> , 2018, 19, 479.	2.8	14
30	Comparative Genomics of Smut Pathogens: Insights From Orphans and Positively Selected Genes Into Host Specialization. <i>Frontiers in Microbiology</i> , 2018, 9, 660.	3.5	33
31	Comparative Methods for Molecular Determination of Host-Specificity Factors in Plant-Pathogenic Fungi. <i>International Journal of Molecular Sciences</i> , 2018, 19, 863.	4.1	51
32	Comprehensive profiling of codon usage signatures and codon context variations in the genus <i>Ustilago</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2019, 35, 118.	3.6	9
33	Molecular Interactions Between Smut Fungi and Their Host Plants. <i>Annual Review of Phytopathology</i> , 2019, 57, 411-430.	7.8	59
34	Transposable Elements Adaptive Role in Genome Plasticity, Pathogenicity and Evolution in Fungal Phytopathogens. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3597.	4.1	50
35	Identification and Functional Analysis of the Pheromone Response Factor Gene of <i>Sporisorium scitamineum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2115.	3.5	15
36	Smut infection of perennial hosts: the genome and the transcriptome of the Brassicaceae smut fungus <i>Thecaphora thlaspeos</i> reveal functionally conserved and novel effectors. <i>New Phytologist</i> , 2019, 222, 1474-1492.	7.3	11
37	A dynamic degradome landscape on miRNAs and their predicted targets in sugarcane caused by <i>Sporisorium scitamineum</i> stress. <i>BMC Genomics</i> , 2019, 20, 57.	2.8	13

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38	Comparative genomics of chytrid fungi reveal insights into the obligate biotrophic and pathogenic lifestyle of <i>Synchytrium endobioticum</i> . <i>Scientific Reports</i> , 2019, 9, 8672.	3.3	36
39	Mitotic Recombination and Rapid Genome Evolution in the Invasive Forest Pathogen <i>Phytophthora ramorum</i> . <i>MBio</i> , 2019, 10, .	4.1	50
40	The emergence of the multi-species NIP1 effector in <i>Rhynchosporium</i> was accompanied by high rates of gene duplications and losses. <i>Environmental Microbiology</i> , 2019, 21, 2677-2695.	3.8	19
41	A chromosome-scale genome assembly reveals a highly dynamic effector repertoire of wheat powdery mildew. <i>New Phytologist</i> , 2019, 221, 2176-2189.	7.3	79
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43	The insertion of a mitochondrial selfish element into the nuclear genome and its consequences. <i>Ecology and Evolution</i> , 2020, 10, 11117-11132.	1.9	4
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45	Genome evolution in fungal plant pathogens: looking beyond the two-speed genome model. <i>Fungal Biology Reviews</i> , 2020, 34, 136-143.	4.7	63
46	Factors Affecting the Synthesis of Cellobiose Lipids by <i>Sporisorium scitamineum</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 555647.	4.1	15
47	Characterization of Two Satellite DNA Families in the Genome of the Oomycete Plant Pathogen <i>Phytophthora parasitica</i> . <i>Frontiers in Genetics</i> , 2020, 11, 557.	2.3	6
48	The functionally conserved effector Sta1 is a fungal cell wall protein required for virulence in <i>Ustilago maydis</i> . <i>New Phytologist</i> , 2020, 227, 185-199.	7.3	20
49	Smut fungal strategies for the successful infection. <i>Microbial Pathogenesis</i> , 2020, 142, 104039.	2.9	9
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52	Physiological Basis of Smut Infectivity in the Early Stages of Sugar Cane Colonization. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 44.	3.5	4
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55	Comparative transcriptome profiling identifies maize line specificity of fungal effectors in the maize- <i>Ustilago maydis</i> interaction. <i>Plant Journal</i> , 2021, 106, 733-752.	5.7	12
56	A cell surface-exposed protein complex with an essential virulence function in <i>Ustilago maydis</i> . <i>Nature Microbiology</i> , 2021, 6, 722-730.	13.3	31
57	Comparative expression analysis of potential pathogenicity-associated genes of high- and low-virulent <i>Sporisorium scitamineum</i> isolates during interaction with sugarcane. <i>3 Biotech</i> , 2021, 11, 353.	2.2	6

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58	Transposable Elements Contribute to Genome Dynamics and Gene Expression Variation in the Fungal Plant Pathogen <i>Verticillium dahliae</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	26
60	The Pleiades are a cluster of fungal effectors that inhibit host defenses. <i>PLoS Pathogens</i> , 2021, 17, e1009641.	4.7	24
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62	Sugarcane Smut, Caused by <i>Sporisorium scitamineum</i> , a Major Disease of Sugarcane: A Contemporary Review. <i>Phytopathology</i> , 2021, 111, 1905-1917.	2.2	27
63	Genome-Wide Analysis of Nutrient Signaling Pathways Conserved in Arbuscular Mycorrhizal Fungi. <i>Microorganisms</i> , 2021, 9, 1557.	3.6	9
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77	Effectors with Different Gears: Divergence of <i>Ustilago maydis</i> Effector Genes Is Associated with Their Temporal Expression Pattern during Plant Infection. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 16.	3.5	11
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110	Squalene Monooxygenase Gene SsCI80130 Regulates Sporisorium scitamineum Mating/Filamentation and Pathogenicity. Journal of Fungi (Basel, Switzerland), 2022, 8, 470.	3.5	1
111	Chromosomal rearrangements with stable repertoires of genes and transposable elements in an invasive forest-pathogenic fungus. , 0, 2, .		1
112	The Sporisorium reilianum Effector Vag2 Promotes Head Smut Disease via Suppression of Plant Defense Responses. Journal of Fungi (Basel, Switzerland), 2022, 8, 498.	3.5	1
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115	Integrative transcriptome analysis revealed the pathogenic molecular basis of Rhizoctonia solani AG-3 TB at three progressive stages of infection. Frontiers in Microbiology, 0, 13, .	3.5	5
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