

Kirk D Broders

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

725
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567281

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1073
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#	ARTICLE	IF	CITATIONS
1	Brome grasses represent the primary source of <i>Claviceps purpurea</i> inoculum associated with barley fields in the San Luis Valley of Colorado. Canadian Journal of Plant Pathology, 2023, 45, 15-29.	1.4	3
2	A large accessory genome and high recombination rates may influence global distribution and broad host range of the fungal plant pathogen <i>Claviceps purpurea</i> . PLoS ONE, 2022, 17, e0263496.	2.5	8
3	Building More Resilient Culture Collections: A Call for Increased Deposits of Plant-Associated Bacteria. Microorganisms, 2022, 10, 741.	3.6	2
4	FUSARIUM-ID v.3.0: An Updated, Downloadable Resource for <i>Fusarium</i> Species Identification. Plant Disease, 2022, 106, 1610-1616.	1.4	27
5	DNA Sequence-Based Identification of <i>Fusarium</i> : A Work in Progress. Plant Disease, 2022, 106, 1597-1609.	1.4	48
6	<i>Phyllachora</i> species infecting maize and other grass species in the Americas represents a complex of closely related species. Ecology and Evolution, 2022, 12, e8832.	1.9	6
7	Sympatric divergence of the ergot fungus, <i>Claviceps purpurea</i> , populations infecting agricultural and nonagricultural grasses in North America. Ecology and Evolution, 2021, 11, 273-293.	1.9	7
8	Whole-Genome Comparisons of Ergot Fungi Reveals the Divergence and Evolution of Species within the Genus <i>Claviceps</i> Are the Result of Varying Mechanisms Driving Genome Evolution and Host Range Expansion. Genome Biology and Evolution, 2021, 13, .	2.5	17
9	Host-generalist fungal pathogens of seedlings may maintain forest diversity via host-specific impacts and differential susceptibility among tree species. New Phytologist, 2021, 231, 460-474.	7.3	14
10	Genome-wide SNP identification in <i>Fraxinus</i> linking genetic characteristics to tolerance of <i>Agrilus planipennis</i> . Ecology and Evolution, 2021, 11, 14775-14788.	1.9	0
11	Mining Indole Alkaloid Synthesis Gene Clusters from Genomes of 53 <i>Claviceps</i> Strains Revealed Redundant Gene Copies and an Approximate Evolutionary Hourglass Model. Toxins, 2021, 13, 799.	3.4	4
12	Genomics-Informed Molecular Detection of <i>Xanthomonas vasicola</i> pv. <i>vasculorum</i> Strains Causing Severe Bacterial Leaf Streak of Corn. Phytopathology, 2020, 110, 1174-1179.	2.2	11
13	Four phylogenetic species of ergot from Canada and their characteristics in morphology, alkaloid production, and pathogenicity. Mycologia, 2020, 112, 974-988.	1.9	13
14	Current Understanding of the History, Global Spread, Ecology, Evolution, and Management of the Corn Bacterial Leaf Streak Pathogen, <i>Xanthomonas vasicola</i> pv. <i>vasculorum</i> . Phytopathology, 2020, 110, 1124-1131.	2.2	15
15	Genomic Acquisitions in Emerging Populations of <i>Xanthomonas vasicola</i> pv. <i>vasculorum</i> Infecting Corn in the United States and Argentina. Phytopathology, 2020, 110, 1161-1173.	2.2	16
16	Transfer of <i>Xanthomonas campestris</i> pv. <i>arecae</i> and <i>X. campestris</i> pv. <i>musacearum</i> to <i>X. vasicola</i> (Vauterin) as <i>X. vasicola</i> pv. <i>arecae</i> comb. nov. and <i>X. vasicola</i> pv. <i>musacearum</i> comb. nov. and Description of <i>X. vasicola</i> pv. <i>vasculorum</i> pv. nov.. Phytopathology, 2020, 110, 1153-1160.	2.2	23
17	Identification of quantitative trait loci associated with maize resistance to bacterial leaf streak. Crop Science, 2020, 60, 226-237.	1.8	13
18	Occurrence in Seeds and Potential Seed Transmission of <i>Xanthomonas vasicola</i> pv. <i>vasculorum</i> in Maize in the United States. Phytopathology, 2020, 110, 1139-1146.	2.2	6

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19	Caliciopsis moriondi, a new species for a fungus long confused with the pine pathogen C. pinea. MycoKeys, 2020, 73, 87-108.	1.9	7
20	Ergochromes: Heretofore Neglected Side of Ergot Toxicity. Toxins, 2019, 11, 439.	3.4	11
21	Response of eastern white pine and associated foliar, blister rust, canker and root rot pathogens to climate change. Forest Ecology and Management, 2018, 423, 18-26.	3.2	18
22	Emergence of white pine needle damage in the northeastern United States is associated with changes in pathogen pressure in response to climate change. Global Change Biology, 2017, 23, 394-405.	9.5	32
23	Impact of climate change and race evolution on the epidemiology and ecology of stripe rust in central and eastern USA and Canada. Canadian Journal of Plant Pathology, 2017, 39, 385-392.	1.4	21
24	Comparative Genomics of Pathogenic and Nonpathogenic Beetle-Vectored Fungi in the Genus Geosmithia. Genome Biology and Evolution, 2017, 9, 3312-3327.	2.5	18
25	Hyperspectral Evaluation of <i>Venturia inaequalis</i> Management Using the Disease Predictive Model RIMpro in the Northeastern U.S.. Agricultural Sciences, 2017, 08, 1358-1371.	0.3	0
26	Corn Yield Loss Estimates Due to Diseases in the United States and Ontario, Canada from 2012 to 2015. Plant Health Progress, 2016, 17, 211-222.	1.4	135
27	The new family Septorioideaceae, within the Botryosphaerales and Septorioides strobis as a new species associated with needle defoliation of Pinus strobus in the United States. Fungal Biology, 2016, 120, 1030-1040.	2.5	28
28	<i>De novo</i> genome assembly of <i>Geosmithia morbida</i>, the causal agent of thousand cankers disease. PeerJ, 2016, 4, e1952.	2.0	9
29	Characterization of Fungal Pathogens Associated with White Pine Needle Damage (WPND) in Northeastern North America. Forests, 2015, 6, 4088-4104.	2.1	33
30	Extent and Severity of Caliciopsis Canker in New England, USA: An Emerging Disease of Eastern White Pine (Pinus strobus L.). Forests, 2015, 6, 4360-4373.	2.1	19
31	Priority of <i>Lophophacidium</i> over <i>Canavirgella</i>: taxonomic status of <i>Lophophacidium dooksii</i> and <i>Canavirgella banfieldii</i>, causal agents of a white pine needle disease. Mycologia, 2015, 107, 745-753.	1.9	7
32	Population Structure of Geosmithia morbida, the Causal Agent of Thousand Cankers Disease of Walnut Trees in the United States. PLoS ONE, 2014, 9, e112847.	2.5	38
33	A Scale-Explicit Framework for Conceptualizing the Environmental Impacts of Agricultural Land Use Changes. Sustainability, 2014, 6, 8432-8451.	3.2	14
34	A Vavilovian approach to discovering crop-associated microbes with potential to enhance plant immunity. Frontiers in Plant Science, 2014, 5, 492.	3.6	22
35	Butternut (<i>Juglans cinerea</i>) health, hybridization, and recruitment in the northeastern United States. Canadian Journal of Forest Research, 2014, 44, 1244-1252.	1.7	12
36	Phylogenetic Diversity of Rhizoctonia solani Associated with Canola and Wheat in Alberta, Manitoba, and Saskatchewan. Plant Disease, 2014, 98, 1695-1701.	1.4	19

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37	Two new species of <i>Pythium</i> , <i>P. schmitthenneri</i> and <i>P. selbyi</i> pathogens of corn and soybean in Ohio. <i>Mycologia</i> , 2012, 104, 477-487.	1.9	15
38	<i>Pythium delawarii</i> a new species isolated from soybean in Ohio. <i>Mycologia</i> , 2009, 101, 232-238.	1.9	15
39	Status of bacterial leaf streak of corn in the United States. , 0, , .		8