## Steven J Klosterman

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2668275/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Attenuation of ethylene signaling increases cotton resistance to a defoliating strain of Verticillium dahliae. Crop Journal, 2023, 11, 89-98.	5.2	5
2	Crustacean Meal Elicits Expression of Growth and Defense-Related Genes in Roots of Lettuce and Tomato. PhytoFrontiers, 2022, 2, 10-20.	1.6	2
3	Composition of the Microbiomes from Spinach Seeds Infested or Noninfested with <i>Peronospora effusa</i> or <i>Verticillium dahliae</i> . Phytobiomes Journal, 2022, 6, 169-180.	2.7	0
4	miR398b negatively regulates cotton immune responses to Verticillium dahliae via multiple targets. Crop Journal, 2022, 10, 1026-1036.	5.2	6
5	Identification of long non-coding RNAs in Verticillium dahliae following inoculation of cotton. Microbiological Research, 2022, 257, 126962.	5.3	4
6	The Verticillium dahliae Spt-Ada-Gcn5 Acetyltransferase Complex Subunit Ada1 Is Essential for Conidia and Microsclerotia Production and Contributes to Virulence. Frontiers in Microbiology, 2022, 13, 852571.	3.5	5
7	Verticillium dahliae CFEM proteins manipulate host immunity and differentially contribute to virulence. BMC Biology, 2022, 20, 55.	3.8	19
8	A secreted ribonuclease effector from <i>Verticillium dahliae</i> localizes in the plant nucleus to modulate host immunity. Molecular Plant Pathology, 2022, 23, 1122-1140.	4.2	15
9	The bZip Transcription Factor VdMRTF1 is a Negative Regulator of Melanin Biosynthesis and Virulence in Verticillium dahliae. Microbiology Spectrum, 2022, 10, e0258121.	3.0	8
10	The secretome of <i>Verticillium dahliae</i> in collusion with plant defence responses modulates <scp>Verticillium</scp> wilt symptoms. Biological Reviews, 2022, 97, 1810-1822.	10.4	15
11	A polyketide synthase from Verticillium dahliae modulates melanin biosynthesis and hyphal growth to promote virulence. BMC Biology, 2022, 20, .	3.8	11
12	Welcoming PhytoFrontiersâ,,¢ into Our APS Family of Journals. PhytoFrontiers, 2021, 1, 2-3.	1.6	0
13	ChMYB4 downregulates lignin biosynthesis and enhances cotton resistance to Verticillium dahliae. Plant Cell Reports, 2021, 40, 735-751.	5.6	31
14	A Singleâ€Nucleotide Mutation in a GLUTAMATE RECEPTORâ€LIKE Gene Confers Resistance to Fusarium Wilt in <i>Gossypium hirsutum</i> . Advanced Science, 2021, 8, 2002723.	11.2	37
15	Genome Sequence Data of MAT1-1 and MAT1-2 Idiomorphs from Verticillium dahliae. Phytopathology, 2021, , PHYTO01210012A.	2.2	1
16	<i>&gt;Verticillium klebahnii</i> and <i>V. isaacii</i> Isolates Exhibit Host-Dependent Biological Control of Verticillium Wilt Caused by <i>V. dahliae</i> . PhytoFrontiers, 2021, 1, 276-290.	1.6	9
17	Cytotoxic function of xylanase VdXyn4 in the plant vascular wilt pathogen <i>Verticillium dahliae</i> . Plant Physiology, 2021, 187, 409-429.	4.8	27
18	Dynamics of Verticillium dahliae race 1 population under managed agricultural ecosystems. BMC Biology, 2021, 19, 131.	3.8	1

STEVEN J KLOSTERMAN

#	Article	IF	CITATIONS
19	Transcriptome Variations in Verticillium dahliae in Response to Two Different Inorganic Nitrogen Sources. Frontiers in Microbiology, 2021, 12, 712701.	3.5	1
20	Biological Characteristics of Verticillium dahliae MAT1-1 and MAT1-2 Strains. International Journal of Molecular Sciences, 2021, 22, 7148.	4.1	2
21	Key Insights and Research Prospects at the Dawn of the Population Genomics Era for Verticillium dahliae. Annual Review of Phytopathology, 2021, 59, 31-51.	7.8	16
22	Functional Genomics and Comparative Lineage-Specific Region Analyses Reveal Novel Insights into Race Divergence in Verticillium dahliae. Microbiology Spectrum, 2021, 9, e0111821.	3.0	7
23	Measurements of Aerial Spore Load by qPCR Facilitates Lettuce Downy Mildew Risk Advisement. Plant Disease, 2020, 104, 82-93.	1.4	23
24	Genome Sequence of <i>Verticillium dahliae</i> Race 1 Isolate VdLs.16 From Lettuce. Molecular Plant-Microbe Interactions, 2020, 33, 1265-1269.	2.6	4
25	Convergent and distinctive functions of transcription factors VdYap1, VdAtf1, and VdSkn7 in the regulation of nitrosative stress resistance, microsclerotia formation, and virulence in Verticillium dahliae. Molecular Plant Pathology, 2020, 21, 1451-1466.	4.2	15
26	Detached leaf inoculation assay for evaluating resistance to the spinach downy mildew pathogen. European Journal of Plant Pathology, 2020, 158, 511-520.	1.7	13
27	Sporangiospore Viability and Oospore Production in the Spinach Downy Mildew Pathogen, <i>Peronospora effusa</i> . Plant Disease, 2020, 104, 2634-2641.	1.4	16
28	Hormone Signaling and Its Interplay With Development and Defense Responses in Verticillium-Plant Interactions. Frontiers in Plant Science, 2020, 11, 584997.	3.6	27
29	Functional analyses of small secreted cysteineâ€ <b>r</b> ich proteins identified candidate effectors in <i>Verticillium dahliae</i> . Molecular Plant Pathology, 2020, 21, 667-685.	4.2	46
30	The Arabidopsis SENESCENCE-ASSOCIATED GENE 13 Regulates Dark-Induced Senescence and Plays Contrasting Roles in Defense Against Bacterial and Fungal Pathogens. Molecular Plant-Microbe Interactions, 2020, 33, 754-766.	2.6	26
31	The bZIP transcription factor VdAtf1 regulates virulence by mediating nitrogen metabolism in <i>Verticillium dahliae</i> . New Phytologist, 2020, 226, 1461-1479.	7.3	41
32	Genome Sequences of <i>Verticillium dahliae</i> Defoliating Strain XJ592 and Nondefoliating Strain XJ511. Molecular Plant-Microbe Interactions, 2020, 33, 565-568.	2.6	5
33	Transcriptional analyses of differential cultivars during resistant and susceptible interactions with Peronospora effusa, the causal agent of spinach downy mildew. Scientific Reports, 2020, 10, 6719.	3.3	22
34	Two Verticillium dahliae MAPKKKs, VdSsk2 and VdSte11, Have Distinct Roles in Pathogenicity, Microsclerotial Formation, and Stress Adaptation. MSphere, 2019, 4, .	2.9	31
35	Proteome and metabolome analyses reveal differential responses in tomato -Verticillium dahliae-interactions. Journal of Proteomics, 2019, 207, 103449.	2.4	51
36	The <i>Verticillium dahliae</i> Sho1â€MAPK pathway regulates melanin biosynthesis and is required for cotton infection. Environmental Microbiology, 2019, 21, 4852-4874.	3.8	36

STEVEN J KLOSTERMAN

#	Article	IF	CITATIONS
37	Insights into VdCmr1â€mediated protection against high temperature stress and UV irradiation in <i>Verticillium dahliae</i> . Environmental Microbiology, 2019, 21, 2977-2996.	3.8	12
38	Arabidopsis defense mutant ndr1-1 displays accelerated development and early flowering mediated by the hormone gibberellic acid. Plant Science, 2019, 285, 200-213.	3.6	9
39	The <i>Gossypium hirsutum</i> TIRâ€NBS‣RR gene <i>GhDSC1 </i> mediates resistance against Verticillium wilt. Molecular Plant Pathology, 2019, 20, 857-876.	4.2	46
40	Spinach Downy Mildew: Advances in Our Understanding of the Disease Cycle and Prospects for Disease Management. Plant Disease, 2019, 103, 791-803.	1.4	38
41	Population genomics demystifies the defoliation phenotype in the plant pathogen <i>Verticillium dahliae</i> . New Phytologist, 2019, 222, 1012-1029.	7.3	41
42	Genomewide Transcriptome Profiles Reveal How Bacillus subtilis Lipopeptides Inhibit Microsclerotia Formation in Verticillium dahliae. Molecular Plant-Microbe Interactions, 2019, 32, 622-634.	2.6	19
43	Detection of Latent <i>Peronospora effusa</i> Infections in Spinach. Plant Disease, 2018, 102, 1766-1771.	1.4	12
44	SNARE-Encoding Genes VdSec22 and VdSso1 Mediate Protein Secretion Required for Full Virulence in Verticillium dahliae. Molecular Plant-Microbe Interactions, 2018, 31, 651-664.	2.6	39
45	Characterization of two homeodomain transcription factors with critical but distinct roles in virulence in the vascular pathogen <i>Verticillium dahliae</i> . Molecular Plant Pathology, 2018, 19, 986-1004.	4.2	39
46	Comparative genomics of downy mildews reveals potential adaptations to biotrophy. BMC Genomics, 2018, 19, 851.	2.8	59
47	Genome-Wide Identification and Functional Analyses of the CRK Gene Family in Cotton Reveals GbCRK18 Confers Verticillium Wilt Resistance in Gossypium barbadense. Frontiers in Plant Science, 2018, 9, 1266.	3.6	30
48	The Transcription Factor VdHapX Controls Iron Homeostasis and Is Crucial for Virulence in the Vascular Pathogen Verticillium dahliae. MSphere, 2018, 3, .	2.9	28
49	Heterologous Expression of the Cotton NBS-LRR Gene GbaNA1 Enhances Verticillium Wilt Resistance in Arabidopsis. Frontiers in Plant Science, 2018, 9, 119.	3.6	36
50	Transcription factor VdCmr1 is required for pigment production, protection from UV irradiation, and regulates expression of melanin biosynthetic genes in Verticillium dahliae. Microbiology (United) Tj ETQq0 0 0 rg	BT1/.®verlc	ock5170 Tf 50 2
51	Spatiotemporal Patterns in the Airborne Dispersal of Spinach Downy Mildew. Phytopathology, 2017, 107, 50-58.	2.2	10
52	The endochitinase VDECH from Verticillium dahliae inhibits spore germination and activates plant defense responses. Plant Science, 2017, 259, 12-23.	3.6	31
53	A Framework for Optimizing Phytosanitary Thresholds in Seed Systems. Phytopathology, 2017, 107, 1219-1228.	2.2	18
54	Vayg1 is required for microsclerotium formation and melanin production in Verticillium dahliae. Fungal Genetics and Biology, 2017, 98, 1-11.	2.1	46

STEVEN J KLOSTERMAN

#	Article	IF	CITATIONS
55	Plasmolysis and Vital Staining Reveal Viable Oospores of <i>Peronospora effusa</i> in Spinach Seed Lots. Plant Disease, 2016, 100, 59-65.	1.4	19
56	Season-Long Dynamics of Spinach Downy Mildew Determined by Spore Trapping and Disease Incidence. Phytopathology, 2016, 106, 1311-1318.	2.2	32
57	Detection and Quantification of <i>Bremia lactucae</i> by Spore Trapping and Quantitative PCR. Phytopathology, 2016, 106, 1426-1437.	2.2	39
58	Disease Management in the Genomics Era—Summaries of Focus Issue Papers. Phytopathology, 2016, 106, 1068-1070.	2.2	14
59	The mitogen-activated protein kinase gene, VdHog1, regulates osmotic stress response, microsclerotia formation and virulence in Verticillium dahliae. Fungal Genetics and Biology, 2016, 88, 13-23.	2.1	71
60	Frequency of <i>Verticillium</i> Species in Commercial Spinach Fields and Transmission of <i>V. dahliae</i> from Spinach to Subsequent Lettuce Crops. Phytopathology, 2015, 105, 80-90.	2.2	25
61	Focus Issue Articles on Emerging and Re-Emerging Plant Diseases. Phytopathology, 2015, 105, 852-854.	2.2	14
62	Genomics Spurs Rapid Advances in Our Understanding of the Biology of Vascular Wilt Pathogens in the Genus <i>Verticillium</i> . Annual Review of Phytopathology, 2015, 53, 181-198.	7.8	96
63	Multi-locus tree and species tree approaches toward resolving a complex clade of downy mildews (Straminipila, Oomycota), including pathogens of beet and spinach. Molecular Phylogenetics and Evolution, 2015, 86, 24-34.	2.7	58
64	VdCYC8, Encoding CYC8 Glucose Repression Mediator Protein, Is Required for Microsclerotia Formation and Full Virulence in Verticillium dahliae. PLoS ONE, 2015, 10, e0144020.	2.5	11
65	Characterization of Spinach Germplasm for Resistance Against Two Races of Verticillium dahliae. Hortscience: A Publication of the American Society for Hortcultural Science, 2015, 50, 1631-1635.	1.0	3
66	Coupling Spore Traps and Quantitative PCR Assays for Detection of the Downy Mildew Pathogens of Spinach ( <i>Peronospora effusa</i> ) and Beet ( <i>P. schachtii</i> ). Phytopathology, 2014, 104, 1349-1359.	2.2	55
67	Deep mRNA sequencing reveals stage-specific transcriptome alterations during microsclerotia development in the smoke tree vascular wilt pathogen, Verticillium dahliae. BMC Genomics, 2014, 15, 324.	2.8	68
68	RNA-seq analyses of gene expression in the microsclerotia of Verticillium dahliae. BMC Genomics, 2013, 14, 607.	2.8	75
69	Colonization of Spinach by <i>Verticillium dahliae</i> and Effects of Pathogen Localization on the Efficacy of Seed Treatments. Phytopathology, 2013, 103, 268-280.	2.2	31
70	Real-Time PCR for the Quantification of Fungi In Planta. Methods in Molecular Biology, 2012, 835, 121-132.	0.9	11
71	A Real-Time PCR Assay for Detection and Quantification of <i>Verticillium dahliae</i> in Spinach Seed. Phytopathology, 2012, 102, 443-451.	2.2	46
72	Transposable elements in phytopathogenic Verticillium spp.: insights into genome evolution and inter- and intra-specific diversification. BMC Genomics, 2012, 13, 314.	2.8	62

#	Article	IF	CITATIONS
73	One Step Construction of Agrobacterium-Recombination-ready-plasmids (OSCAR), an efficient and robust tool for ATMT based gene deletion construction in fungi. Fungal Genetics and Biology, 2011, 48, 677-684.	2.1	88
74	SSH reveals a linkage between a senescence-associated protease and Verticillium wilt symptom development in lettuce (Lactuca sativa). Physiological and Molecular Plant Pathology, 2011, 76, 48-58.	2.5	21
75	Identification of Pathogenicity-Related Genes in the Vascular Wilt Fungus Verticillium dahliae by Agrobacterium tumefaciens-Mediated T-DNA Insertional Mutagenesis. Molecular Biotechnology, 2011, 49, 209-221.	2.4	71
76	Comparative Genomics Yields Insights into Niche Adaptation of Plant Vascular Wilt Pathogens. PLoS Pathogens, 2011, 7, e1002137.	4.7	477
77	Analysis of <i>Verticillium dahliae</i> Suggests a Lack of Correlation Between Genotypic Diversity and Virulence Phenotypes. Plant Disease, 2011, 95, 1224-1232.	1.4	18
78	Selection for Resistance to Verticillium Wilt Caused by Race 2 Isolates of Verticillium dahliae in Accessions of Lettuce (Lactuca sativa L.). Hortscience: A Publication of the American Society for Hortcultural Science, 2011, 46, 201-206.	1.0	19
79	Iceberg Lettuce Breeding Lines with Resistance to Verticillium Wilt Caused by Race 1 Isolates of Verticillium dahliae. Hortscience: A Publication of the American Society for Hortcultural Science, 2011, 46, 501-504.	1.0	13
80	Population analyses of the vascular plant pathogen Verticillium dahliae detect recombination and transcontinental gene flow. Fungal Genetics and Biology, 2010, 47, 416-422.	2.1	86
81	Molecular Variation Among Isolates of <i>Verticillium dahliae</i> and Polymerase Chain Reaction-Based Differentiation of Races. Phytopathology, 2010, 100, 1222-1230.	2.2	55
82	Diversity, Pathogenicity, and Management of Verticillium Species. Annual Review of Phytopathology, 2009, 47, 39-62.	7.8	624
83	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 May 2009–31 July 2009. Molecular Ecology Resources, 2009, 9, 1460-1466.	4.8	128
84	A Soilless Verticillium Wilt Assay Using an Early Flowering Lettuce Line. Plant Disease, 2009, 93, 691-698.	1.4	10
85	Ubc2, an Ortholog of the Yeast Ste50p Adaptor, Possesses a Basidiomycete-Specific Carboxy Terminal Extension Essential for Pathogenicity Independent of Pheromone Response. Molecular Plant-Microbe Interactions, 2008, 21, 110-121.	2.6	25
86	Genetics of Morphogenesis and Pathogenic Development of Ustilago maydis. Advances in Genetics, 2007, 57, 1-47.	1.8	69
87	Insights from the genome of the biotrophic fungal plant pathogen Ustilago maydis. Nature, 2006, 444, 97-101.	27.8	1,113
88	Genetics of Morphogenesis in Basidiomycetes. Applied Mycology and Biotechnology, 2005, , 353-422.	0.3	5
89	Analysis of pea HMG-I/Y expression suggests a role in defence gene regulation. Molecular Plant Pathology, 2003, 4, 249-258.	4.2	26
90	Plant HMG proteins bearing the AT-hook motif. Plant Science, 2002, 162, 855-866.	3.6	32

#	Article	IF	CITATIONS
91	Characterization of a 20ÂkDa DNase elicitor from <i>Fusarium solani</i> f. sp. <i>phaseoli</i> and its expression at the onset of induced resistance in <i>Pisum sativum</i> . Molecular Plant Pathology, 2001, 2, 147-158.	4.2	33
92	A Comparison of the Effects of DNA-Damaging Agents and Biotic Elicitors on the Induction of Plant Defense Genes, Nuclear Distortion, and Cell Death. Plant Physiology, 2001, 125, 752-762.	4.8	47