

Yonglin Wang

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	A Cytochrome P450 Monooxygenase in Nondefoliating Strain of <i>Verticillium dahliae</i> Manipulates Virulence via Scavenging Reactive Oxygen Species. <i>Phytopathology</i> , 2022, 112, 1723-1729.	1.1	2
2	The bZip Transcription Factor VdMRTF1 is a Negative Regulator of Melanin Biosynthesis and Virulence in <i>Verticillium dahliae</i> . <i>Microbiology Spectrum</i> , 2022, 10, e0258121.	1.2	8
3	Genomic Characterization Provides an Insight into the Pathogenicity of the Poplar Canker Bacterium <i>Lonsdalea populi</i> . <i>Genes</i> , 2021, 12, 246.	1.0	0
4	Transcriptome Variations in <i>Verticillium dahliae</i> in Response to Two Different Inorganic Nitrogen Sources. <i>Frontiers in Microbiology</i> , 2021, 12, 712701.	1.5	1
5	CgHog1 controls the adaptation to both sorbitol and fludioxonil in <i>Colletotrichum gloeosporioides</i> . <i>Fungal Genetics and Biology</i> , 2020, 135, 103289.	0.9	11
6	Convergent and distinctive functions of transcription factors VdYap1, VdAtf1, and VdSkn7 in the regulation of nitrosative stress resistance, microsclerotia formation, and virulence in <i>Verticillium dahliae</i> . <i>Molecular Plant Pathology</i> , 2020, 21, 1451-1466.	2.0	15
7	Oxalic Acid Metabolism Contributes to Full Virulence and Pycnidial Development in the Poplar Canker Fungus <i>Cytospora chrysosperma</i> . <i>Phytopathology</i> , 2020, 110, 1319-1325.	1.1	8
8	The bZIP transcription factor VdAtf1 regulates virulence by mediating nitrogen metabolism in <i>Verticillium dahliae</i> . <i>New Phytologist</i> , 2020, 226, 1461-1479.	3.5	41
9	Two <i>Verticillium dahliae</i> MAPKKs, VdSsk2 and VdSte11, Have Distinct Roles in Pathogenicity, Microsclerotial Formation, and Stress Adaptation. <i>MSphere</i> , 2019, 4, .	1.3	31
10	Insights into VdCmr1-mediated protection against high temperature stress and UV irradiation in <i>Verticillium dahliae</i> . <i>Environmental Microbiology</i> , 2019, 21, 2977-2996.	1.8	12
11	Involvement of a Response Regulator VdSsk1 in Stress Response, Melanin Biosynthesis and Full Virulence in <i>Verticillium dahliae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 606.	1.5	14
12	Genomewide Transcriptome Profiles Reveal How <i>Bacillus subtilis</i> Lipopeptides Inhibit Microsclerotia Formation in <i>Verticillium dahliae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 622-634.	1.4	19
13	A novel gene from a secondary metabolism gene cluster is required for microsclerotia formation and virulence in <i>Verticillium dahliae</i> . <i>Phytopathology Research</i> , 2019, 1, .	0.9	4
14	A Cdc42 homolog in <i>Colletotrichum gloeosporioides</i> regulates morphological development and is required for ROS-mediated plant infection. <i>Current Genetics</i> , 2018, 64, 1153-1169.	0.8	15
15	Deletion of VdKu80 enhances targeted gene replacement in <i>Verticillium dahliae</i> . <i>Australasian Plant Pathology</i> , 2018, 47, 601-608.	0.5	0
16	The Transcription Factor VdHapX Controls Iron Homeostasis and Is Crucial for Virulence in the Vascular Pathogen <i>Verticillium dahliae</i> . <i>MSphere</i> , 2018, 3, .	1.3	28
17	Poplar miR472a targeting NBS-LRRs is involved in effective defence against the necrotrophic fungus <i>Cytospora chrysosperma</i> . <i>Journal of Experimental Botany</i> , 2018, 69, 5519-5530.	2.4	28
18	Transcription factor VdCmr1 is required for pigment production, protection from UV irradiation, and regulates expression of melanin biosynthetic genes in <i>Verticillium dahliae</i> . <i>Microbiology (United Kingdom)</i> , 2017, 157, 105-115.	1.0	5

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19	The C2H2 transcription factor VdMsn2 controls hyphal growth, microsclerotia formation, and virulence of <i>Verticillium dahliae</i> . <i>Fungal Biology</i> , 2017, 121, 1001-1010.	1.1	36
20	The two-component response regulator VdSkn7 plays key roles in microsclerotial development, stress resistance and virulence of <i>Verticillium dahliae</i> . <i>Fungal Genetics and Biology</i> , 2017, 108, 26-35.	0.9	20
21	The Mitogen-Activated Protein Kinase CgMK1 Governs Appressorium Formation, Melanin Synthesis, and Plant Infection of <i>Colletotrichum gloeosporioides</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2216.	1.5	41
22	Functional characterization of two bZIP transcription factors in <i>Verticillium dahliae</i> . <i>Gene</i> , 2017, 626, 386-394.	1.0	22
23	MADS-Box Transcription Factor VdMcm1 Regulates Conidiation, Microsclerotia Formation, Pathogenicity, and Secondary Metabolism of <i>Verticillium dahliae</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1192.	1.5	77
24	The Mitogen-Activated Protein Kinase Kinase VdPbs2 of <i>Verticillium dahliae</i> Regulates Microsclerotia Formation, Stress Response, and Plant Infection. <i>Frontiers in Microbiology</i> , 2016, 7, 1532.	1.5	55
25	High-resolution transcript profiling reveals shoot abscission process of spruce dwarf mistletoe <i>Arceuthobium sichuanense</i> in response to ethephon. <i>Scientific Reports</i> , 2016, 6, 38889.	1.6	3
26	The <i>Colletotrichum gloeosporioides</i> RhoB regulates cAMP and stress response pathways and is required for pathogenesis. <i>Fungal Genetics and Biology</i> , 2016, 96, 12-24.	0.9	18
27	De novo assembly and transcriptome characterization of spruce dwarf mistletoe <i>Arceuthobium sichuanense</i> uncovers gene expression profiling associated with plant development. <i>BMC Genomics</i> , 2016, 17, 771.	1.2	27
28	bZIP transcription factor CgAP1 is essential for oxidative stress tolerance and full virulence of the poplar anthracnose fungus <i>Colletotrichum gloeosporioides</i> . <i>Fungal Genetics and Biology</i> , 2016, 95, 58-66.	0.9	24
29	The mitogen-activated protein kinase gene, VdHog1, regulates osmotic stress response, microsclerotia formation and virulence in <i>Verticillium dahliae</i> . <i>Fungal Genetics and Biology</i> , 2016, 88, 13-23.	0.9	71
30	VdCrz1 is involved in microsclerotia formation and required for full virulence in <i>Verticillium dahliae</i> . <i>Fungal Genetics and Biology</i> , 2015, 82, 201-212.	0.9	54
31	Transcriptomic profiles of the smoke tree wilt fungus <i>Verticillium dahliae</i> under nutrient starvation stresses. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1963-1977.	1.0	13
32	Phylogenetic analysis revealed an expanded C2H2-homeobox subfamily and expression profiles of C2H2 zinc finger gene family in <i>Verticillium dahliae</i> . <i>Gene</i> , 2015, 562, 169-179.	1.0	30
33	Deep mRNA sequencing reveals stage-specific transcriptome alterations during microsclerotia development in the smoke tree vascular wilt pathogen, <i>Verticillium dahliae</i> . <i>BMC Genomics</i> , 2014, 15, 324.	1.2	68
34	Genetic transformation, infection process and qPCR quantification of <i>Verticillium dahliae</i> on smoke-tree <i>Cotinus coggygria</i> . <i>Australasian Plant Pathology</i> , 2013, 42, 33-41.	0.5	33
35	Quantitative Detection of Pathogen DNA of <i>Verticillium</i> Wilt on Smoke Tree <i>Cotinus coggygria</i> . <i>Plant Disease</i> , 2013, 97, 1645-1651.	0.7	22
36	Genome-Wide Identification, Phylogeny and Expression Profile of Vesicle Fusion Components in <i>Verticillium dahliae</i> . <i>PLoS ONE</i> , 2013, 8, e68681.	1.1	16

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37	PsSAK1, a Stress-Activated MAP Kinase of <i>Phytophthora sojae</i> , Is Required for Zoospore Viability and Infection of Soybean. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 1022-1031.	1.4	45