

Yueqiang Leng

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	A conserved hypothetical gene is required but not sufficient for Ptr ToxC production in <i>Pyrenophora tritici-repentis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2022, , .	2.6	11
2	Genome Sequence Resources for the Maize Pathogen <i>Fusarium temperatum</i> Isolated in Poland. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 214-217.	2.6	2
3	Molecular Mapping of Quantitative Trait Loci for <i>Fusarium</i> Head Blight Resistance in the Brazilian Spring Wheat Cultivar ‘Surpresa’. <i>Frontiers in Plant Science</i> , 2021, 12, 778472.	3.6	3
4	Molecular Mapping of Loci Conferring Susceptibility to Spot Blotch and Resistance to Powdery Mildew in Barley Using the Sequencing-Based Genotyping Approach. <i>Phytopathology</i> , 2020, 110, 440-446.	2.2	11
5	Fine mapping of a dominant gene conferring resistance to spot blotch caused by a new pathotype of <i>Bipolaris sorokiniana</i> in barley. <i>Theoretical and Applied Genetics</i> , 2019, 132, 41-51.	3.6	11
6	The gene conferring susceptibility to spot blotch caused by <i>Cochliobolus sativus</i> is located at the <i>Mla</i> locus in barley cultivar Bowman. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1531-1539.	3.6	21
7	Molecular Mapping of <i>Fusarium</i> Head Blight Resistance in the Spring Wheat Line ND2710. <i>Phytopathology</i> , 2018, 108, 972-979.	2.2	32
8	Molecular mapping of QTL for <i>Fusarium</i> head blight resistance introgressed into durum wheat. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1939-1951.	3.6	57
9	Genome-wide association mapping of spot blotch resistance to three different pathotypes of <i>Cochliobolus sativus</i> in the USDA barley core collection. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	17
10	Sources and Genetics of Spot Blotch Resistance to a New Pathotype of <i>Cochliobolus sativus</i> in the USDA National Small Grains Collection. <i>Plant Disease</i> , 2016, 100, 1988-1993.	1.4	33
11	Coordinated and independent functions of velvet-complex genes in fungal development and virulence of the fungal cereal pathogen <i>Cochliobolus sativus</i> . <i>Fungal Biology</i> , 2016, 120, 948-960.	2.5	25
12	RNA-Seq Revealed Differences in Transcriptomes between 3ADON and 15ADON Populations of <i>Fusarium graminearum</i> In Vitro and In Planta. <i>PLoS ONE</i> , 2016, 11, e0163803.	2.5	25
13	Prevalence of inversion positive and inversion negative mating type (MAT) alleles and MAT heterokaryons in <i>Sclerotinia sclerotiorum</i> in the United States. <i>Botany</i> , 2015, 93, 497-505.	1.0	3
14	The regulatory gene <i>VosA</i> affects conidiogenesis and is involved in virulence of the fungal cereal pathogen <i>Cochliobolus sativus</i> . <i>Fungal Biology</i> , 2015, 119, 884-900.	2.5	13
15	<i>Brachypodium distachyon</i> – <i>Cochliobolus sativus</i> Pathosystem is a New Model for Studying Plant–Fungal Interactions in Cereal Crops. <i>Phytopathology</i> , 2015, 105, 482-489.	2.2	13
16	The Role of Mitogen-Activated Protein (MAP) Kinase Signaling Components in the Fungal Development, Stress Response and Virulence of the Fungal Cereal Pathogen <i>Bipolaris sorokiniana</i> . <i>PLoS ONE</i> , 2015, 10, e0128291.	2.5	35
17	Functional characterization of the gene <i>FoOCH1</i> encoding a putative α -1,6-mannosyltransferase in <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> . <i>Fungal Genetics and Biology</i> , 2014, 65, 1-13.	2.1	40
18	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	3.5	232

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19	Identification and application of a unique genetic locus in diagnosis of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> tropical race 4. <i>Canadian Journal of Plant Pathology</i> , 2013, 35, 482-493.	1.4	21
20	Construction of Hairpin RNA-Expressing Vectors for RNA-Mediated Gene Silencing in Fungi. <i>Methods in Molecular Biology</i> , 2012, 835, 623-633.	0.9	6
21	Sfp type 4 phosphopantetheinyl transferase is required for lysine synthesis, tolerance to oxidative stress and virulence in the plant pathogenic fungus <i>Cochliobolus sativus</i> . <i>Molecular Plant Pathology</i> , 2012, 13, 375-387.	4.2	49
22	RNA-mediated gene silencing in the cereal fungal pathogen <i>Cochliobolus sativus</i> . <i>Molecular Plant Pathology</i> , 2011, 12, 289-298.	4.2	25