

# Yulin Jia

## List of Publications by Year in descending order

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116  
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docs citations

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| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | Analysis of Differentially Expressed Rice Genes Reveals the ATP-Binding Cassette Transporters as Candidate Genes Against the Sheath Blight Pathogen, <i>Rhizoctonia solani</i> . <i>PhytoFrontiers</i> , 2022, 2, 105-115. | 0.8 | 4         |
| 2  | An Allelic Variant of the Broad-Spectrum Blast Resistance Gene <i>Ptr</i> in Weedy Rice Is Associated with Resistance to the Most Virulent Blast Race IB-33. <i>Plant Disease</i> , 2022, 106, 1675-1680.                  | 0.7 | 2         |
| 3  | Registration of two rice mapping populations using weedy rice ecotypes as a novel germplasm resource. <i>Journal of Plant Registrations</i> , 2022, 16, 162-175.   | 0.4 | 2         |
| 4  | Transgenic Rice Expressing Isoflavone Synthase Gene from Soybean Shows Resistance Against Blast Fungus ( <i>Magnaporthe oryzae</i> ). <i>Plant Disease</i> , 2021, 105, 3141-3146.   | 0.7 | 8         |
| 5  | <i>Bacillus subtilis</i> GB519 Promotes Rice Growth and Reduces the Damages Caused by Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>PhytoFrontiers</i> , 2021, 1, 330-338.  | 0.8 | 4         |
| 6  | Mapping Blast Resistance Genes in Rice Varieties ‘Minghui 63’™ and ‘M-202’™. <i>Plant Disease</i> , 2021, , .  | 0.7 | 0         |
| 7  | A Rapid Survey of Avirulence Genes in Field Isolates of <i>Magnaporthe oryzae</i> . <i>Plant Disease</i> , 2020, 104, 717-723.   | 0.7 | 3         |
| 8  | Identification of Novel QTL Conferring Sheath Blight Resistance in Two Weedy Rice Mapping Populations. <i>Rice</i> , 2020, 13, 21.   | 1.7 | 18        |
| 9  | Selection and mutation of the avirulence gene <i>AVR-Pii</i> of the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Plant Pathology</i> , 2019, 68, 127-134.  | 1.2 | 10        |
| 10 | Evaluation of Rice Responses to the Blast Fungus <i>Magnaporthe oryzae</i> at Different Growth Stages. <i>Plant Disease</i> , 2019, 103, 132-136.  | 0.7 | 11        |
| 11 | A Toolbox for Managing Blast and Sheath Blight Diseases of Rice in the United States of America. , , .   |     | 5         |
| 12 | Integration Analysis of Small RNA and Degradome Sequencing Reveals MicroRNAs Responsive to <i>Dickeya zea</i> in Resistant Rice. <i>International Journal of Molecular Sciences</i> , 2019, 20, 222.                       | 1.8 | 25        |
| 13 | Exploring natural variation for rice sheath blight resistance in <i>Brachypodium distachyon</i> . <i>Plant Signaling and Behavior</i> , 2019, 14, 1546527.   | 1.2 | 2         |
| 14 | Call of the wild rice: <i>Oryza rufipogon</i> shapes weedy rice evolution in Southeast Asia. <i>Evolutionary Applications</i> , 2019, 12, 93-104.  | 1.5 | 45        |
| 15 | Functional Interactions Between Major Rice Blast Resistance Genes, <i>Pi-ta</i> and <i>Pi-b</i> , and Minor Blast Resistance Quantitative Trait Loci. <i>Phytopathology</i> , 2018, 108, 1095-1103.                        | 1.1 | 9         |
| 16 | Novel QTLs Affecting Rice Kernel Fissure Resistance Discovered in the Cultivar ‘Saber’ Augment Those from ‘Cybonnet’. <i>Crop Science</i> , 2018, 58, 1531-1541.   | 0.8 | 4         |
| 17 | The Role of Standing Variation in the Evolution of Weediness Traits in South Asian Weedy Rice ( <i>Oryza</i> spp.). <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3679-3690.  | 0.8 | 17        |
| 18 | The rice blast resistance gene <i>Ptr</i> encodes an atypical protein required for broad-spectrum disease resistance. <i>Nature Communications</i> , 2018, 9, 2039.  | 5.8 | 128       |

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|----|---|-----|-----------|
| 19 | Weedy red rice has novel sources of resistance to biotic stress. <i>Crop Journal</i> , 2018, 6, 443-450.  | 2.3 | 22        |
| 20 | Signatures of adaptation in the weedy rice genome. <i>Nature Genetics</i> , 2017, 49, 811-814.  | 9.4 | 146       |
| 21 | All roads lead to weediness: Patterns of genomic divergence reveal extensive recurrent weedy rice origins from South Asian <i>Oryza</i> . <i>Molecular Ecology</i> , 2017, 26, 3151-3167.               | 2.0 | 51        |
| 22 | Dynamic Changes in the Rice Blast Population in the United States Over Six Decades. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 803-812.  | 1.4 | 28        |
| 23 | Characterization of Molecular Identity and Pathogenicity of Rice Blast Fungus in Hunan Province of China. <i>Plant Disease</i> , 2017, 101, 557-561.  | 0.7 | 20        |
| 24 | Registration of 42 Blast Resistant Medium Grain Rice Genetic Stocks with Suitable Agronomic, Yield, Milling Yield, and Seed Characteristics. <i>Journal of Plant Registrations</i> , 2016, 10, 316-324. | 0.4 | 3         |
| 25 | Marker Development for Rice Blast Resistance Gene Pi66(t) and Application in the USDA Rice Mini-Core Collection. <i>Crop Science</i> , 2016, 56, 1001-1008.   | 0.8 | 4         |
| 26 | Characterization of Field Isolates of <i>Magnaporthe oryzae</i> with Mating Type, DNA Fingerprinting, and Pathogenicity Assays. <i>Plant Disease</i> , 2016, 100, 298-303.                              | 0.7 | 10        |
| 27 | Coevolutionary Dynamics of Rice Blast Resistance Gene <i>Pi-ta</i> and <i>Magnaporthe oryzae</i> Avirulence Gene <i>AVR-Pita 1</i> . <i>Phytopathology</i> , 2016, 106, 676-683.                        | 1.1 | 30        |
| 28 | Little White Lies: Pericarp Color Provides Insights into the Origins and Evolution of Southeast Asian Weedy Rice. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 4105-4114.                             | 0.8 | 36        |
| 29 | Identification of a <i>Pi9</i> -Containing Rice Germplasm with a Newly Developed Robust Marker. <i>Phytopathology</i> , 2016, 106, 871-876.   | 1.1 | 12        |
| 30 | QTLs for Early Tiller Production and Relationships with Rapid Seedling Growth and Increased Panicle Number in Rice. <i>Crop Science</i> , 2016, 56, 505-519.  | 0.8 | 6         |
| 31 | Genome-Wide Association of Rice Blast Disease Resistance and Yield-Related Components of Rice. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 1383-1392.                                       | 1.4 | 68        |
| 32 | Registration of a Rice Gene Mapping Population of Lemont × Jasmine 85 Recombinant Inbred Lines. <i>Journal of Plant Registrations</i> , 2015, 9, 128-132.   | 0.4 | 3         |
| 33 | More than one way to evolve a weed: parallel evolution of <i>US</i> weedy rice through independent genetic mechanisms. <i>Molecular Ecology</i> , 2015, 24, 3329-3344.                                  | 2.0 | 51        |
| 34 | Confirming and Identifying New Loci for Rice Blast Disease Resistance using <i>Magnaporthe oryzae</i> Field Isolates in the US. <i>Crop Science</i> , 2015, 55, 2620-2627.                              | 0.8 | 7         |
| 35 | Natural variation of rice blast resistance gene <i>Pi-d2</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 1235-1249.  | 0.3 | 17        |
| 36 | QTL Analysis for Resistance to Blast Disease in U.S. Weedy Rice. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 834-844.   | 1.4 | 23        |

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|----|---|-----|-----------|
| 37 | Characterization of resistance genes to rice blast fungus <i>Magnaporthe oryzae</i> in a "Green Revolution" rice variety. <i>Molecular Breeding</i> , 2015, 35, 1.  | 1.0 | 13        |
| 38 | Characterization of rice blast resistance genes in rice germplasm with monogenic lines and pathogenicity assays. <i>Crop Protection</i> , 2015, 72, 132-138.  | 1.0 | 22        |
| 39 | Identification of Candidate Genes Associated with Positive and Negative Heterosis in Rice. <i>PLoS ONE</i> , 2014, 9, e95178.   | 1.1 | 11        |
| 40 | Characterization of Rice Blast Resistance Gene <i>Pi61(t)</i> in Rice Germplasm. <i>Plant Disease</i> , 2014, 98, 1200-1204.  | 0.7 | 8         |
| 41 | Effectiveness and Durability of the Rice <i>Pi-ta</i> Gene in Yunnan Province of China. <i>Phytopathology</i> , 2014, 104, 762-768.   | 1.1 | 14        |
| 42 | Tagging quantitative trait loci for heading date and plant height in important breeding parents of rice ( <i>Oryza sativa</i> ). <i>Euphytica</i> , 2014, 197, 191-200.                                     | 0.6 | 17        |
| 43 | Genetic variation and evolution of the <i>Pit</i> blast resistance locus in rice. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 473-489.  | 0.8 | 5         |
| 44 | Statistical Inference of Selection and Divergence of the Rice Blast Resistance Gene <i>Pi-ta</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2425-2432.  | 0.8 | 6         |
| 45 | The evolution of flowering strategies in US weedy rice. <i>American Journal of Botany</i> , 2014, 101, 1737-1747.   | 0.8 | 28        |
| 46 | An expedited method for isolation of DNA for PCR from <i>Magnaporthe oryzae</i> stored on filter paper. <i>Crop Journal</i> , 2014, 2, 267-271.   | 2.3 | 7         |
| 47 | Induction of avirulence by AVR-Pita1 in virulent U.S. field isolates of <i>Magnaporthe oryzae</i> . <i>Crop Journal</i> , 2014, 2, 1-9.   | 2.3 | 7         |
| 48 | Deep transcriptome sequencing reveals the expression of key functional and regulatory genes involved in the abiotic stress signaling pathways in rice. <i>Journal of Plant Biology</i> , 2013, 56, 216-231. | 0.9 | 27        |
| 49 | Molecular mapping of four blast resistance genes using recombinant inbred lines of 93-11 and nipponbare. <i>Journal of Plant Biology</i> , 2013, 56, 91-97.   | 0.9 | 6         |
| 50 | Identification of rice blast resistance genes using international monogenic differentials. <i>Crop Protection</i> , 2013, 45, 109-116.  | 1.0 | 26        |
| 51 | Inoculation and Scoring Methods for Rice Sheath Blight Disease. <i>Methods in Molecular Biology</i> , 2013, 956, 257-268.   | 0.4 | 26        |
| 52 | Analysis of Genetic and Molecular Identity Among Field Isolates of the Rice Blast Fungus with an International Differential System, Rep-PCR, and DNA Sequencing. <i>Plant Disease</i> , 2013, 97, 491-495.  | 0.7 | 25        |
| 53 | Similar traits, different genes? Examining convergent evolution in related weedy rice populations. <i>Molecular Ecology</i> , 2013, 22, 685-698.  | 2.0 | 50        |
| 54 | Confirming QTLs and Finding Additional Loci Responsible for Resistance to Rice Sheath Blight Disease. <i>Plant Disease</i> , 2013, 97, 113-117.   | 0.7 | 46        |

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|----|---|-----|-----------|
| 55 | Three Quantitative Trait Loci Conferring Resistance to Kernel Fissuring in Rice Identified by Selective Genotyping in Two Tropical Japonica Populations. <i>Crop Science</i> , 2013, 53, 2434-2443.     | 0.8 | 16        |
| 56 | Response to Early Generation Selection for Resistance to Rice Kernel Fissuring. <i>Crop Science</i> , 2012, 52, 1482-1492.  | 0.8 | 11        |
| 57 | Registration of Four Rice Germplasm Lines with Improved Resistance to Sheath Blight and Blast Diseases. <i>Journal of Plant Registrations</i> , 2012, 6, 95-100.  | 0.4 | 13        |
| 58 | Indica and Japonica Crosses Resulting in Linkage Block and Recombination Suppression on Rice Chromosome 12. <i>PLoS ONE</i> , 2012, 7, e43066.  | 1.1 | 20        |
| 59 | Transcriptome and methylome interactions in rice hybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12040-12045.                              | 3.3 | 203       |
| 60 | Identification of the Rice Blast Resistance Gene <i>Pib</i> in the National Small Grains Collection. <i>Phytopathology</i> , 2012, 102, 700-706.  | 1.1 | 32        |
| 61 | Sheath-blight resistance QTLs in japonica rice germplasm. <i>Euphytica</i> , 2012, 184, 23-34.  | 0.6 | 33        |
| 62 | Analysis of rice blast resistance gene <i>Pi-z</i> in rice germplasm using pathogenicity assays and DNA markers. <i>Euphytica</i> , 2012, 184, 35-46.   | 0.6 | 48        |
| 63 | Registration of a Rice Gene Mapping Population Consisting of Teqing <sup>TM</sup> into Lemont <sup>TM</sup> Backcross Introgression Lines. <i>Journal of Plant Registrations</i> , 2012, 6, 128-135.    | 0.4 | 14        |
| 64 | Mapping Quantitative Trait Loci for Resistance to Rice Blast. <i>Phytopathology</i> , 2011, 101, 176-181.   | 1.1 | 25        |
| 65 | The long and the short of it: <i>SD1</i> polymorphism and the evolution of growth trait divergence in U.S. weedy rice. <i>Molecular Ecology</i> , 2011, 20, 3743-3756.                                  | 2.0 | 36        |
| 66 | Comparative analysis of putative pathogenesis-related gene expression in two <i>Rhizoctonia solani</i> pathosystems. <i>Current Genetics</i> , 2011, 57, 391-408.                                       | 0.8 | 21        |
| 67 | Molecular Evolution of the Rice Blast Resistance Gene <i>Pi-ta</i> in Invasive Weedy Rice in the USA. <i>PLoS ONE</i> , 2011, 6, e26260.  | 1.1 | 30        |
| 68 | Structural and expressional analysis of the B-hordein genes in Tibetan hull-less barley. <i>Genetica</i> , 2010, 138, 227-239.  | 0.5 | 17        |
| 69 | Genomic patterns of nucleotide diversity in divergent populations of U.S. weedy rice. <i>BMC Evolutionary Biology</i> , 2010, 10, 180.  | 3.2 | 98        |
| 70 | Seeing red: the origin of grain pigmentation in US weedy rice. <i>Molecular Ecology</i> , 2010, 19, 3380-3393.  | 2.0 | 79        |
| 71 | Molecular evolution of shattering loci in U.S. weedy rice. <i>Molecular Ecology</i> , 2010, 19, 3271-3284.  | 2.0 | 112       |
| 72 | Development of Monogenic and Digenic Rice Lines for Blast Resistance Genes <i>Pi-ta</i> , <i>Pi-k<sup>h</sup></i> , <i>Pi-k<sup>s</sup></i> . <i>Journal of Plant Registrations</i> , 2010, 4, 163-166. | 0.4 | 16        |

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|----|---|-----|-----------|
| 73 | Diversification and evolution of the avirulence gene AVR-Pita1 in field isolates of <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2010, 47, 973-980.   | 0.9 | 116       |
| 74 | Sequence variation at the rice blast resistance gene Pi-km locus: Implications for the development of allele specific markers. <i>Plant Science</i> , 2010, 178, 523-530.   | 1.7 | 68        |
| 75 | A User-Friendly Method to Isolate and Single Spore the Fungi <i>Magnaporthe oryzae</i> and <i>Magnaporthe grisea</i> Obtained from Diseased Field Samples. <i>Plant Health Progress</i> , 2009, 10, 37.                               | 0.8 | 15        |
| 76 | Examination of the Rice Blast Pathogen Population Diversity in Arkansas, USA – Stable or Unstable?. , 2009, , 217-228.  |     | 9         |
| 77 | Evolutionary Dynamics of the Genomic Region Around the Blast Resistance Gene <i>Pi-ta</i> in AA Genome <i>Oryza</i> Species. <i>Genetics</i> , 2009, 183, 1315-1325.  | 1.2 | 48        |
| 78 | Identification of two major resistance genes against race IE-1k of <i>Magnaporthe oryzae</i> in the indica rice cultivar Zhe733. <i>Molecular Breeding</i> , 2009, 24, 127-134.   | 1.0 | 27        |
| 79 | Exploring genetic diversity and potential novel disease resistance genes in a collection of rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT /Ove   | 0.8 | 31        |
| 80 | Current progress on genetic interactions of rice with rice blast and sheath blight fungi. <i>Frontiers of Agriculture in China</i> , 2009, 3, 231-239.  | 0.2 | 40        |
| 81 | Artificial introgression of a large chromosome fragment around the rice blast resistance gene <i>Pi-ta</i> in backcross progeny and several elite rice cultivars. <i>Heredity</i> , 2009, 103, 333-339.                               | 1.2 | 32        |
| 82 | Alternatively spliced transcripts of <i>Pi-ta</i> blast resistance gene in <i>Oryza sativa</i> . <i>Plant Science</i> , 2009, 177, 468-478.   | 1.7 | 36        |
| 83 | Determination of Resistance Spectra of the <i>Pi-ta</i> and <i>Pi-k</i> Genes to U.S. Races of <i>Magnaporthe oryzae</i> Causing Rice Blast in a Recombinant Inbred Line Population. <i>Plant Disease</i> , 2009, 93, 639-644.        | 0.7 | 27        |
| 84 | Mapping Quantitative Trait Loci Responsible for Resistance to Sheath Blight in Rice. <i>Phytopathology</i> , 2009, 99, 1078-1084.   | 1.1 | 115       |
| 85 | Understanding the Co-evolution of the Rice Blast Resistance Gene <i>PI-TA</i> and <i>Magnaporthe oryzae</i> Avirulence Gene <i>AVR-PITA</i> . , 2009, , 137-147.  |     | 4         |
| 86 | Field Resistance Expressed when the <i>Pi-ta</i> Gene is Compromised by <i>Magnaporthe oryzae</i> . , 2009, , 281-289.  |     | 8         |
| 87 | Identification of SSR markers for a broad-spectrum blast resistance gene <i>Pi20(t)</i> for marker-assisted breeding. <i>Molecular Breeding</i> , 2008, 22, 141-149.  | 1.0 | 48        |
| 88 | Identification of a New Locus, <i>Ptr(t)</i> , Required for Rice Blast Resistance Gene <i>Pi-ta</i> -Mediated Resistance. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 396-403.  | 1.4 | 53        |
| 89 | Haplotype Diversity at the <i>Pi-ta</i> Locus in Cultivated Rice and Its Wild Relatives. <i>Phytopathology</i> , 2008, 98, 1305-1311.   | 1.1 | 43        |
| 90 | Carolina Foxtail ( <i>Alopecurus carolinianus</i> ): Susceptibility and Suitability as an Alternative Host to Rice Blast Disease ( <i>Magnaporthe oryzae</i> [formerly <i>M. grisea</i> ]). <i>Plant Disease</i> , 2008, 92, 504-507. | 0.7 | 7         |

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|-----|---|-----|-----------|
| 91  | Registration of TIL:455, TIL:514, and TIL:642, Three Rice Germplasm Lines Containing Introgressed Sheath Blight Resistance Alleles. <i>Journal of Plant Registrations</i> , 2008, 2, 251-254.     | 0.4 | 19        |
| 92  | Rapid Determination of Rice Cultivar Responses to the Sheath Blight Pathogen <i>Rhizoctonia solani</i> Using a Micro-Chamber Screening Method. <i>Plant Disease</i> , 2007, 91, 485-489.          | 0.7 | 92        |
| 93  | Instability of the <i>Magnaporthe oryzae</i> avirulence gene AVR-Pita alters virulence. <i>Fungal Genetics and Biology</i> , 2007, 44, 1024-1034.   | 0.9 | 157       |
| 94  | Host Active Defense Responses Occur within 24 Hours after Pathogen Inoculation in the Rice Blast System. <i>Rice Science</i> , 2007, 14, 302-310.   | 1.7 | 4         |
| 95  | Rapid survey for presence of a blast resistance gene Pi-ta in rice cultivars using the dominant DNA markers derived from portions of the Pi-ta gene. <i>Plant Breeding</i> , 2007, 126, 36-42.    | 1.0 | 54        |
| 96  | Evolutionary Genomics of Weedy Rice in the USA. <i>Journal of Integrative Plant Biology</i> , 2007, 49, 811-816.  | 4.1 | 39        |
| 97  | An early response regulatory cluster induced by low temperature and hydrogen peroxide in seedlings of chilling-tolerant japonica rice. <i>BMC Genomics</i> , 2007, 8, 175.                        | 1.2 | 123       |
| 98  | Molecular characterization of the recombinant inbred line population derived from a japonica-indica rice cross. <i>Euphytica</i> , 2007, 159, 73-82.  | 0.6 | 30        |
| 99  | RL-SAGE and microarray analysis of the rice transcriptome after <i>Rhizoctonia solani</i> infection. <i>Molecular Genetics and Genomics</i> , 2007, 278, 421-431.                                 | 1.0 | 50        |
| 100 | Identification of field isolates of <i>Rhizoctonia solani</i> to detect quantitative resistance in rice under greenhouse conditions. <i>Frontiers of Agriculture in China</i> , 2007, 1, 361-367. | 0.2 | 30        |
| 101 | Identifying Novel Resistance Genes in Newly Introduced Blast Resistant Rice Germplasm. <i>Crop Science</i> , 2006, 46, 1870-1878.   | 0.8 | 51        |
| 102 | Development of a SNLP marker from the Pi-ta blast resistance gene by tri-primer PCR. <i>Euphytica</i> , 2004, 138, 97-105.  | 0.6 | 52        |
| 103 | Rice Pi-ta gene Confers Resistance to the Major Pathotypes of the Rice Blast Fungus in the United States. <i>Phytopathology</i> , 2004, 94, 296-301.  | 1.1 | 78        |
| 104 | Marker assisted selection for the control of rice blast disease. <i>Outlooks on Pest Management</i> , 2003, 14, 150.  | 0.2 | 24        |
| 105 | Determination of Host Responses to <i>Magnaporthe grisea</i> on Detached Rice Leaves Using a Spot Inoculation Method. <i>Plant Disease</i> , 2003, 87, 129-133.                                   | 0.7 | 86        |
| 106 | Natural Variation at the Pi-ta Rice Blast Resistance Locus. <i>Phytopathology</i> , 2003, 93, 1452-1459.  | 1.1 | 70        |
| 107 | Development of Dominant Rice Blast <i>Pi-ta</i> Resistance Gene Markers. <i>Crop Science</i> , 2002, 42, 2145-2149.   | 0.8 | 112       |
| 108 | Direct interaction of resistance gene and avirulence gene products confers rice blast resistance. <i>EMBO Journal</i> , 2000, 19, 4004-4014.  | 3.5 | 943       |

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|-----|---|-----|-----------|
| 109 | tA Single Amino Acid Difference Distinguishes Resistant and Susceptible Alleles of the Rice Blast Resistance Gene Pi-ta. <i>Plant Cell</i> , 2000, 12, 2033.  | 3.1 | 33        |
| 110 | A Single Amino Acid Difference Distinguishes Resistant and Susceptible Alleles of the Rice Blast Resistance Gene Pi-ta. <i>Plant Cell</i> , 2000, 12, 2033-2045.  | 3.1 | 544       |
| 111 | Rapid transcript accumulation of pathogenesis-related genes during an incompatible interaction in bacterial speck disease-resistant tomato plants. , 1999, 40, 455-465.   |     | 61        |
| 112 | Initiation of Plant Disease Resistance by Physical Interaction of AvrPto and Pto Kinase. <i>Science</i> , 1996, 274, 2060-2063.   | 6.0 | 630       |
| 113 | Cloning and Characterization of Two Members of the Pto Gene Family: the Pto Bacterial Resistance Gene and the Fen Insecticide Sensitivity Gene.. <i>Current Plant Science and Biotechnology in Agriculture</i> , 1994, , 273-282. | 0.0 | 0         |
| 114 | Physiological, Ecological and Genetic Interactions of Rice with Harmful Microbes. , 0, , .  |     | 2         |
| 115 | Effectiveness and durability of the ricePi-tagene in Yunnan province of China. <i>Phytopathology</i> , 0, , PHYTO-11-13-000.  | 1.1 | 0         |
| 116 | Introductory Chapter: Protecting Rice Grains in the Post-Genomic Era: Are We There Yet?. , 0, , .   |     | 2         |