

Longfu Zhu

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ext. papers

4,851
ext. citations

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avg, IF

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| # | Paper | IF | Citations |
|----|--|------|-----------|
| 72 | Lignin metabolism has a central role in the resistance of cotton to the wilt fungus <i>Verticillium dahliae</i> as revealed by RNA-Seq-dependent transcriptional analysis and histochemistry. <i>Journal of Experimental Botany</i> , 2011 , 62, 5607-21 | 7 | 284 |
| 71 | Reference genome sequences of two cultivated allotetraploid cottons, <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> . <i>Nature Genetics</i> , 2019 , 51, 224-229 | 36.3 | 266 |
| 70 | Asymmetric subgenome selection and cis-regulatory divergence during cotton domestication. <i>Nature Genetics</i> , 2017 , 49, 579-587 | 36.3 | 229 |
| 69 | Expression of an <i>Arabidopsis</i> vacuolar H ⁺ -pyrophosphatase gene (AVP1) in cotton improves drought- and salt tolerance and increases fibre yield in the field conditions. <i>Plant Biotechnology Journal</i> , 2011 , 9, 88-99 | 11.6 | 209 |
| 68 | The genome sequence of Sea-Island cotton (<i>Gossypium barbadense</i>) provides insights into the allopolyploidization and development of superior spinnable fibres. <i>Scientific Reports</i> , 2015 , 5, 17662 | 4.9 | 181 |
| 67 | Proteomic and virus-induced gene silencing (VIGS) Analyses reveal that gossypol, brassinosteroids, and jasmonic acid contribute to the resistance of cotton to <i>Verticillium dahliae</i> . <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 3690-703 | 7.6 | 167 |
| 66 | Overexpression of rice NAC gene SNAC1 improves drought and salt tolerance by enhancing root development and reducing transpiration rate in transgenic cotton. <i>PLoS ONE</i> , 2014 , 9, e86895 | 3.7 | 139 |
| 65 | Sugar and auxin signaling pathways respond to high-temperature stress during anther development as revealed by transcript profiling analysis in cotton. <i>Plant Physiology</i> , 2014 , 164, 1293-308 | 6.6 | 129 |
| 64 | Cotton WRKY1 mediates the plant defense-to-development transition during infection of cotton by <i>Verticillium dahliae</i> by activating JASMONATE ZIM-DOMAIN1 expression. <i>Plant Physiology</i> , 2014 , 166, 2179-94 | 6.6 | 94 |
| 63 | Laccase GhLac1 Modulates Broad-Spectrum Biotic Stress Tolerance via Manipulating Phenylpropanoid Pathway and Jasmonic Acid Synthesis. <i>Plant Physiology</i> , 2018 , 176, 1808-1823 | 6.6 | 94 |
| 62 | Isolation and characterization of genes associated to cotton somatic embryogenesis by suppression subtractive hybridization and microarray. <i>Plant Molecular Biology</i> , 2006 , 60, 167-83 | 4.6 | 91 |
| 61 | Long noncoding RNAs involve in resistance to <i>Verticillium dahliae</i> , a fungal disease in cotton. <i>Plant Biotechnology Journal</i> , 2018 , 16, 1172-1185 | 11.6 | 77 |
| 60 | GhJAZ2 negatively regulates cotton fiber initiation by interacting with the R2R3-MYB transcription factor GhMYB25-like. <i>Plant Journal</i> , 2016 , 88, 921-935 | 6.9 | 76 |
| 59 | Cotton cytochrome P450 CYP82D regulates systemic cell death by modulating the octadecanoid pathway. <i>Nature Communications</i> , 2014 , 5, 5372 | 17.4 | 75 |
| 58 | An ethylene response-related factor, GBERF1-like, from <i>Gossypium barbadense</i> improves resistance to <i>Verticillium dahliae</i> via activating lignin synthesis. <i>Plant Molecular Biology</i> , 2016 , 91, 305-18 | 4.6 | 65 |
| 57 | Suitable internal control genes for qRT-PCR normalization in cotton fiber development and somatic embryogenesis. <i>Science Bulletin</i> , 2007 , 52, 3110-3117 | | 64 |
| 56 | microRNAs involved in auxin signalling modulate male sterility under high-temperature stress in cotton (<i>Gossypium hirsutum</i>). <i>Plant Journal</i> , 2017 , 91, 977-994 | 6.9 | 63 |

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|----|---|-----|----|
| 55 | Molecular cloning and functional characterization of a novel cotton CBL-interacting protein kinase gene (GhCIPK6) reveals its involvement in multiple abiotic stress tolerance in transgenic plants. <i>Biochemical and Biophysical Research Communications</i> , 2013 , 435, 209-15 | 3.4 | 62 |
| 54 | Expression of an Arabidopsis sodium/proton antiporter gene (AtNHX1) in peanut to improve salt tolerance. <i>Plant Biotechnology Reports</i> , 2012 , 6, 59-67 | 2.5 | 60 |
| 53 | GhATAF1, a NAC transcription factor, confers abiotic and biotic stress responses by regulating phytohormonal signaling networks. <i>Plant Cell Reports</i> , 2016 , 35, 2167-79 | 5.1 | 51 |
| 52 | Expression of the Arabidopsis vacuolar H ⁺ -pyrophosphatase gene AVP1 in peanut to improve drought and salt tolerance. <i>Plant Biotechnology Reports</i> , 2013 , 7, 345-355 | 2.5 | 51 |
| 51 | Physiological and molecular mechanism of defense in cotton against <i>Verticillium dahliae</i> . <i>Plant Physiology and Biochemistry</i> , 2018 , 125, 193-204 | 5.4 | 49 |
| 50 | Suppression of GhAGP4 gene expression repressed the initiation and elongation of cotton fiber. <i>Plant Cell Reports</i> , 2010 , 29, 193-202 | 5.1 | 49 |
| 49 | A draft gene regulatory network for cellular totipotency reprogramming during plant somatic embryogenesis. <i>Genomics</i> , 2007 , 90, 620-8 | 4.3 | 48 |
| 48 | Cotton GhCKI disrupts normal male reproduction by delaying tapetum programmed cell death via inactivating starch synthase. <i>Plant Journal</i> , 2013 , 75, 823-35 | 6.9 | 47 |
| 47 | Suppression of the homeobox gene HDTF1 enhances resistance to <i>Verticillium dahliae</i> and <i>Botrytis cinerea</i> in cotton. <i>Journal of Integrative Plant Biology</i> , 2016 , 58, 503-13 | 8.3 | 43 |
| 46 | Expression profile analysis of genes involved in cell wall regeneration during protoplast culture in cotton by suppression subtractive hybridization and macroarray. <i>Journal of Experimental Botany</i> , 2008 , 59, 3661-74 | 7 | 41 |
| 45 | Functional characterization of cotton genes responsive to <i>Verticillium dahliae</i> through bioinformatics and reverse genetics strategies. <i>Journal of Experimental Botany</i> , 2014 , 65, 6679-92 | 7 | 40 |
| 44 | Differential Gene Expression in Cotton Defence Response to <i>Verticillium dahliae</i> by SSH. <i>Journal of Phytopathology</i> , 2011 , 159, 606-615 | 1.8 | 38 |
| 43 | GhJAZ2 attenuates cotton resistance to biotic stresses via the inhibition of the transcriptional activity of GhbHLH171. <i>Molecular Plant Pathology</i> , 2018 , 19, 896-908 | 5.7 | 35 |
| 42 | GbMPK3, a mitogen-activated protein kinase from cotton, enhances drought and oxidative stress tolerance in tobacco. <i>Plant Cell, Tissue and Organ Culture</i> , 2014 , 116, 153-162 | 2.7 | 34 |
| 41 | Defective pollen wall contributes to male sterility in the male sterile line 1355A of cotton. <i>Scientific Reports</i> , 2015 , 5, 9608 | 4.9 | 33 |
| 40 | GhCPK33 Negatively Regulates Defense against by Phosphorylating GhOPR3. <i>Plant Physiology</i> , 2018 , 178, 876-889 | 6.6 | 32 |
| 39 | Overexpression of GbWRKY1 positively regulates the Pi starvation response by alteration of auxin sensitivity in Arabidopsis. <i>Plant Cell Reports</i> , 2012 , 31, 2177-88 | 5.1 | 27 |
| 38 | LEAFY COTYLEDON1-CASEIN KINASE I-TCP15-PHYTOCHROME INTERACTING FACTOR4 Network Regulates Somatic Embryogenesis by Regulating Auxin Homeostasis. <i>Plant Physiology</i> , 2015 , 169, 2805-21 | 6.6 | 24 |

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| 37 | Genome-wide identification of lipoxygenase gene family in cotton and functional characterization in response to abiotic stresses. <i>BMC Genomics</i> , 2018 , 19, 599 | 4.5 | 23 |
| 36 | Transfer of tomato immune receptor Ve1 confers Ave1-dependent Verticillium resistance in tobacco and cotton. <i>Plant Biotechnology Journal</i> , 2018 , 16, 638-648 | 11.6 | 23 |
| 35 | Suppression of tryptophan synthase activates cotton immunity by triggering cell death via promoting SA synthesis. <i>Plant Journal</i> , 2019 , 98, 329-345 | 6.9 | 22 |
| 34 | Genes Encoding Fasciclin-Like Arabinogalactan Proteins are Specifically Expressed During Cotton Fiber Development. <i>Plant Molecular Biology Reporter</i> , 2008 , 26, 98-113 | 1.7 | 21 |
| 33 | GbSOBIR1 confers Verticillium wilt resistance by phosphorylating the transcriptional factor GbbHLH171 in <i>Gossypium barbadense</i> . <i>Plant Biotechnology Journal</i> , 2019 , 17, 152-163 | 11.6 | 20 |
| 32 | ABA signaling is negatively regulated by GbWRKY1 through JAZ1 and ABI1 to affect salt and drought tolerance. <i>Plant Cell Reports</i> , 2020 , 39, 181-194 | 5.1 | 18 |
| 31 | Effects of Long-term Cotton Continuous Cropping on Soil Microbiome. <i>Scientific Reports</i> , 2019 , 9, 18297 | 4.9 | 17 |
| 30 | GhCAX3 gene, a novel Ca(2+)/H(+) exchanger from cotton, confers regulation of cold response and ABA induced signal transduction. <i>PLoS ONE</i> , 2013 , 8, e66303 | 3.7 | 15 |
| 29 | GhHB12, a HD-ZIP I Transcription Factor, Negatively Regulates the Cotton Resistance to. <i>International Journal of Molecular Sciences</i> , 2018 , 19, | 6.3 | 15 |
| 28 | GhUMC1, a blue copper-binding protein, regulates lignin synthesis and cotton immune response. <i>Biochemical and Biophysical Research Communications</i> , 2018 , 504, 75-81 | 3.4 | 13 |
| 27 | ????????????????<itali>Ve1</itali>. <i>Scientia Sinica Vitae</i> , 2014 , 44, 803-814 | 1.4 | 11 |
| 26 | Cotton pan-genome retrieves the lost sequences and genes during domestication and selection. <i>Genome Biology</i> , 2021 , 22, 119 | 18.3 | 10 |
| 25 | GhCyP3 improves the resistance of cotton to Verticillium dahliae by inhibiting the E3 ubiquitin ligase activity of GhPUB17. <i>Plant Molecular Biology</i> , 2019 , 99, 379-393 | 4.6 | 9 |
| 24 | Genome-Wide Identification of Papain-Like Cysteine Proteases in and Functional Characterization in Response to. <i>Frontiers in Plant Science</i> , 2019 , 10, 134 | 6.2 | 9 |
| 23 | Comprehensive Genome-Wide Analysis of Thaumatin-Like Gene Family in Four Cotton Species and Functional Identification of Involved in Regulating Tolerance to and Drought. <i>Frontiers in Plant Science</i> , 2020 , 11, 575015 | 6.2 | 9 |
| 22 | A Single-Nucleotide Mutation in a GLUTAMATE RECEPTOR-LIKE Gene Confers Resistance to Fusarium Wilt in. <i>Advanced Science</i> , 2021 , 8, 2002723 | 13.6 | 8 |
| 21 | The cotton HD-Zip transcription factor GhHB12 regulates flowering time and plant architecture via the GhmiR157-GhSPL pathway. <i>Communications Biology</i> , 2018 , 1, 229 | 6.7 | 8 |
| 20 | GhWRKY1-like enhances cotton resistance to Verticillium dahliae via an increase in defense-induced lignification and S monolignol content. <i>Plant Science</i> , 2021 , 305, 110833 | 5.3 | 7 |

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| 19 | Genome-Wide Analysis of Family Genes in Cotton Identified a Role for in Resistance. <i>Genes</i> , 2020 , 11, | 4.2 | 6 |
| 18 | GhTULP34, a member of tubby-like proteins, interacts with GhSKP1A to negatively regulate plant osmotic stress. <i>Genomics</i> , 2021 , 113, 462-474 | 4.3 | 6 |
| 17 | GhMYB4 downregulates lignin biosynthesis and enhances cotton resistance to <i>Verticillium dahliae</i> . <i>Plant Cell Reports</i> , 2021 , 40, 735-751 | 5.1 | 6 |
| 16 | Promoters of Arabidopsis Casein kinase I-like 2 and 7 confer specific high-temperature response in anther. <i>Plant Molecular Biology</i> , 2018 , 98, 33-49 | 4.6 | 5 |
| 15 | Phosphate deficiency enhances cotton resistance to <i>Verticillium dahliae</i> through activating jasmonic acid biosynthesis and phenylpropanoid pathway. <i>Plant Science</i> , 2021 , 302, 110724 | 5.3 | 5 |
| 14 | Effects of cotton-maize rotation on soil microbiome structure. <i>Molecular Plant Pathology</i> , 2021 , 22, 673-682 | 5.8 | 5 |
| 13 | GhHB12 negatively regulates abiotic stress tolerance in Arabidopsis and cotton. <i>Environmental and Experimental Botany</i> , 2020 , 176, 104087 | 5.9 | 4 |
| 12 | Deficiencies in the formation and regulation of anther cuticle and tryphine contribute to male sterility in cotton PGMS line. <i>BMC Genomics</i> , 2020 , 21, 825 | 4.5 | 4 |
| 11 | An enhanced photosynthesis and carbohydrate metabolic capability contributes to heterosis of the cotton (<i>Gossypium hirsutum</i>) hybrid Huaza Mian H318R as revealed by genome-wide gene expression analysis. <i>BMC Genomics</i> , 2021 , 22, 277 | 4.5 | 4 |
| 10 | Orchestration of plant development and defense by indirect crosstalk of salicylic acid and brassinosteroid signaling via transcription factor GhTINY2. <i>Journal of Experimental Botany</i> , 2021 , 72, 4721-4743 | 7 | 4 |
| 9 | A combination of genome-wide and transcriptome-wide association studies reveals genetic elements leading to male sterility during high temperature stress in cotton. <i>New Phytologist</i> , 2021 , 231, 165-181 | 9.8 | 4 |
| 8 | The Sophora Alopecuroid H ⁺ -PPase Gene SaVP1 Confers Multiple Abiotic Stress Tolerance in Arabidopsis. <i>Plant Molecular Biology Reporter</i> , 2015 , 33, 923-930 | 1.7 | 3 |
| 7 | Isolation and characterization of a conserved domain in the eremophyte H ⁺ -PPase family. <i>PLoS ONE</i> , 2013 , 8, e70099 | 3.7 | 3 |
| 6 | Association mapping and domestication analysis to dissect genetic improvement process of upland cotton yield-related traits in China. <i>Journal of Cotton Research</i> , 2021 , 4, | 2.3 | 2 |
| 5 | Down regulation of cotton GbTRP1 leads to accumulation of anthranilates and confers resistance to <i>Verticillium dahliae</i> . <i>Journal of Cotton Research</i> , 2019 , 2, | 2.3 | 1 |
| 4 | Genome-wide identification, evolutionary estimation and functional characterization of two cotton CKI gene types. <i>BMC Plant Biology</i> , 2021 , 21, 229 | 5.3 | 1 |
| 3 | Dynamic 3D genome architecture of cotton fiber reveals subgenome-coordinated chromatin topology for 4-staged single-cell differentiation.. <i>Genome Biology</i> , 2022 , 23, 45 | 18.3 | 0 |
| 2 | Fast anther dehiscence status recognition system established by deep learning to screen heat tolerant cotton.. <i>Plant Methods</i> , 2022 , 18, 53 | 5.8 | |

- 1 Genetic Mapping and Analysis of a Compact Plant Architecture and Precocious Mutant in Upland Cotton. *Plants*, **2022**, 11, 1483

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