# Mu-Qing Zhang

List of Publications by Year
in descending order

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| 88 | 1,771 | 304743 | 345221 |
|---|---|---|---|
| papers | citations | 22 h-index | 36 g-index |

| 94 | 94 | 94 | 1267 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Heat Treatment Eliminates â€˜CandidatusLiberibacter asiaticusâ€™ from Infected Citrus Trees Under Controlled Conditions. Phytopathology, 2013, 103, 15-22. | 2.2 | 119 |
| 2 | Effective Antibiotics against â€˜Candidatus Liberibacter asiaticusâ€™ in HLB-Affected Citrus Plants Identified via the Graft-Based Evaluation. PLoS ONE, 2014, 9, e111032. | 2.5 | 95 |
| 3 | Chemical Compounds Effective Against the Citrus Huanglongbing Bacterium â€˜Candidatus Liberibacter asiaticusâ€™ In Planta. Phytopathology, 2011, 101, 1097-1103. | 2.2 | 89 |
| 4 | Species-Specific Detection and Identification of Fusarium Species Complex, the Causal Agent of Sugarcane Pokkah Boeng in China. PLoS ONE, 2014, 9, e104195. | 2.5 | 70 |
| 5 | Sugarcane for bioethanol production: Potential of bagasse in Chinese perspective. Renewable and Sustainable Energy Reviews, 2020, 133, 110296. | 16.4 | 54 |
| 6 | Screening Molecules for Control of Citrus Huanglongbing Using an Optimized Regeneration System for â€˜Candidatus Liberibacter asiaticusâ€™-Infected Periwinkle (Catharanthus roseus) Cuttings. Phytopathology, 2010, 100, 239-245. | 2.2 | 53 |
| 7 | A Graft-Based Chemotherapy Method for Screening Effective Molecules and Rescuing Huanglongbing-Affected Citrus Plants. Phytopathology, 2012, 102, 567-574. | 2.2 | 53 |
| 8 | Transcriptomic characterization and potential marker development of contrasting sugarcane cultivars. Scientific Reports, 2018, 8, 1683. | 3.3 | 46 |
| 9 | Antimicrobial Nanoemulsion Formulation with Improved Penetration of Foliar Spray through Citrus Leaf Cuticles to Control Citrus Huanglongbing. PLoS ONE, 2015, 10, e0133826. | 2.5 | 45 |
| 10 | Genome-wide identification and expression analysis of AP2/ERF transcription factors in sugarcane (Saccharum spontaneum L.). BMC Genomics, 2020, 21, 685. | 2.8 | 44 |
| 11 | Characterization of the microbial community structure in Candidatus Liberibacter asiaticus-infected citrus plants treated with antibiotics in the field. BMC Microbiology, 2013, 13, 112. | 3.3 | 42 |
| 12 | Characterization of a Saccharum spontaneum with a basic chromosome number of xâ€‰=â€‰10 provides new insights on genome evolution in genus Saccharum. Theoretical and Applied Genetics, 2020, 133, 187-199. | 3.6 | 42 |
| 13 | Differential Protein Expression in Sugarcane during Sugarcane-Sporisorium scitamineumInteraction Revealed by 2-DE and MALDI-TOF-TOF/MS. Comparative and Functional Genomics, 2011, 2011, 1-10. | 2.0 | 39 |
| 14 | Field Evaluation of Integrated Management for Mitigating Citrus Huanglongbing in Florida. Frontiers in Plant Science, 2018, 9, 1890. | 3.6 | 34 |
| 15 | Field Performance of Transgenic Sugarcane Lines Resistant to Sugarcane Mosaic Virus. Frontiers in Plant Science, 2017, 8, 104. | 3.6 | 33 |
| 16 | Deciphering the Bacterial Microbiome in Huanglongbing-Affected Citrus Treated with Thermotherapy and Sulfonamide Antibiotics. PLoS ONE, 2016, 11, e0155472. | 2.5 | 33 |
| 17 | Genomic insights into the recent chromosome reduction of autopolyploid sugarcane Saccharum spontaneum. Nature Genetics, 2022, 54, 885-896. | 21.4 | 33 |
| 18 | Unexpected Inheritance Pattern of Erianthus arundinaceus Chromosomes in the Intergeneric Progeny between Saccharum spp. and Erianthus arundinaceus. PLoS ONE, 2014, 9, e110390. | 2.5 | 31 |

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|---|---|---|---|
| 19 | Deciphering the Bacterial Microbiome of Citrus Plants in Response to â€˜Candidatus Liberibacter asiaticusâ€™-Infection and Antibiotic Treatments. PLoS ONE, 2013, 8, e76331. | 2.5 | 31 |
| 20 | Mitigating citrus huanglongbing via effective application of antimicrobial compounds and thermotherapy. Crop Protection, 2016, 84, 150-158. | 2.1 | 29 |
| 21 | Effects of Drought-Tolerant Ea-DREB2B Transgenic Sugarcane on Bacterial Communities in Soil. Frontiers in Microbiology, 2020, 11, 704. | 3.5 | 29 |
| 22 | Comparative analysis of sucrose phosphate synthase (SPS) gene family between Saccharum officinarum and Saccharum spontaneum. BMC Plant Biology, 2020, 20, 422. | 3.6 | 27 |
| 23 | Molecular characterization of carbendazim resistance of Fusarium species complex that causes sugarcane pokkah boeng disease. BMC Genomics, 2019, 20, 115. | 2.8 | 26 |
| 24 | Characterization of Chromosome Inheritance of the Intergeneric BC2 and BC3 Progeny between Saccharum spp. and Erianthus arundinaceus. PLoS ONE, 2015, 10, e0133722. | 2.5 | 25 |
| 25 | Comparison and analysis of tomato flavor compounds using different extraction methods. Journal of Food Measurement and Characterization, 2020, 14, 465-475. | 3.2 | 25 |
| 26 | The formation and evolution of centromeric satellite repeats in Saccharum species. Plant Journal, 2021, 106, 616-629. | 5.7 | 24 |
| 27 | Deciphering the transcriptomic response of Fusarium verticillioides in relation to nitrogen availability and the development of sugarcane pokkah boeng disease. Scientific Reports, 2016, 6, 29692. | 3.3 | 23 |
| 28 | Banana Fusarium Wilt Disease Detection by Supervised and Unsupervised Methods from UAV-Based Multispectral Imagery. Remote Sensing, 2022, 14, 1231. | 4.0 | 23 |
| 29 | RNA Interference: Promising Approach to Combat Plant Viruses. International Journal of Molecular Sciences, 2022, 23, 5312. | 4.1 | 22 |
| 30 | Evolutionary expansion and functional divergence of sugar transporters in Saccharum (S.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 | 5.7 | 20 |
| 31 | Genome-wide identification and expression profiling of DREB genes in Saccharum spontaneum. BMC Genomics, 2021, 22, 456. | 2.8 | 20 |
| 32 | Genome-wide analysis of R2R3-MYB transcription factors family in the autopolyploid Saccharum spontaneum: an exploration of dominance expression and stress response. BMC Genomics, 2021, 22, 622. | 2.8 | 20 |
| 33 | Identification and Characterization of a New Fungal Pathogen Causing Twisted Leaf Disease of Sugarcane in China. Plant Disease, 2015, 99, 325-332. | 1.4 | 19 |
| 34 | Sugarcane Production in China. , 2018, , . | | 19 |
| 35 | Gene expression profiling of reactive oxygen species (ROS) and antioxidant defense system following Sugarcane mosaic virus (SCMV) infection. BMC Plant Biology, 2020, 20, 532. | 3.6 | 19 |
| 36 | Chromosomeâ€specific painting unveils chromosomal fusions and distinct allopolyploid species in the Saccharum complex. New Phytologist, 2022, 233, 1953-1965. | 7.3 | 19 |

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|---|---|---|---|
| 37 | Virome Identification and Characterization of Fusarium sacchari and F. andiyazi: Causative Agents of Pokkah Boeng Disease in Sugarcane. Frontiers in Microbiology, 2020, 11, 240. | 3.5 | 18 |
| 38 | Predication of the Effector Proteins Secreted by Fusarium sacchari Using Genomic Analysis and Heterogenous Expression. Journal of Fungi (Basel, Switzerland), 2022, 8, 59. | 3.5 | 18 |
| 39 | A high-quality genome assembly of Morinda officinalis, a famous native southern herb in the Lingnan region of southern China. Horticulture Research, 2021, 8, 135. | 6.3 | 17 |
| 40 | First Report of Fusarium commune Causing Root Rot Disease of Sugarcane (var. Badila) in China. Plant Disease, 2018, 102, 1660. | 1.4 | 15 |
| 41 | Characterization of chromosome composition of sugarcane in nobilization by using genomic in situ hybridization. Molecular Cytogenetics, 2018, 11, 35. | 0.9 | 15 |
| 42 | Interactions between ScNAC23 and ScGAI regulate GA-mediated flowering and senescence in sugarcane. Plant Science, 2021, 304, 110806. | 3.6 | 15 |
| 43 | Antimicrobial Compounds Effective against Candidatus Liberibacter asiaticus Discovered via Graft-based Assay in Citrus. Scientific Reports, 2018, 8, 17288. | 3.3 | 14 |
| 44 | An insight to rhizosphere bacterial community composition and structure of consecutive winter-initiated sugarcane ratoon crop in Southern China. BMC Plant Biology, 2022, 22, 74. | 3.6 | 13 |
| 45 | Effective selection and regeneration of transgenic sugarcane plants using positive selection system. In Vitro Cellular and Developmental Biology - Plant, 2015, 51, 52-61. | 2.1 | 12 |
| 46 | A new method based on SNP of nrDNA-ITS to identify Saccharum spontaneum and its progeny in the genus Saccharum. PLoS ONE, 2018, 13, e0197458. | 2.5 | 12 |
| 47 | Evolution and Expression Analysis of Starch Synthase Gene Families in Saccharum spontaneum. Tropical Plant Biology, 2019, 12, 158-173. | 1.9 | 12 |
| 48 | Photosynthetic characterization and expression profiles of sugarcane infected by Sugarcane mosaic virus (SCMV). Photosynthesis Research, 2021, 150, 279-294. | 2.9 | 11 |
| 49 | A systematic high-throughput phenotyping assay for sugarcane stalk quality characterization by near-infrared spectroscopy. Plant Methods, 2021, 17, 76. | 4.3 | 11 |
| 50 | Investigation of soil nutrients and associated rhizobacterial communities in different sugarcane genotypes in relation to sugar content. Chemical and Biological Technologies in Agriculture, 2021, 8, . | 4.6 | 11 |
| 51 | Untangling the Rhizosphere Bacterial Community Composition and Response of Soil Physiochemical Properties to Different Nitrogen Applications in Sugarcane Field. Frontiers in Microbiology, 2022, 13, 856078. | 3.5 | 11 |
| 52 | Characterization, Genomic Organization, Abundance, and Chromosomal Distribution of Ty1-copia Retrotransposons in Erianthus arundinaceus. Frontiers in Plant Science, 2017, 8, 924. | 3.6 | 10 |
| 53 | Chromosome transmission in BC4 progenies of intergeneric hybrids between Saccharum spp. and Erianthus arundinaceus (Retz.) Jeswiet. Scientific Reports, 2019, 9, 2528. | 3.3 | 10 |
| 54 | Response of Soil Fungal Community to Drought-Resistant Ea-DREB2B Transgenic Sugarcane. Frontiers in Microbiology, 2020, 11, 562775. | 3.5 | 10 |

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|---|---|---|---|
| 55 | Selective Interaction of Sugarcane eIF4E with VPgs from Sugarcane Mosaic Pathogens. Viruses, 2021, 13, 518. | 3.3 | 10 |
| 56 | Comparative Analysis of Sugar Metabolites and Their Transporters in Sugarcane Following Sugarcane mosaic virus (SCMV) Infection. International Journal of Molecular Sciences, 2021, 22, 13574. | 4.1 | 10 |
| 57 | Transcriptomic analysis reveals root metabolic alteration and induction of huanglongbing resistance by sulphonamide antibiotics in huanglongbingâ€affected citrus plants. Plant Pathology, 2020, 69, 733-743. | 2.4 | 9 |
| 58 | Precise high-throughput online near-infrared spectroscopy assay to determine key cell wall features associated with sugarcane bagasse digestibility. Biotechnology for Biofuels, 2021, 14, 123. | 6.2 | 9 |
| 59 | First Report of Fusarium oxysporum Isolate gx3 Causing Sugarcane Pokkah Boeng in Guangxi of China. Plant Disease, 2016, 100, 1785-1785. | 1.4 | 9 |
| 60 | First Report of Fusarium andiyazi Causing Sugarcane Pokkah Boeng Disease in China. Plant Disease, 2020, 104, 286-286. | 1.4 | 9 |
| 61 | ScGAIL, a sugarcane N-terminal truncated DELLA-like protein, participates in gibberellin signaling in Arabidopsis. Journal of Experimental Botany, 2022, 73, 3462-3476. | 4.8 | 8 |
| 62 | Analysis of Disequilibrium Hybridization in Hybrid and Backcross Progenies of Saccharum officinarum Ã— Erianthus arundinaceus. Agricultural Sciences in China, 2010, 9, 1271-1277. | 0.6 | 7 |
| 63 | First Report of Fusarium sacchari That Causes Sugarcane Wilt Disease in China. Plant Disease, 2020, 104, 2289-2289. | 1.4 | 7 |
| 64 | Metabolic and proteomic analysis of nitrogen metabolism mechanisms involved in the sugarcane â€“ Fusarium verticillioides interaction. Journal of Plant Physiology, 2020, 251, 153207. | 3.5 | 7 |
| 65 | Field Evaluation of Chemotherapy on HLB-Affected Citrus Trees With Emphasis on Fruit Yield and Quality. Frontiers in Plant Science, 2021, 12, 611287. | 3.6 | 7 |
| 66 | Phosphomannose isomerase affects the key enzymes of glycolysis and sucrose metabolism in transgenic sugarcane overexpressing the manA gene. Molecular Breeding, 2015, 35, 100. | 2.1 | 6 |
| 67 | Sugarcane Nitrogen Concentration and Irrigation Level Prediction Based on UAV Multispectral Imagery. Sensors, 2022, 22, 2711. | 3.8 | 6 |
| 68 | Function Analysis of Sugarcane A20/AN1 Zincâ€Finger Protein Gene ShSAP1 in Transgenic Tobacco. Crop Science, 2014, 54, 2724-2734. | 1.8 | 5 |
| 69 | Development and Evaluation of SSR Markers Based on Large Scale Full-Length Transcriptome Sequencing in Sugarcane. Tropical Plant Biology, 2020, 13, 343-352. | 1.9 | 5 |
| 70 | A flow cytometry-based analysis to establish a cell cycle synchronization protocol for Saccharum spp.. Scientific Reports, 2020, 10, 5016. | 3.3 | 5 |
| 71 | Considerations regarding centromere assembly in plant whole-genome sequencing. Methods, 2021, 187, 54-56. | 3.8 | 5 |
| 72 | Molecular marker application in sugarcane. Sugar Tech, 2004, 6, 251-259. | 1.8 | 4 |

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|---|---|---|---|
| 73 | Fusarium Species Complex Causing Pokkah Boeng in China. , 0, , . | | 4 |
| 74 | Fungal deterioration of the bagasse storage from the harvested sugarcane. Biotechnology for Biofuels, 2021, 14, 152. | 6.2 | 4 |
| 75 | Quantitative evaluation of variation in defoliation traits among sugarcane genotypes. PLoS ONE, 2018, 13, e0196071. | 2.5 | 3 |
| 76 | Photosynthesis-related protein expression in sugarcane during sugarcaneâ€“Fusarium verticillioides interaction revealed by iTRAQ. Plant Growth Regulation, 2020, 91, 237-248. | 3.4 | 3 |
| 77 | First Report of Stalk Bacterial Soft Rot of Sugarcane Caused by Dickeya zeae in China. Plant Disease, 2021, 105, 1188-1188. | 1.4 | 3 |
| 78 | Field Evaluation of New Promising Sugarcane Cultivars for Cold Tolerance in Guangxi, China. Sugar Tech, 2020, 22, 1007-1017. | 1.8 | 2 |
| 79 | High-Quality Genome Sequence Resource for Fusarium andiyazi Causing Pokkah Boeng Disease of Sugarcane in China. Molecular Plant-Microbe Interactions, 2021, 34, MPMI-11-20-0331. | 2.6 | 2 |
| 80 | Authenticity Identification of Saccharum officinarum and Saccharum spontaneum Germplasm Materials. Agronomy, 2022, 12, 819. | 3.0 | 2 |
| 81 | The alleviation of manganese toxicity by ammonium in sugarcane is related to pectin content, pectin methyl esterification, and nitric oxide. GCB Bioenergy, 0, , . | 5.6 | 2 |
| 82 | Key Role of Heat Shock Protein Expression Induced by Ampicillin in Citrus Defense against Huanglongbing: A Transcriptomics Study. Agronomy, 2022, 12, 1356. | 3.0 | 2 |
| 83 | Genome Sequence of Phoma sorghina var. saccharum That Causes Sugarcane Twisted Leaf Disease in China. Molecular Plant-Microbe Interactions, 2020, 33, 1092-1094. | 2.6 | 1 |
| 84 | Repetitive Sequence Barcode Probe for Karyotype Analysis in Tripidium arundinaceum. International Journal of Molecular Sciences, 2022, 23, 6726. | 4.1 | 1 |
| 85 | Sequence analysis of Erianthus arundinaceus chromosome 1 isolated by flow sorting after genomic in situ hybridization in suspension. Crop Journal, 2022, , . | 5.2 | 0 |
| 86 | Quantitative estimating nutrient uptake requirements for sugarcane based on QUEFTS model in China. Journal of Plant Nutrition, 2022, 45, 1504-1515. | 1.9 | 0 |
| 87 | Diversity Chromosome Evolution of Ty1-copia Retrotransposons in Pennisetum purpureum Revealed by FISH. Agronomy, 2022, 12, 1312. | 3.0 | 0 |
| 88 | Devious Phloem Intruder Candidatus Liberibacter Species Causing Huanglongbing: History, Symptoms, Mechanism, and Current Strategies. , 0, , . | | 0 |