# Xuecai Zhang

List of Publications by Year
in descending order

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|---|---|---|---|
| 52<br>papers | 3,801<br>citations | 257450<br>24<br>h-index | 182427<br>51<br>g-index |
| 55<br>all docs | 55<br>docs citations | 55<br>times ranked | 3586<br>citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. Trends in Plant Science, 2017, 22, 961-975. | 8.8 | 1,004 |
| 2 | Genomic prediction in CIMMYT maize and wheat breeding programs. Heredity, 2014, 112, 48-60. | 2.6 | 357 |
| 3 | High-resolution genetic mapping of maize pan-genome sequence anchors. Nature Communications, 2015, 6, 6914. | 12.8 | 213 |
| 4 | Enhancing genetic gain in the era of molecular breeding. Journal of Experimental Botany, 2017, 68, 2641-2666. | 4.8 | 197 |
| 5 | Genomic prediction in biparental tropical maize populations in water-stressed and well-watered environments using low-density and GBS SNPs. Heredity, 2015, 114, 291-299. | 2.6 | 187 |
| 6 | Effect of Trait Heritability, Training Population Size and Marker Density on Genomic Prediction Accuracy Estimation in 22 bi-parental Tropical Maize Populations. Frontiers in Plant Science, 2017, 8, 1916. | 3.6 | 145 |
| 7 | Molecular Breeding for Nutritionally Enriched Maize: Status and Prospects. Frontiers in Genetics, 2019, 10, 1392. | 2.3 | 131 |
| 8 | Combined Linkage and Association Mapping Reveals QTL and Candidate Genes for Plant and Ear Height in Maize. Frontiers in Plant Science, 2016, 7, 833. | 3.6 | 117 |
| 9 | Genome-Wide Association Mapping and Genomic Prediction Analyses Reveal the Genetic Architecture of Grain Yield and Flowering Time Under Drought and Heat Stress Conditions in Maize. Frontiers in Plant Science, 2018, 9, 1919. | 3.6 | 102 |
| 10 | Optimal Design of Preliminary Yield Trials with Genome-Wide Markers. Crop Science, 2014, 54, 48-59. | 1.8 | 100 |
| 11 | Molecular characterization of CIMMYT maize inbred lines with genotyping-by-sequencing SNPs. Theoretical and Applied Genetics, 2016, 129, 753-765. | 3.6 | 94 |
| 12 | Rapid Cycling Genomic Selection in a Multiparental Tropical Maize Population. G3: Genes, Genomes, Genetics, 2017, 7, 2315-2326. | 1.8 | 92 |
| 13 | Beat the stress: breeding for climate resilience in maize for the tropical rainfed environments. Theoretical and Applied Genetics, 2021, 134, 1729-1752. | 3.6 | 92 |
| 14 | Genome-wide Association for Plant Height and Flowering Time across 15 Tropical Maize Populations under Managed Drought Stress and Well-Watered Conditions in Sub-Saharan Africa. Crop Science, 2016, 56, 2365-2378. | 1.8 | 88 |
| 15 | Genomic Selection Outperforms Marker Assisted Selection for Grain Yield and Physiological Traits in a Maize Doubled Haploid Population Across Water Treatments. Frontiers in Plant Science, 2018, 9, 366. | 3.6 | 83 |
| 16 | Genome-Wide Analysis of Tar Spot Complex Resistance in Maize Using Genotyping-by-Sequencing SNPs and Whole-Genome Prediction. Plant Genome, 2017, 10, plantgenome2016.10.0099. | 2.8 | 69 |
| 17 | Natural antisense transcripts are significantly involved in regulation of drought stress in maize. Nucleic Acids Research, 2017, 45, 5126-5141. | 14.5 | 53 |
| 18 | Genomic-enabled prediction with classification algorithms. Heredity, 2014, 112, 616-626. | 2.6 | 52 |

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|---|---------|-----|-----------|
| 19 | Applications of genotyping-by-sequencing (GBS) in maize genetics and breeding. Scientific Reports, 2020, 10, 16308. | 3.3 | 49 |
| 20 | Identification of QTL for Early Vigor and Stay-Green Conferring Tolerance to Drought in Two Connected Advanced Backcross Populations in Tropical Maize (Zea mays L.). PLoS ONE, 2016, 11, e0149636. | 2.5 | 41 |
| 21 | Dissecting the genetic architecture of Fusarium verticillioides seed rot resistance in maize by combining QTL mapping and genome-wide association analysis. Scientific Reports, 2017, 7, 46446. | 3.3 | 41 |
| 22 | Maximizing efficiency of genomic selection in CIMMYTâ€™s tropical maize breeding program. Theoretical and Applied Genetics, 2021, 134, 279-294. | 3.6 | 36 |
| 23 | Strategies for Effective Use of Genomic Information in Crop Breeding Programs Serving Africa and South Asia. Frontiers in Plant Science, 2020, 11, 353. | 3.6 | 33 |
| 24 | Genomic Prediction of Kernel Zinc Concentration in Multiple Maize Populations Using Genotyping-by-Sequencing and Repeat Amplification Sequencing Markers. Frontiers in Plant Science, 2020, 11, 534. | 3.6 | 30 |
| 25 | Genome-wide association study and genomic prediction of Fusarium ear rot resistance in tropical maize germplasm. Crop Journal, 2021, 9, 325-341. | 5.2 | 30 |
| 26 | A teosinte-derived allele of a MYB transcription repressor confers multiple disease resistance in maize. Molecular Plant, 2021, 14, 1846-1863. | 8.3 | 29 |
| 27 | Incorporation of parental phenotypic data into multiâ€omic models improves prediction of yieldâ€related traits in hybrid rice. Plant Biotechnology Journal, 2021, 19, 261-272. | 8.3 | 27 |
| 28 | Genomic prediction across years in a maize doubled haploid breeding program to accelerate early-stage testcross testing. Theoretical and Applied Genetics, 2020, 133, 2869-2879. | 3.6 | 26 |
| 29 | Genomic Prediction in a Large African Maize Population. Crop Science, 2017, 57, 2361-2371. | 1.8 | 25 |
| 30 | Linkage mapping and genome-wide association study reveals conservative QTL and candidate genes for Fusarium rot resistance in maize. BMC Genomics, 2020, 21, 357. | 2.8 | 23 |
| 31 | Probability of success of breeding strategies for improving pro-vitamin A content in maize. Theoretical and Applied Genetics, 2012, 125, 235-246. | 3.6 | 21 |
| 32 | Genomic Prediction with Genotype by Environment Interaction Analysis for Kernel Zinc Concentration in Tropical Maize Germplasm. G3: Genes, Genomes, Genetics, 2020, 10, 2629-2639. | 1.8 | 21 |
| 33 | Exogenous Pi supplementation improved the salt tolerance of maize (Zea mays L.) by promoting Na+ exclusion. Scientific Reports, 2018, 8, 16203. | 3.3 | 20 |
| 34 | Genome-wide association study and genomic prediction analyses of drought stress tolerance in China in a collection of off-PVP maize inbred lines. Molecular Breeding, 2019, 39, 1. | 2.1 | 17 |
| 35 | Fine mapping of Rscmv2, a major gene for resistance to sugarcane mosaic virus in maize. Molecular Breeding, 2012, 30, 1593-1600. | 2.1 | 15 |
| 36 | Genetic analysis of cob resistance to F. verticillioides: another step towards the protection of maize from ear rot. Theoretical and Applied Genetics, 2019, 132, 1049-1059. | 3.6 | 15 |

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|---|---------|-----|-----------|
| 37 | Genomic prediction of the general combining ability of maize lines (<i>Zea mays</i> L.) and the performance of their single crosses. Plant Breeding, 2018, 137, 379-387. | 1.9 | 14 |
| 38 | Genetic Dissection of Quantitative Resistance to Common Rust (Puccinia sorghi) in Tropical Maize (Zea) Tj ETQq0 0 0 rgBT /Overlock 10 Frontiers in Plant Science, 2021, 12, 692205. | 3.6 | 14 |
| 39 | Association mapping resolving the major loci Scmv2 conferring resistance to sugarcane mosaic virus in maize. European Journal of Plant Pathology, 2016, 145, 385-391. | 1.7 | 13 |
| 40 | Using genomic data to improve the estimation of general combining ability based on sparse partial diallel cross designs in maize. Crop Journal, 2020, 8, 819-829. | 5.2 | 12 |
| 41 | Natural variations in the non-coding region of ZmNAC080308 contributes maintaining grain yield under drought stress in maize. BMC Plant Biology, 2021, 21, 305. | 3.6 | 12 |
| 42 | New QTL for resistance to Puccinia polysora Underw in maize. Journal of Applied Genetics, 2019, 60, 147-150. | 1.9 | 8 |
| 43 | The genetic structure of CIMMYT and U.S. inbreds and its implications for tropical maize breeding. Crop Science, 2021, 61, 1666-1681. | 1.8 | 7 |
| 44 | Genomic prediction of the performance of hybrids and the combining abilities for line by tester trials in maize. Crop Journal, 2022, 10, 109-116. | 5.2 | 7 |
| 45 | Combining Three Mapping Strategies to Reveal Quantitative Trait Loci and Candidate Genes for Maize Ear Length. Plant Genome, 2018, 11, 170107. | 2.8 | 6 |
| 46 | Genomic Prediction of Resistance to Tar Spot Complex of Maize in Multiple Populations Using Genotyping-by-Sequencing SNPs. Frontiers in Plant Science, 2021, 12, 672525. | 3.6 | 6 |
| 47 | Increasing Genetic Gains in Maize in Stress-Prone Environments of the Tropics. , 2020, , 97-132. | | 6 |
| 48 | Identification of QTL for early vigor and leaf senescence across two tropical maize doubled haploid populations under nitrogen deficient conditions. Euphytica, 2020, 216, 1. | 1.2 | 5 |
| 49 | Kernel metabolites depict the diversity of relationship between maize hybrids and their parental lines. Crop Journal, 2021, 9, 181-191. | 5.2 | 5 |
| 50 | Identification and fine mapping of a major QTL (qRtsc8-1) conferring resistance to maize tar spot complex and validation of production markers in breeding lines. Theoretical and Applied Genetics, 2022, 135, 1551-1563. | 3.6 | 4 |
| 51 | Evaluation and Identification of Resistance Lines and QTLs of Maize to Seedborne <i>Fusarium verticillioides</i>. Plant Disease, 2022, 106, 2066-2073. | 1.4 | 4 |
| 52 | Diallelic Analysis of Tropical Maize Germplasm Response to Spontaneous Chromosomal Doubling. Plants, 2020, 9, 1224. | 3.5 | 0 |