

# Michael A Gore

## List of Publications by Year in descending order

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125  
papers

12,698  
citations

87888

38  
h-index

28297

105  
g-index

171  
all docs

171  
docs citations

171  
times ranked

11617  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mixed linear model approach adapted for genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 355-360.	21.4	2,022
2	GAPIT: genome association and prediction integrated tool. <i>Bioinformatics</i> , 2012, 28, 2397-2399.	4.1	2,016
3	Status and Prospects of Association Mapping in Plants. <i>Plant Genome</i> , 2008, 1, .	2.8	1,118
4	A First-Generation Haplotype Map of Maize. <i>Science</i> , 2009, 326, 1115-1117.	12.6	747
5	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	21.4	577
6	Field-based phenomics for plant genetics research. <i>Field Crops Research</i> , 2012, 133, 101-112.	5.1	521
7	The Genetic Architecture Of Maize Height. <i>Genetics</i> , 2014, 196, 1337-1356.	2.9	329
8	Development and evaluation of a field-based high-throughput phenotyping platform. <i>Functional Plant Biology</i> , 2014, 41, 68.	2.1	316
9	Automated Identification of Northern Leaf Blight-Infected Maize Plants from Field Imagery Using Deep Learning. <i>Phytopathology</i> , 2017, 107, 1426-1432.	2.2	254
10	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of <i>Gossypium</i> spp.. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1187-1209.	1.8	226
11	Decreased CO <sub>2</sub> availability and inactivation of Rubisco limit photosynthesis in cotton plants under heat and drought stress in the field. <i>Environmental and Experimental Botany</i> , 2012, 83, 1-11.	4.2	200
12	<i>CAROTENOID CLEAVAGE DIOXYGENASE4</i> Is a Negative Regulator of $\beta$ -Carotene Content in <i>Arabidopsis</i> Seeds. <i>Plant Cell</i> , 2014, 25, 4812-4826.	6.6	180
13	A Foundation for Provitamin A Biofortification of Maize: Genome-Wide Association and Genomic Prediction Models of Carotenoid Levels. <i>Genetics</i> , 2014, 198, 1699-1716.	2.9	180
14	From association to prediction: statistical methods for the dissection and selection of complex traits in plants. <i>Current Opinion in Plant Biology</i> , 2015, 24, 110-118.	7.1	166
15	Genome-Wide Association Study and Pathway-Level Analysis of Tocochromanol Levels in Maize Grain. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1287-1299.	1.8	152
16	Genetic diversity and population structure in the US Upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Theoretical and Applied Genetics</i> , 2014, 127, 283-295.	3.6	151
17	Genome-Wide Analysis of Branched-Chain Amino Acid Levels in <i>Arabidopsis</i> Seeds. <i>Plant Cell</i> , 2014, 25, 4827-4843.	6.6	121
18	Re-evaluating the phylogeny of allopolyploid <i>Gossypium</i> L.. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 45-52.	2.7	110

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19	Field-Based High-Throughput Plant Phenotyping Reveals the Temporal Patterns of Quantitative Trait Loci Associated with Stress-Responsive Traits in Cotton. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 865-879.	1.8	105
20	The quest for understanding phenotypic variation via integrated approaches in the field environment. <i>Plant Physiology</i> , 2016, 172, pp.00592.2016.	4.8	99
21	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1231-1247.	1.8	96
22	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. <i>Plant Cell</i> , 2017, 29, 2374-2392.	6.6	93
23	Sustaining the Future of Plant Breeding: The Critical Role of the USDAâ€™ARS National Plant Germplasm System. <i>Crop Science</i> , 2018, 58, 451-468.	1.8	91
24	Image set for deep learning: field images of maize annotated with disease symptoms. <i>BMC Research Notes</i> , 2018, 11, 440.	1.4	91
25	Autonomous Detection of Plant Disease Symptoms Directly from Aerial Imagery. <i>The Plant Phenome Journal</i> , 2019, 2, 1-9.	2.0	73
26	Quantitative Phenotyping of Northern Leaf Blight in UAV Images Using Deep Learning. <i>Remote Sensing</i> , 2019, 11, 2209.	4.0	69
27	Millimeter-Level Plant Disease Detection From Aerial Photographs via Deep Learning and Crowdsourced Data. <i>Frontiers in Plant Science</i> , 2019, 10, 1550.	3.6	68
28	Genetic Analysis of Visually Scored Orange Kernel Color in Maize. <i>Crop Science</i> , 2013, 53, 189-200.	1.8	66
29	Proximal hyperspectral sensing and data analysis approaches for field-based plant phenomics. <i>Computers and Electronics in Agriculture</i> , 2015, 118, 225-236.	7.7	66
30	Transcriptome-Wide Association Supplements Genome-Wide Association in <i>Zea mays</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3023-3033.	1.8	64
31	Linkage Map Construction and Quantitative Trait Locus Analysis of Agronomic and Fiber Quality Traits in Cotton. <i>Plant Genome</i> , 2014, 7, plantgenome2013.07.0023.	2.8	62
32	Large-scale Discovery of Gene-Enriched SNPs. <i>Plant Genome</i> , 2009, 2, .	2.8	55
33	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. <i>Plant Genome</i> , 2020, 13, e20009.	2.8	54
34	NLR locus-mediated trade-off between abiotic and biotic stress adaptation in <i>Arabidopsis</i> . <i>Nature Plants</i> , 2017, 3, 17072.	9.3	53
35	Population Structure and Phylogenetic Relationships in a Diverse Panel of <i>Brassica rapa</i> L.. <i>Frontiers in Plant Science</i> , 2017, 8, 321.	3.6	53
36	Network-Guided GWAS Improves Identification of Genes Affecting Free Amino Acids. <i>Plant Physiology</i> , 2017, 173, 872-886.	4.8	52

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37	The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale public cooperative maize experiment. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	52
38	Comparative evolutionary genetics of deleterious load in sorghum and maize. <i>Nature Plants</i> , 2021, 7, 17-24.	9.3	52
39	Deleterious Mutation Burden and Its Association with Complex Traits in Sorghum (<i>Sorghum</i> Tj ETQq1 1 0.784314 rgBT /Overlock	2.9	51
40	The patterns of deleterious mutations during the domestication of soybean. <i>Nature Communications</i> , 2021, 12, 97.	12.8	49
41	The Evolutionary History of Wild, Domesticated, and Feral<i>Brassica oleracea</i> (Brassicaceae). <i>Molecular Biology and Evolution</i> , 2021, 38, 4419-4434.	8.9	49
42	Quantitative trait locus analysis of Verticillium wilt resistance in an introgressed recombinant inbred population of Upland cotton. <i>Molecular Breeding</i> , 2014, 33, 709-720.	2.1	48
43	<i>ZEAXANTHIN EPOXIDASE</i> Activity Potentiates Carotenoid Degradation in Maturing Seed. <i>Plant Physiology</i> , 2016, 171, 1837-1851.	4.8	44
44	Multivariate Genome-Wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat (<i>Avena sativa</i>L.). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2963-2975.	1.8	44
45	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. <i>Frontiers in Genetics</i> , 2020, 11, 592769.	2.3	44
46	Machine learning-enabled phenotyping for GWAS and TWAS of WUE traits in 869 field-grown sorghum accessions. <i>Plant Physiology</i> , 2021, 187, 1481-1500.	4.8	44
47	Genetic Diversity of the Two Commercial Tetraploid Cotton Species in the<i>Gossypium</i> Diversity Reference Set. <i>Journal of Heredity</i> , 2016, 107, 274-286.	2.4	43
48	Genome-wide analysis of the omega-3 fatty acid desaturase gene family in <i>Gossypium</i> . <i>BMC Plant Biology</i> , 2014, 14, 312.	3.6	41
49	A community resource for exploring and utilizing genetic diversity in the USDA pea single plant plus collection. <i>Horticulture Research</i> , 2017, 4, 17017.	6.3	41
50	Molecular characterization of the <i>Gossypium</i> Diversity Reference Set of the US National Cotton Germplasm Collection. <i>Theoretical and Applied Genetics</i> , 2015, 128, 313-327.	3.6	39
51	Maize genomes to fields (G2F): 2014â€“2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. <i>BMC Research Notes</i> , 2020, 13, 71.	1.4	38
52	Identification of haplotypes at the Rsv4 genomic region in soybean associated with durable resistance to soybean mosaic virus. <i>Theoretical and Applied Genetics</i> , 2016, 129, 453-468.	3.6	37
53	Genomeâ€“Wide Association and Genomic Prediction Models of Tocochromanols in Fresh Sweet Corn Kernels. <i>Plant Genome</i> , 2019, 12, 180038.	2.8	37
54	Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. <i>Nature Communications</i> , 2021, 12, 1227.	12.8	37

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55	Evaluation of Target Preparation Methods for Singleâ€Feature Polymorphism Detection in Large Complex Plant Genomes. <i>Crop Science</i> , 2007, 47, S-135.	1.8	36
56	Closing the Divide between Human Nutrition and Plant Breeding. <i>Crop Science</i> , 2015, 55, 1437-1448.	1.8	36
57	Natural variation for carotenoids in fresh kernels is controlled by uncommon variants in sweet corn. <i>Plant Genome</i> , 2020, 13, e20008.	2.8	34
58	Population Genomic Analysis Reveals Differential Evolutionary Histories and Patterns of Diversity across Subgenomes and Subpopulations of <i>Brassica napus</i> L.. <i>Frontiers in Plant Science</i> , 2016, 7, 525.	3.6	33
59	Aerial highâ€throughput phenotyping enables indirect selection for grain yield at the early generation, seedâ€limited stages in breeding programs. <i>Crop Science</i> , 2020, 60, 3096-3114.	1.8	31
60	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. <i>Plant Cell</i> , 2021, 33, 882-900.	6.6	31
61	A century of guayule: Comprehensive genetic characterization of the US national guayule ( <i>Parthenium</i> ) Tj ETQq1 1 0,784314,rgBT /Over	5.2	30
62	Chemical variation for leaf cuticular waxes and their levels revealed in a diverse panel of <i>Brassica napus</i> L.. <i>Industrial Crops and Products</i> , 2016, 79, 77-83.	5.2	26
63	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. <i>BMC Research Notes</i> , 2018, 11, 452.	1.4	25
64	Novel Bayesian Networks for Genomic Prediction of Developmental Traits in Biomass Sorghum. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 769-781.	1.8	25
65	Scienceâ€graphic art partnerships to increase research impact. <i>Communications Biology</i> , 2019, 2, 295.	4.4	24
66	Stomatal conductance, xylem water transport, and root traits underpin improved performance under drought and well-watered conditions across a diverse panel of maize inbred lines. <i>Field Crops Research</i> , 2019, 234, 119-128.	5.1	24
67	Structureâ€function analysis of the maize bulliform cell cuticle and its potential role in dehydration and leaf rolling. <i>Plant Direct</i> , 2020, 4, e00282.	1.9	24
68	Inâ€Field Wholeâ€Plant Maize Architecture Characterized by Subcanopy Rovers and Latent Space Phenotyping. <i>The Plant Phenome Journal</i> , 2019, 2, 1-11.	2.0	23
69	Phenotyping stomatal closure by thermal imaging for GWAS and TWAS of water use efficiency-related genes. <i>Plant Physiology</i> , 2021, 187, 2544-2562.	4.8	23
70	A combined BSA-Seq and linkage mapping approach identifies genomic regions associated with <i>Phytophthora</i> root and crown rot resistance in squash. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1015-1031.	3.6	23
71	Investigation of the Influence of Leaf Thickness on Canopy Reflectance and Physiological Traits in Upland and Pima Cotton Populations. <i>Frontiers in Plant Science</i> , 2017, 8, 1405.	3.6	22
72	Genomic characterization of the Native Seeds/SEARCH common bean ( <i>Phaseolus vulgaris</i> L.) collection and its seed coat patterns. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 1469-1482.	1.6	22

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73	Relative utility of agronomic, phenological, and morphological traits for assessing genotype×environment interaction in maize inbreds. <i>Crop Science</i> , 2020, 60, 62-81.	1.8	21
74	Registration of the TM61/NM24016 Cotton Recombinant Inbred Mapping Population. <i>Journal of Plant Registrations</i> , 2012, 6, 124-127.	0.5	21
75	Genome-Wide Association Study and Pathway-Level Analysis of Kernel Color in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1945-1955.	1.8	20
76	Acylsugars protect <i>Nicotiana benthamiana</i> against insect herbivory and desiccation. <i>Plant Molecular Biology</i> , 2022, 109, 505-522.	3.9	20
77	Multi-omics prediction of oat agronomic and seed nutritional traits across environments and in distantly related populations. <i>Theoretical and Applied Genetics</i> , 2021, 134, 4043-4054.	3.6	20
78	Temporal Genetic Dynamics of an Experimental, Biparental Field Population of <i>Phytophthora capsici</i> . <i>Frontiers in Genetics</i> , 2017, 08, 26.	2.3	19
79	Heritable temporal gene expression patterns correlate with metabolomic seed content in developing hexaploid oat seed. <i>Plant Biotechnology Journal</i> , 2020, 18, 1211-1222.	8.3	19
80	Transcriptomic network analyses shed light on the regulation of cuticle development in maize leaves. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12464-12471.	7.1	19
81	A minimally disruptive method for measuring water potential in planta using hydrogel nanoreporters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	19
82	High-resolution genome-wide association study pinpoints metal transporter and chelator genes involved in the genetic control of element levels in maize grain. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	18
83	Genomic diversity and phylogenetic relationships in the genus <i>Parthenium</i> (Asteraceae). <i>Industrial Crops and Products</i> , 2015, 76, 920-929.	5.2	17
84	Genome-Wide Association Study in New York <i>Phytophthora capsici</i> Isolates Reveals Loci Involved in Mating Type and Mefenoxam Sensitivity. <i>Phytopathology</i> , 2021, 111, 204-216.	2.2	17
85	Translating insights from the seed metabolome into improved prediction for lipid-composition traits in oat ( <i>Avena sativa</i> L.). <i>Genetics</i> , 2021, 217, .	2.9	17
86	Breedbase: a digital ecosystem for modern plant breeding. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	17
87	Divergence of defensive cucurbitacins in independent <i>Cucurbita pepo</i> domestication events leads to differences in specialist herbivore preference. <i>Plant, Cell and Environment</i> , 2020, 43, 2812-2825.	5.7	16
88	ImageBreed: Open-access plant breeding web database for image-based phenotyping. <i>The Plant Phenome Journal</i> , 2020, 3, e20004.	2.0	16
89	Combining GWAS and TWAS to identify candidate causal genes for tocochromanol levels in maize grain. <i>Genetics</i> , 2022, 221, .	2.9	15
90	Effects of temperature and salinity on germination of non-pelleted and pelleted guayule ( <i>Parthenium</i> ) Tj ETQq0 0 0,rgBT /Overlock 10 Tf	5.2	14

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91	Multivariate Analysis of the Cotton Seed Ionome Reveals a Shared Genetic Architecture. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1147-1160.	1.8	14
92	Improving Genomic Prediction for Seed Quality Traits in Oat ( <i>Avena sativa</i> L.) Using Trait-Specific Relationship Matrices. <i>Frontiers in Genetics</i> , 2021, 12, 643733.	2.3	14
93	Genetic Analysis of the Transition from Wild to Domesticated Cotton ( <i>Gossypium hirsutum</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 731-754.	1.8	14
94	Genome-Wide Association Study for Maize Leaf Cuticular Conductance Identifies Candidate Genes Involved in the Regulation of Cuticle Development. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1671-1683.	1.8	13
95	Complex Ploidy Level Variation in Guayule Breeding Programs. <i>Crop Science</i> , 2011, 51, 210-216.	1.8	12
96	Chemical variation for fiber cuticular wax levels in upland cotton ( <i>Gossypium hirsutum</i> L.) evaluated under contrasting irrigation regimes. <i>Industrial Crops and Products</i> , 2017, 100, 153-162.	5.2	12
97	Genomic characterization of Ugandan smallholder farmer-preferred cassava varieties. <i>Crop Science</i> , 2020, 60, 1450-1461.	1.8	12
98	Random forest regression for optimizing variable planting rates for corn and soybean using topographical and soil data. <i>Agronomy Journal</i> , 2020, 112, 5045-5066.	1.8	11
99	Temporal covariance structure of multi-spectral phenotypes and their predictive ability for end-of-season traits in maize. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2853-2868.	3.6	11
100	Genome-wide association identifies a missing hydrolase for tocopherol synthesis in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	11
101	Use of hydraulic traits for modeling genotype-specific acclimation in cotton under drought. <i>New Phytologist</i> , 2020, 228, 898-909.	7.3	10
102	Transcriptome-wide association and prediction for carotenoids and tocopherols in fresh sweet corn kernels. <i>Plant Genome</i> , 2022, 15, e20197.	2.8	10
103	Genome size variation in guayule and mariola: Fundamental descriptors for polyploid plant taxa. <i>Industrial Crops and Products</i> , 2014, 54, 1-5.	5.2	9
104	Influences of the combination of high temperature and water deficit on the heritabilities and correlations of agronomic and fiber quality traits in upland cotton. <i>Euphytica</i> , 2017, 213, 1.	1.2	9
105	Machine Learning Enables High-Throughput Phenotyping for Analyses of the Genetic Architecture of Bulliform Cell Patterning in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 4235-4243.	1.8	9
106	The Germ Fraction Inhibits Iron Bioavailability of Maize: Identification of an Approach to Enhance Maize Nutritional Quality via Processing and Breeding. <i>Nutrients</i> , 2019, 11, 833.	4.1	9
107	Making waves in Breedbase: An integrated spectral data storage and analysis pipeline for plant breeding programs. <i>The Plant Phenome Journal</i> , 2021, 4, e20012.	2.0	9
108	Effectiveness of genomic selection for improving provitamin A carotenoid content and associated traits in cassava. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	9

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109	Selection for seed size has uneven effects on specialized metabolite abundance in oat (<i>Avena) Tj ETQq1 1 0.784314 rgBT 9 Overloc	1.8	9
110	Integrating GWAS and TWAS to elucidate the genetic architecture of maize leaf cuticular conductance. <i>Plant Physiology</i> , 2022, 189, 2144-2158.	4.8	9
111	Genome-wide association study identifies acyl-lipid metabolism candidate genes involved in the genetic control of natural variation for seed fatty acid traits in <i>Brassica napus</i> L.. <i>Industrial Crops and Products</i> , 2020, 145, 112080.	5.2	8
112	Generalizable approaches for genomic prediction of metabolites in plants. <i>Plant Genome</i> , 2022, 15, e20205.	2.8	8
113	A Low-Cost Automated System for High-Throughput Phenotyping of Single Oat Seeds. <i>The Plant Phenome Journal</i> , 2018, 1, 1-13.	2.0	7
114	Genome-wide association study suggests an independent genetic basis of zinc and cadmium concentrations in fresh sweet corn kernels. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	7
115	Wild relatives of potato may bolster its adaptation to new niches under future climate scenarios. <i>Food and Energy Security</i> , 2022, 11, e360.	4.3	7
116	A maize LIPID TRANSFER PROTEIN may bridge the gap between PHYTOCHROME-mediated light signaling and cuticle biosynthesis. <i>Plant Signaling and Behavior</i> , 2020, 15, 1790824.	2.4	6
117	Low-cost, handheld near-infrared spectroscopy for root dry matter content prediction in cassava. <i>The Plant Phenome Journal</i> , 2022, 5, .	2.0	6
118	Cotton phenotyping with lidar from a track-mounted platform. <i>Proceedings of SPIE</i> , 2016, , .	0.8	4
119	Nucleotide diversity in the two co-resident genomes of allopolyploid cotton. <i>Plant Systematics and Evolution</i> , 2017, 303, 1021-1042.	0.9	4
120	Genotypic evaluation of twenty-eight high- and low-cyanide cassava in low-land tropics, southeast Nigeria. <i>Heliyon</i> , 2019, 5, e01855.	3.2	4
121	High-Quality Reference Genome Sequence for the Oomycete Vegetable Pathogen <i>Phytophthora capsici</i> Strain LT1534. <i>Microbiology Resource Announcements</i> , 2021, 10, e0029521.	0.6	4
122	Undisciplining the university through shared purpose, practice, and place. <i>Humanities and Social Sciences Communications</i> , 2022, 9, .	2.9	3
123	Interactions between breeding system and ploidy affect niche breadth in <i>Solanum</i> . <i>Royal Society Open Science</i> , 2022, 9, 211862.	2.4	2
124	Prospector: A mobile application for portable, high-throughput near-infrared spectroscopy phenotyping. <i>The Plant Phenome Journal</i> , 2021, 4, e20024.	2.0	0
125	Sugarcane Mosaic Virus Resistance in the Wisconsin Sweet Corn Diversity Panel. <i>Journal of the American Society for Horticultural Science</i> , 2021, 146, 435-444.	1.0	0