Michael A Gore

List of Publications by Citations

135 papers	**7,918** citations	**32** h-index	**88** g-index
171 ext. papers	**11,072** ext. citations	**5.8** avg, IF	**5.71** L-index

#	Paper	IF	Citations
135	Mixed linear model approach adapted for genome-wide association studies. *Nature Genetics*, **2010**, 42, 355-60	36.3	1259
134	GAPIT: genome association and prediction integrated tool. *Bioinformatics*, **2012**, 28, 2397-9	7.2	1135
133	Status and Prospects of Association Mapping in Plants. *Plant Genome*, **2008**, 1,	4.4	818
132	A first-generation haplotype map of maize. *Science*, **2009**, 326, 1115-7	33.3	613
131	Maize HapMap2 identifies extant variation from a genome in flux. *Nature Genetics*, **2012**, 44, 803-7	36.3	470
130	Field-based phenomics for plant genetics research. *Field Crops Research*, **2012**, 133, 101-112	5.5	404
129	Development and evaluation of a field-based high-throughput phenotyping platform. *Functional Plant Biology*, **2013**, 41, 68-79	2.7	225
128	The genetic architecture of maize height. *Genetics*, **2014**, 196, 1337-56	4	211
127	Decreased CO2 availability and inactivation of Rubisco limit photosynthesis in cotton plants under heat and drought stress in the field. *Environmental and Experimental Botany*, **2012**, 83, 1-11	5.9	148
126	Carotenoid cleavage dioxygenase4 is a negative regulator of β-carotene content in Arabidopsis seeds. *Plant Cell*, **2013**, 25, 4812-26	11.6	139
125	Automated Identification of Northern Leaf Blight-Infected Maize Plants from Field Imagery Using Deep Learning. *Phytopathology*, **2017**, 107, 1426-1432	3.8	136
124	A foundation for provitamin A biofortification of maize: genome-wide association and genomic prediction models of carotenoid levels. *Genetics*, **2014**, 198, 1699-716	4	129
123	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of Gossypium spp. *G3: Genes, Genomes, Genetics*, **2015**, 5, 1187-209	3.2	117
122	Genome-wide association study and pathway-level analysis of tocochromanol levels in maize grain. *G3: Genes, Genomes, Genetics*, **2013**, 3, 1287-99	3.2	111
121	Genetic diversity and population structure in the US Upland cotton (Gossypium hirsutum L.). *Theoretical and Applied Genetics*, **2014**, 127, 283-95	6	107
120	From association to prediction: statistical methods for the dissection and selection of complex traits in plants. *Current Opinion in Plant Biology*, **2015**, 24, 110-8	9.9	94
119	Genome-wide analysis of branched-chain amino acid levels in Arabidopsis seeds. *Plant Cell*, **2013**, 25, 4827-43	11.6	93

118	The Quest for Understanding Phenotypic Variation via Integrated Approaches in the Field Environment. *Plant Physiology*, **2016**, 172, 622-634	6.6	75
117	Field-Based High-Throughput Plant Phenotyping Reveals the Temporal Patterns of Quantitative Trait Loci Associated with Stress-Responsive Traits in Cotton. *G3: Genes, Genomes, Genetics*, **2016**, 6, 865-79	3.2	63
116	Re-evaluating the phylogeny of allopolyploid Gossypium L. *Molecular Phylogenetics and Evolution*, **2015**, 92, 45-52	4.1	63
115	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. *Plant Cell*, **2017**, 29, 2374-2392	11.6	57
114	Sustaining the Future of Plant Breeding: The Critical Role of the USDA-ARS National Plant Germplasm System. *Crop Science*, **2018**, 58, 451-468	2.4	55
113	Genetic Analysis of Visually Scored Orange Kernel Color in Maize. *Crop Science*, **2013**, 53, 189-200	2.4	49
112	Linkage Map Construction and Quantitative Trait Locus Analysis of Agronomic and Fiber Quality Traits in Cotton. *Plant Genome*, **2014**, 7, plantgenome2013.07.0023	4.4	48
111	Large-Scale Discovery of Gene-Enriched SNPs. *Plant Genome*, **2009**, 2,	4.4	48
110	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat. *G3: Genes, Genomes, Genetics*, **2019**, 9, 1231-1247	3.2	44
109	Image set for deep learning: field images of maize annotated with disease symptoms. *BMC Research Notes*, **2018**, 11, 440	2.3	43
108	Proximal hyperspectral sensing and data analysis approaches for field-based plant phenomics. *Computers and Electronics in Agriculture*, **2015**, 118, 225-236	6.5	40
107	Network-Guided GWAS Improves Identification of Genes Affecting Free Amino Acids. *Plant Physiology*, **2017**, 173, 872-886	6.6	36
106	Quantitative Phenotyping of Northern Leaf Blight in UAV Images Using Deep Learning. *Remote Sensing*, **2019**, 11, 2209	5	34
105	Genome-wide analysis of the omega-3 fatty acid desaturase gene family in Gossypium. *BMC Plant Biology*, **2014**, 14, 312	5.3	33
104	Evaluation of Target Preparation Methods for Single-Feature Polymorphism Detection in Large Complex Plant Genomes. *Crop Science*, **2007**, 47, S-135	2.4	32
103	ZEAXANTHIN EPOXIDASE Activity Potentiates Carotenoid Degradation in Maturing Seed. *Plant Physiology*, **2016**, 171, 1837-51	6.6	31
102	Millimeter-Level Plant Disease Detection From Aerial Photographs Deep Learning and Crowdsourced Data. *Frontiers in Plant Science*, **2019**, 10, 1550	6.2	31
101	NLR locus-mediated trade-off between abiotic and biotic stress adaptation in Arabidopsis. *Nature Plants*, **2017**, 3, 17072	11.5	30

100	Genetic Diversity of the Two Commercial Tetraploid Cotton Species in the Gossypium Diversity Reference Set. *Journal of Heredity*, **2016**, 107, 274-86	2.4	30
99	Quantitative trait locus analysis of Verticillium wilt resistance in an introgressed recombinant inbred population of Upland cotton. *Molecular Breeding*, **2014**, 33, 709-720	3.4	30
98	Identification of haplotypes at the Rsv4 genomic region in soybean associated with durable resistance to soybean mosaic virus. *Theoretical and Applied Genetics*, **2016**, 129, 453-68	6	28
97	Transcriptome-Wide Association Supplements Genome-Wide Association in. *G3: Genes, Genomes, Genetics*, **2019**, 9, 3023-3033	3.2	28
96	Autonomous Detection of Plant Disease Symptoms Directly from Aerial Imagery. *The Plant Phenome Journal*, **2019**, 2, 1-9	5	28
95	Molecular characterization of the Gossypium Diversity Reference Set of the US National Cotton Germplasm Collection. *Theoretical and Applied Genetics*, **2015**, 128, 313-27	6	27
94	Deleterious Mutation Burden and Its Association with Complex Traits in Sorghum (). *Genetics*, **2019**, 211, 1075-1087	4	27
93	Population Structure and Phylogenetic Relationships in a Diverse Panel of L. *Frontiers in Plant Science*, **2017**, 8, 321	6.2	26
92	Closing the Divide between Human Nutrition and Plant Breeding. *Crop Science*, **2015**, 55, 1437-1448	2.4	26
91	rAmpSeq: Using repetitive sequences for robust genotyping		26
90	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. *Plant Genome*, **2020**, 13, e20009	4.4	24
89	A community resource for exploring and utilizing genetic diversity in the USDA pea single plant plus collection. *Horticulture Research*, **2017**, 4, 17017	7.7	23
88	A century of guayule: Comprehensive genetic characterization of the US national guayule (Parthenium argentatum A. Gray) germplasm collection. *Industrial Crops and Products*, **2017**, 109, 300-309	5.9	20
87	Population Genomic Analysis Reveals Differential Evolutionary Histories and Patterns of Diversity across Subgenomes and Subpopulations of Brassica napus L. *Frontiers in Plant Science*, **2016**, 7, 525	6.2	20
86	Multivariate Genome-Wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat (L.). *G3: Genes, Genomes, Genetics*, **2019**, 9, 2963-2975	3.2	20
85	Genome-Wide Association and Genomic Prediction Models of Tocochromanols in Fresh Sweet Corn Kernels. *Plant Genome*, **2019**, 12, 180038	4.4	20
84	Chemical variation for leaf cuticular waxes and their levels revealed in a diverse panel of Brassica napus L .. *Industrial Crops and Products*, **2016**, 79, 77-83	5.9	19
83	Registration of the TM-1/NM24016 Cotton Recombinant Inbred Mapping Population. *Journal of Plant Registrations*, **2012**, 6, 124-127	0.7	19

82	Natural variation for carotenoids in fresh kernels is controlled by uncommon variants in sweet corn. *Plant Genome*, **2020**, 13, e20008	4.4	17
81	Maize genomes to fields (G2F): 2014-2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. *BMC Research Notes*, **2020**, 13, 71	2.3	16
80	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. *BMC Research Notes*, **2018**, 11, 452	2.3	16
79	Genomic diversity and phylogenetic relationships in the genus Parthenium (Asteraceae). *Industrial Crops and Products*, **2015**, 76, 920-929	5.9	14
78	Aerial high-throughput phenotyping enables indirect selection for grain yield at the early generation, seed-limited stages in breeding programs. *Crop Science*, **2020**, 60, 3096-3114	2.4	14
77	Science-graphic art partnerships to increase research impact. *Communications Biology*, **2019**, 2, 295	6.7	13
76	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. *Field Crops Research*, **2019**, 234, 119-128	5.5	12
75	The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale public cooperative maize experiment. *G3: Genes, Genomes, Genetics*, **2021**, 11,	3.2	12
74	Comparative evolutionary genetics of deleterious load in sorghum and maize. *Nature Plants*, **2021**, 7, 17-24	11.5	12
73	Chemical variation for fiber cuticular wax levels in upland cotton (Gossypium hirsutum L.) evaluated under contrasting irrigation regimes. *Industrial Crops and Products*, **2017**, 100, 153-162	5.9	11
72	Complex Ploidy Level Variation in Guayule Breeding Programs. *Crop Science*, **2011**, 51, 210-216	2.4	11
71	Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. *Frontiers in Genetics*, **2020**, 11, 592769	4.5	11
70	In-Field Whole-Plant Maize Architecture Characterized by Subcanopy Rovers and Latent Space Phenotyping. *The Plant Phenome Journal*, **2019**, 2, 1-11	5	11
69	Genome-Wide Association Study and Pathway-Level Analysis of Kernel Color in Maize. *G3: Genes, Genomes, Genetics*, **2019**, 9, 1945-1955	3.2	10
68	Investigation of the Influence of Leaf Thickness on Canopy Reflectance and Physiological Traits in Upland and Pima Cotton Populations. *Frontiers in Plant Science*, **2017**, 8, 1405	6.2	10
67	Temporal Genetic Dynamics of an Experimental, Biparental Field Population of. *Frontiers in Genetics*, **2017**, 8, 26	4.5	10
66	Novel Bayesian Networks for Genomic Prediction of Developmental Traits in Biomass Sorghum. *G3: Genes, Genomes, Genetics*, **2020**, 10, 769-781	3.2	10
65	Effects of temperature and salinity on germination of non-pelleted and pelleted guayule (Parthenium argentatum A. Gray) seeds. *Industrial Crops and Products*, **2014**, 55, 90-96	5.9	9

64	The Evolutionary History of Wild, Domesticated, and Feral Brassica oleracea (Brassicaceae). *Molecular Biology and Evolution*, **2021**, 38, 4419-4434	8.3	9
63	The patterns of deleterious mutations during the domestication of soybean. *Nature Communications*, **2021**, 12, 97	17.4	9
62	Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. *Nature Communications*, **2021**, 12, 1227	17.4	9
61	Transcriptomic network analyses shed light on the regulation of cuticle development in maize leaves. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 12464-12471	11.5	8
60	ImageBreed: Open-access plant breeding web database for image-based phenotyping. *The Plant Phenome Journal*, **2020**, 3, e20004	5	8
59	Multivariate Analysis of the Cotton Seed Ionome Reveals a Shared Genetic Architecture. *G3: Genes, Genomes, Genetics*, **2018**, 8, 1147-1160	3.2	8
58	Heritable temporal gene expression patterns correlate with metabolomic seed content in developing hexaploid oat seed. *Plant Biotechnology Journal*, **2020**, 18, 1211-1222	11.6	8
57	Genome size variation in guayule and mariola: Fundamental descriptors for polyploid plant taxa. *Industrial Crops and Products*, **2014**, 54, 1-5	5.9	7
56	Genetic Analysis of the Transition from Wild to Domesticated Cotton (L.). *G3: Genes, Genomes, Genetics*, **2020**, 10, 731-754	3.2	7
55	Relative utility of agronomic, phenological, and morphological traits for assessing genotype-by-environment interaction in maize inbreds. *Crop Science*, **2020**, 60, 62-81	2.4	7
54	Translating insights from the seed metabolome into improved prediction for lipid-composition traits in oat (Avena sativa L.). *Genetics*, **2021**, 217,	4	7
53	Influences of the combination of high temperature and water deficit on the heritabilities and correlations of agronomic and fiber quality traits in upland cotton. *Euphytica*, **2017**, 213, 1	2.1	6
52	The Germ Fraction Inhibits Iron Bioavailability of Maize: Identification of an Approach to Enhance Maize Nutritional Quality via Processing and Breeding. *Nutrients*, **2019**, 11,	6.7	6
51	Genomic characterization of Ugandan smallholder farmer-preferred cassava varieties. *Crop Science*, **2020**, 60, 1450-1461	2.4	6
50	Machine Learning Enables High-Throughput Phenotyping for Analyses of the Genetic Architecture of Bulliform Cell Patterning in Maize. *G3: Genes, Genomes, Genetics*, **2019**, 9, 4235-4243	3.2	6
49	Divergence of defensive cucurbitacins in independent Cucurbita pepo domestication events leads to differences in specialist herbivore preference. *Plant, Cell and Environment*, **2020**, 43, 2812-2825	8.4	6
48	Temporal covariance structure of multi-spectral phenotypes and their predictive ability for end-of-season traits in maize. *Theoretical and Applied Genetics*, **2020**, 133, 2853-2868	6	6
47	Genome-Wide Association Study for Maize Leaf Cuticular Conductance Identifies Candidate Genes Involved in the Regulation of Cuticle Development. *G3: Genes, Genomes, Genetics*, **2020**, 10, 1671-1683	3.2	5

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46	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat		5
45	Structure-function analysis of the maize bulliform cell cuticle and its potential role in dehydration and leaf rolling. *Plant Direct*, **2020**, 4, e00282	3.3	5
44	A Low-Cost Automated System for High-Throughput Phenotyping of Single Oat Seeds. *The Plant Phenome Journal*, **2018**, 1, 1-13	5	5
43	A combined BSA-Seq and linkage mapping approach identifies genomic regions associated with Phytophthora root and crown rot resistance in squash. *Theoretical and Applied Genetics*, **2021**, 134, 1015-1031	6	5
42	Multi-omics prediction of oat agronomic and seed nutritional traits across environments and in distantly related populations. *Theoretical and Applied Genetics*, **2021**, 134, 4043-4054	6	4
41	Genome-wide association study identifies acyl-lipid metabolism candidate genes involved in the genetic control of natural variation for seed fatty acid traits in Brassica napus L.. *Industrial Crops and Products*, **2020**, 145, 112080	5.9	4
40	A minimally disruptive method for measuring water potential in planta using hydrogel nanoreporters. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	4
39	Cotton phenotyping with lidar from a track-mounted platform **2016**,		4
38	Nucleotide diversity in the two co-resident genomes of allopolyploid cotton. *Plant Systematics and Evolution*, **2017**, 303, 1021-1042	1.3	3
37	Genomic characterization of the Native Seeds/SEARCH common bean (Phaseolus vulgaris L.) collection and its seed coat patterns. *Genetic Resources and Crop Evolution*, **2019**, 66, 1469-1482	2	3
36	Genotypic evaluation of twenty-eight high- and low-cyanide cassava in low-land tropics, southeast Nigeria. *Heliyon*, **2019**, 5, e01855	3.6	3
35	Use of hydraulic traits for modeling genotype-specific acclimation in cotton under drought. *New Phytologist*, **2020**, 228, 898-909	9.8	3
34	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. *Plant Cell*, **2021**, 33, 882-900	11.6	3
33	Leveraging mutational burden for complex trait prediction in sorghum		3
32	Transcriptome-wide association supplements genome-wide association in Zea mays		3
31	In-field whole plant maize architecture characterized by Latent Space Phenotyping		3
30	A maize LIPID TRANSFER PROTEIN may bridge the gap between PHYTOCHROME-mediated light signaling and cuticle biosynthesis. *Plant Signaling and Behavior*, **2020**, 15, 1790824	2.5	3
29	High-resolution genome-wide association study pinpoints metal transporter and chelator genes involved in the genetic control of element levels in maize grain. *G3: Genes, Genomes, Genetics*, **2021**, 11,	3.2	3

28	Machine learning-enabled phenotyping for GWAS and TWAS of WUE traits in 869 field-grown sorghum accessions. *Plant Physiology*, **2021**, 187, 1481-1500	6.6	3
27	Genome-Wide Association Study in New York Isolates Reveals Loci Involved in Mating Type and Mefenoxam Sensitivity. *Phytopathology*, **2021**, 111, 204-216	3.8	3
26	Improving Genomic Prediction for Seed Quality Traits in Oat (Avena sativa L.) Using Trait-Specific Relationship Matrices. *Frontiers in Genetics*, **2021**, 12, 643733	4.5	3
25	Phenotyping stomatal closure by thermal imaging for GWAS and TWAS of water use efficiency-related genes. *Plant Physiology*, **2021**, 187, 2544-2562	6.6	3
24	Elemental Accumulation in Kernels of the Maize Nested Association Mapping Panel Reveals Signals of Gene by Environment Interactions		2
23	Eleven biosynthetic genes explain the majority of natural variation for carotenoid levels in maize grain		2
22	Genetic analysis of the transition from wild to domesticated cotton (G. hirsutum L.)		2
21	Genome-wide association study suggests an independent genetic basis of zinc and cadmium concentrations in fresh sweet corn kernels. *G3: Genes, Genomes, Genetics*, **2021**, 11,	3.2	2
20	Effectiveness of genomic selection for improving provitamin A carotenoid content and associated traits in cassava. *G3: Genes, Genomes, Genetics*, **2021**, 11,	3.2	2
19	Making waves in Breedbase: An integrated spectral data storage and analysis pipeline for plant breeding programs. *The Plant Phenome Journal*, **2021**, 4, e20012	5	2
18	Interactions between breeding system and ploidy affect niche breadth in .. *Royal Society Open Science*, **2022**, 9, 211862	3.3	1
17	Accelerating Crop Domestication in the Era of Gene Editing **2021**, 185-211		1
16	Wild relatives of potato may bolster its adaptation to new niches under future climate scenarios. *Food and Energy Security*,e360	4.1	1
15	Network analyses implicate a role for PHYTOCHROME-mediated light signaling in the regulation of cuticle development in plant leaves		1
14	Structure-function analysis of the maize bulliform cell cuticle and its role in dehydration and leaf rolling		1
13	Random Forest Regression for Optimizing Variable Planting Rates for Corn and Soybean Using High-Resolution Topographical and Soil Data		1
12	Machine learning enabled phenotyping for GWAS and TWAS of WUE traits in 869 field-grown sorghum accessions		1
11	Multivariate Genome-wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat (Avena sativaL.)		1

LIST OF PUBLICATIONS

10	Comparative evolutionary analysis and prediction of deleterious mutation patterns between sorghum and maize		1
9	Temporal Genetic Dynamics of an Experimental, Biparental Field Population of Phytophthora capsici		1
8	High-Quality Reference Genome Sequence for the Oomycete Vegetable Pathogen Phytophthora capsici Strain LT1534. *Microbiology Resource Announcements*, **2021**, 10, e0029521	1.3	1
7	Selection for seed size has uneven effects on specialized metabolite abundance in oat (Avena sativa L). *G3: Genes, Genomes, Genetics*, **2021**,	3.2	1
6	Random forest regression for optimizing variable planting rates for corn and soybean using topographical and soil data. *Agronomy Journal*, **2020**, 112, 5045-5066	2.2	0
5	Acylsugars protect Nicotiana benthamiana against insect herbivory and desiccation. *Plant Molecular Biology*, **2021**, 1	4.6	0
4	Transcriptome-wide association and prediction for carotenoids and tocochromanols in fresh sweet corn kernels.. *Plant Genome*, **2022**, e20197	4.4	0
3	Generalizable approaches for genomic prediction of metabolites in plants.. *Plant Genome*, **2022**, e20205	4.4	0
2	Sugarcane Mosaic Virus Resistance in the Wisconsin Sweet Corn Diversity Panel. *Journal of the American Society for Horticultural Science*, **2021**, 1-10	2.3	
1	Prospector: A mobile application for portable, high-throughput near-infrared spectroscopy phenotyping. *The Plant Phenome Journal*, **2021**, 4, e20024	5	