

# Michael A Gore

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/907689/publications.pdf>

Version: 2024-02-01

125  
papers

12,698  
citations

87843

38  
h-index

28275

105  
g-index

171  
all docs

171  
docs citations

171  
times ranked

11617  
citing authors

#	ARTICLE	IF	CITATIONS
1	Acylsugars protect <i>Nicotiana benthamiana</i> against insect herbivory and desiccation. <i>Plant Molecular Biology</i> , 2022, 109, 505-522.	2.0	20
2	Wild relatives of potato may bolster its adaptation to new niches under future climate scenarios. <i>Food and Energy Security</i> , 2022, 11, e360.	2.0	7
3	Interactions between breeding system and ploidy affect niche breadth in <i>Solanum</i> . <i>Royal Society Open Science</i> , 2022, 9, 211862.	1.1	2
4	Low-cost, handheld near-infrared spectroscopy for root dry matter content prediction in cassava. <i>The Plant Phenome Journal</i> , 2022, 5, .	1.0	6
5	Transcriptome-wide association and prediction for carotenoids and tocochromanols in fresh sweet corn kernels. <i>Plant Genome</i> , 2022, 15, e20197.	1.6	10
6	Breedbase: a digital ecosystem for modern plant breeding. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	17
7	Selection for seed size has uneven effects on specialized metabolite abundance in oat ( <i>Avena</i> ). <i>Journal of Experimental Botany</i> , 2022, 63, 1081-1092.	0.8	9
8	Generalizable approaches for genomic prediction of metabolites in plants. <i>Plant Genome</i> , 2022, 15, e20205.	1.6	8
9	Integrating GWAS and TWAS to elucidate the genetic architecture of maize leaf cuticular conductance. <i>Plant Physiology</i> , 2022, 189, 2144-2158.	2.3	9
10	Undisciplining the university through shared purpose, practice, and place. <i>Humanities and Social Sciences Communications</i> , 2022, 9, .	1.3	3
11	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, .	3.3	11
12	Combining GWAS and TWAS to identify candidate causal genes for tocochromanol levels in maize grain. <i>Genetics</i> , 2022, 221, .	1.2	15
13	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.	1.1	17
14	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.	1.0	9
15	Prospector: A mobile application for portable, high-throughput near-infrared spectroscopy phenotyping. <i>The Plant Phenome Journal</i> , 2021, 4, e20024.	1.0	0
16	The patterns of deleterious mutations during the domestication of soybean. <i>Nature Communications</i> , 2021, 12, 97.	5.8	49
17	Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. <i>Nature Communications</i> , 2021, 12, 1227.	5.8	37
18	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, .	1.2	17

#	ARTICLE	IF	CITATIONS
19	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.	1.1	14
20	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, .	0.8	18
21	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, .	0.8	7
22	Effectiveness of genomic selection for improving provitamin A carotenoid content and associated traits in cassava. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	9
23	High-Quality Reference Genome Sequence for the Oomycete Vegetable Pathogen <i>Phytophthora capsici</i> Strain LT1534. <i>Microbiology Resource Announcements</i> , 2021, 10, e0029521.	0.3	4
24	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, .	3.3	19
25	The Evolutionary History of Wild, Domesticated, and Feral <i>Brassica oleracea</i> ( <i>Brassicaceae</i> ). <i>Molecular Biology and Evolution</i> , 2021, 38, 4419-4434.	3.5	49
26	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.	2.3	44
27	Phenotyping stomatal closure by thermal imaging for GWAS and TWAS of water use efficiency-related genes. <i>Plant Physiology</i> , 2021, 187, 2544-2562.	2.3	23
28	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.	1.8	23
29	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, .	0.8	52
30	Comparative evolutionary genetics of deleterious load in sorghum and maize. <i>Nature Plants</i> , 2021, 7, 17-24.	4.7	52
31	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. <i>Plant Cell</i> , 2021, 33, 882-900.	3.1	31
32	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.	0.5	0
33	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.	1.8	20
34	Heritable temporal gene expression patterns correlate with metabolomic seed content in developing hexaploid oat seed. <i>Plant Biotechnology Journal</i> , 2020, 18, 1211-1222.	4.1	19
35	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.	2.5	8
36	Relative utility of agronomic, phenological, and morphological traits for assessing genotype-by-environment interaction in maize inbreds. <i>Crop Science</i> , 2020, 60, 62-81.	0.8	21

#	ARTICLE	IF	CITATIONS
37	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.	2.8	16
38	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.	0.8	31
39	A maize LIPID TRANSFER PROTEIN may bridge the gap between PHYTOCHROME-mediated light signaling and cuticle biosynthesis. Plant Signaling and Behavior, 2020, 15, 1790824.	1.2	6
40	Structure-function analysis of the maize bulliform cell cuticle and its potential role in dehydration and leaf rolling. Plant Direct, 2020, 4, e00282.	0.8	24
41	Novel Bayesian Networks for Genomic Prediction of Developmental Traits in Biomass Sorghum. G3: Genes, Genomes, Genetics, 2020, 10, 769-781.	0.8	25
42	Random forest regression for optimizing variable planting rates for corn and soybean using topographical and soil data. Agronomy Journal, 2020, 112, 5045-5066.	0.9	11
43	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.	1.8	11
44	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.	3.3	19
45	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.	0.8	13
46	Use of hydraulic traits for modeling genotype-specific acclimation in cotton under drought. New Phytologist, 2020, 228, 898-909.	3.5	10
47	Natural variation for carotenoids in fresh kernels is controlled by uncommon variants in sweet corn. Plant Genome, 2020, 13, e20008.	1.6	34
48	Genomic characterization of Ugandan smallholder farmer-preferred cassava varieties. Crop Science, 2020, 60, 1450-1461.	0.8	12
49	ImageBreed: Open-access plant breeding web-database for image-based phenotyping. The Plant Phenome Journal, 2020, 3, e20004.	1.0	16
50	Maize genomes to fields (G2F): 2014-2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. BMC Research Notes, 2020, 13, 71.	0.6	38
51	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. Plant Genome, 2020, 13, e20009.	1.6	54
52	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.	1.1	44
53	Genetic Analysis of the Transition from Wild to Domesticated Cotton ( <i>Gossypium hirsutum</i> L.). G3: Genes, Genomes, Genetics, 2020, 10, 731-754.	0.8	14
54	Science-graphic art partnerships to increase research impact. Communications Biology, 2019, 2, 295.	2.0	24

#	ARTICLE	IF	CITATIONS
55	Millimeter-Level Plant Disease Detection From Aerial Photographs via Deep Learning and Crowdsourced Data. <i>Frontiers in Plant Science</i> , 2019, 10, 1550.	1.7	68
56	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.	0.8	9
57	Quantitative Phenotyping of Northern Leaf Blight in UAV Images Using Deep Learning. <i>Remote Sensing</i> , 2019, 11, 2209.	1.8	69
58	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.	0.8	22
59	Genotypic evaluation of twenty-eight high- and low-cyanide cassava in low-land tropics, southeast Nigeria. <i>Heliyon</i> , 2019, 5, e01855.	1.4	4
60	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.	1.7	9
61	Genome-Wide Association Study and Pathway-Level Analysis of Kernel Color in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1945-1955.	0.8	20
62	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1231-1247.	0.8	96
63	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.	2.3	24
64	Transcriptome-Wide Association Supplements Genome-Wide Association in <i>Zea mays</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3023-3033.	0.8	64
65	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.	0.8	44
66	In-Field Whole-Plant Maize Architecture Characterized by Subcanopy Rovers and Latent Space Phenotyping. <i>The Plant Phenome Journal</i> , 2019, 2, 1-11.	1.0	23
67	Autonomous Detection of Plant Disease Symptoms Directly from Aerial Imagery. <i>The Plant Phenome Journal</i> , 2019, 2, 1-9.	1.0	73
68	Deleterious Mutation Burden and Its Association with Complex Traits in Sorghum ( <i>Sorghum</i> ). <i>Overlook</i> , 2019, 10, 51.	1.2	51
69	Genome-Wide Association and Genomic Prediction Models of Tocochromanols in Fresh Sweet Corn Kernels. <i>Plant Genome</i> , 2019, 12, 180038.	1.6	37
70	Multivariate Analysis of the Cotton Seed Ionome Reveals a Shared Genetic Architecture. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1147-1160.	0.8	14
71	A Low-Cost Automated System for High-Throughput Phenotyping of Single Oat Seeds. <i>The Plant Phenome Journal</i> , 2018, 1, 1-13.	1.0	7
72	Sustaining the Future of Plant Breeding: The Critical Role of the USDA-ARS National Plant Germplasm System. <i>Crop Science</i> , 2018, 58, 451-468.	0.8	91

#	ARTICLE	IF	CITATIONS
73	Image set for deep learning: field images of maize annotated with disease symptoms. BMC Research Notes, 2018, 11, 440.	0.6	91
74	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. BMC Research Notes, 2018, 11, 452.	0.6	25
75	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.	0.6	9
76	Chemical variation for fiber cuticular wax levels in upland cotton ( <i>Gossypium hirsutum</i> L.) evaluated under contrasting irrigation regimes. Industrial Crops and Products, 2017, 100, 153-162.	2.5	12
77	Nucleotide diversity in the two co-resident genomes of allopolyploid cotton. Plant Systematics and Evolution, 2017, 303, 1021-1042.	0.3	4
78	A community resource for exploring and utilizing genetic diversity in the USDA pea single plant plus collection. Horticulture Research, 2017, 4, 17017.	2.9	41
79	NLR locus-mediated trade-off between abiotic and biotic stress adaptation in Arabidopsis. Nature Plants, 2017, 3, 17072.	4.7	53
80	Network-Guided GWAS Improves Identification of Genes Affecting Free Amino Acids. Plant Physiology, 2017, 173, 872-886.	2.3	52
81	A century of guayule: Comprehensive genetic characterization of the US national guayule ( <i>Parthenium</i> ) Tj ETQq1 1.0, 784314, rgBT / Over	2.5	36
82	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. Plant Cell, 2017, 29, 2374-2392.	3.1	93
83	Automated Identification of Northern Leaf Blight-Infected Maize Plants from Field Imagery Using Deep Learning. Phytopathology, 2017, 107, 1426-1432.	1.1	254
84	Population Structure and Phylogenetic Relationships in a Diverse Panel of Brassica rapa L.. Frontiers in Plant Science, 2017, 8, 321.	1.7	53
85	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.	1.7	22
86	Temporal Genetic Dynamics of an Experimental, Biparental Field Population of Phytophthora capsici. Frontiers in Genetics, 2017, 08, 26.	1.1	19
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.	1.7	33
88	The quest for understanding phenotypic variation via integrated approaches in the field environment. Plant Physiology, 2016, 172, pp.00592.2016.	2.3	99
89	Cotton phenotyping with lidar from a track-mounted platform. Proceedings of SPIE, 2016, , .	0.8	4
90	<i>ZEAXANTHIN EPOXIDASE</i> Activity Potentiates Carotenoid Degradation in Maturing Seed. Plant Physiology, 2016, 171, 1837-1851.	2.3	44

#	ARTICLE	IF	CITATIONS
91	Identification of haplotypes at the Rsv4 genomic region in soybean associated with durable resistance to soybean mosaic virus. Theoretical and Applied Genetics, 2016, 129, 453-468.	1.8	37
92	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.	2.5	26
93	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, 865-879.	0.8	105
94	Genetic Diversity of the Two Commercial Tetraploid Cotton Species in the <i>Gossypium</i> Diversity Reference Set. Journal of Heredity, 2016, 107, 274-286.	1.0	43
95	Closing the Divide between Human Nutrition and Plant Breeding. Crop Science, 2015, 55, 1437-1448.	0.8	36
96	Re-evaluating the phylogeny of allopolyploid <i>Gossypium</i> L.. Molecular Phylogenetics and Evolution, 2015, 92, 45-52.	1.2	110
97	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of <i>Gossypium</i> spp.. G3: Genes, Genomes, Genetics, 2015, 5, 1187-1209.	0.8	226
98	From association to prediction: statistical methods for the dissection and selection of complex traits in plants. Current Opinion in Plant Biology, 2015, 24, 110-118.	3.5	166
99	Proximal hyperspectral sensing and data analysis approaches for field-based plant phenomics. Computers and Electronics in Agriculture, 2015, 118, 225-236.	3.7	66
100	Genomic diversity and phylogenetic relationships in the genus <i>Parthenium</i> (Asteraceae). Industrial Crops and Products, 2015, 76, 920-929.	2.5	17
101	Molecular characterization of the <i>Gossypium</i> Diversity Reference Set of the US National Cotton Germplasm Collection. Theoretical and Applied Genetics, 2015, 128, 313-327.	1.8	39
102	Linkage Map Construction and Quantitative Trait Locus Analysis of Agronomic and Fiber Quality Traits in Cotton. Plant Genome, 2014, 7, plantgenome2013.07.0023.	1.6	62
103	<i>CAROTENOID CLEAVAGE DIOXYGENASE4</i> Is a Negative Regulator of $\beta^2$ -Carotene Content in <i>Arabidopsis</i> Seeds. Plant Cell, 2014, 25, 4812-4826.	3.1	180
104	Genome-wide analysis of the omega-3 fatty acid desaturase gene family in <i>Gossypium</i> . BMC Plant Biology, 2014, 14, 312.	1.6	41
105	The Genetic Architecture Of Maize Height. Genetics, 2014, 196, 1337-1356.	1.2	329
106	Development and evaluation of a field-based high-throughput phenotyping platform. Functional Plant Biology, 2014, 41, 68.	1.1	316
107	Effects of temperature and salinity on germination of non-pelleted and pelleted guayule ( <i>Parthenium</i> ) Tj ETQq1 1 0.784314 r <sub>BT</sub> /Overl	2.5	14
108	Genetic diversity and population structure in the US Upland cotton ( <i>Gossypium hirsutum</i> L.). Theoretical and Applied Genetics, 2014, 127, 283-295.	1.8	151

#	ARTICLE	IF	CITATIONS
109	Genome-Wide Analysis of Branched-Chain Amino Acid Levels in <i>Arabidopsis</i> Seeds. <i>Plant Cell</i> , 2014, 25, 4827-4843.	3.1	121
110	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.	1.0	48
111	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.	1.2	180
112	Genome size variation in guayule and mariola: Fundamental descriptors for polyploid plant taxa. <i>Industrial Crops and Products</i> , 2014, 54, 1-5.	2.5	9
113	Genome-Wide Association Study and Pathway-Level Analysis of Tocochromanol Levels in Maize Grain. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1287-1299.	0.8	152
114	Genetic Analysis of Visually Scored Orange Kernel Color in Maize. <i>Crop Science</i> , 2013, 53, 189-200.	0.8	66
115	GAPIT: genome association and prediction integrated tool. <i>Bioinformatics</i> , 2012, 28, 2397-2399.	1.8	2,016
116	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	9.4	577
117	Field-based phenomics for plant genetics research. <i>Field Crops Research</i> , 2012, 133, 101-112.	2.3	521
118	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.	2.0	200
119	Registration of the TM <sup>6</sup> 1/NM24016 Cotton Recombinant Inbred Mapping Population. <i>Journal of Plant Registrations</i> , 2012, 6, 124-127.	0.4	21
120	Complex Ploidy Level Variation in Guayule Breeding Programs. <i>Crop Science</i> , 2011, 51, 210-216.	0.8	12
121	Mixed linear model approach adapted for genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 355-360.	9.4	2,022
122	Large-scale Discovery of Gene-Enriched SNPs. <i>Plant Genome</i> , 2009, 2, .	1.6	55
123	A First-Generation Haplotype Map of Maize. <i>Science</i> , 2009, 326, 1115-1117.	6.0	747
124	Status and Prospects of Association Mapping in Plants. <i>Plant Genome</i> , 2008, 1, .	1.6	1,118
125	Evaluation of Target Preparation Methods for Single-Feature Polymorphism Detection in Large Complex Plant Genomes. <i>Crop Science</i> , 2007, 47, S-135.	0.8	36