

# Michael A Gore

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Interactions between breeding system and ploidy affect niche breadth in .. <i>Royal Society Open Science</i> , <b>2022</b> , 9, 211862	3.3	1
134	Transcriptome-wide association and prediction for carotenoids and tocochromanols in fresh sweet corn kernels.. <i>Plant Genome</i> , <b>2022</b> , e20197	4.4	0
133	Generalizable approaches for genomic prediction of metabolites in plants.. <i>Plant Genome</i> , <b>2022</b> , e20205	4.4	0
132	Multi-omics prediction of oat agronomic and seed nutritional traits across environments and in distantly related populations. <i>Theoretical and Applied Genetics</i> , <b>2021</b> , 134, 4043-4054	6	4
131	Accelerating Crop Domestication in the Era of Gene Editing <b>2021</b> , 185-211		1
130	Sugarcane Mosaic Virus Resistance in the Wisconsin Sweet Corn Diversity Panel. <i>Journal of the American Society for Horticultural Science</i> , <b>2021</b> , 1-10	2.3	
129	Eleven biosynthetic genes explain the majority of natural variation in carotenoid levels in maize grain. <i>Plant Cell</i> , <b>2021</b> , 33, 882-900	11.6	3
128	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> , <b>2021</b> , 11,	3.2	3
127	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> , <b>2021</b> , 11,	3.2	2
126	Effectiveness of genomic selection for improving provitamin A carotenoid content and associated traits in cassava. <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> , 11,	3.2	2
125	High-Quality Reference Genome Sequence for the Oomycete Vegetable Pathogen <i>Phytophthora capsici</i> Strain LT1534. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10, e0029521	1.3	1
124	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> , <b>2021</b> , 118,	11.5	4
123	The Evolutionary History of Wild, Domesticated, and Feral <i>Brassica oleracea</i> (Brassicaceae). <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 4419-4434	8.3	9
122	Machine learning-enabled phenotyping for GWAS and TWAS of WUE traits in 869 field-grown sorghum accessions. <i>Plant Physiology</i> , <b>2021</b> , 187, 1481-1500	6.6	3
121	Genome-Wide Association Study in New York Isolates Reveals Loci Involved in Mating Type and Mefenoxam Sensitivity. <i>Phytopathology</i> , <b>2021</b> , 111, 204-216	3.8	3
120	Making waves in Breedbase: An integrated spectral data storage and analysis pipeline for plant breeding programs. <i>The Plant Phenome Journal</i> , <b>2021</b> , 4, e20012	5	2
119	Prospector: A mobile application for portable, high-throughput near-infrared spectroscopy phenotyping. <i>The Plant Phenome Journal</i> , <b>2021</b> , 4, e20024	5	

118	The patterns of deleterious mutations during the domestication of soybean. <i>Nature Communications</i> , <b>2021</b> , 12, 97	17.4	9
117	Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. <i>Nature Communications</i> , <b>2021</b> , 12, 1227	17.4	9
116	Translating insights from the seed metabolome into improved prediction for lipid-composition traits in oat ( <i>Avena sativa</i> L.). <i>Genetics</i> , <b>2021</b> , 217,	4	7
115	Improving Genomic Prediction for Seed Quality Traits in Oat ( <i>Avena sativa</i> L.) Using Trait-Specific Relationship Matrices. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 643733	4.5	3
114	Phenotyping stomatal closure by thermal imaging for GWAS and TWAS of water use efficiency-related genes. <i>Plant Physiology</i> , <b>2021</b> , 187, 2544-2562	6.6	3
113	Acylsugars protect <i>Nicotiana benthamiana</i> against insect herbivory and desiccation. <i>Plant Molecular Biology</i> , <b>2021</b> , 1	4.6	0
112	A combined BSA-Seq and linkage mapping approach identifies genomic regions associated with Phytophthora root and crown rot resistance in squash. <i>Theoretical and Applied Genetics</i> , <b>2021</b> , 134, 1015-1031	6	5
111	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> , <b>2021</b> , 11,	3.2	12
110	Comparative evolutionary genetics of deleterious load in sorghum and maize. <i>Nature Plants</i> , <b>2021</b> , 7, 17-24	11.5	12
109	Selection for seed size has uneven effects on specialized metabolite abundance in oat ( <i>Avena sativa</i> L.). <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> ,	3.2	1
108	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> , <b>2020</b> , 117, 12464-12471	11.5	8
107	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> , <b>2020</b> , 10, 1671-1683	3.2	5
106	Use of hydraulic traits for modeling genotype-specific acclimation in cotton under drought. <i>New Phytologist</i> , <b>2020</b> , 228, 898-909	9.8	3
105	Natural variation for carotenoids in fresh kernels is controlled by uncommon variants in sweet corn. <i>Plant Genome</i> , <b>2020</b> , 13, e20008	4.4	17
104	Genomic characterization of Ugandan smallholder farmer-preferred cassava varieties. <i>Crop Science</i> , <b>2020</b> , 60, 1450-1461	2.4	6
103	ImageBreed: Open-access plant breeding web database for image-based phenotyping. <i>The Plant Phenome Journal</i> , <b>2020</b> , 3, e20004	5	8
102	Maize genomes to fields (G2F): 2014-2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. <i>BMC Research Notes</i> , <b>2020</b> , 13, 71	2.3	16
101	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. <i>Plant Genome</i> , <b>2020</b> , 13, e20009	4.4	24

100	Genetic Analysis of the Transition from Wild to Domesticated Cotton ( L.). <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 731-754	3.2	7
99	Heritable temporal gene expression patterns correlate with metabolomic seed content in developing hexaploid oat seed. <i>Plant Biotechnology Journal</i> , <b>2020</b> , 18, 1211-1222	11.6	8
98	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.. <i>Industrial Crops and Products</i> , <b>2020</b> , 145, 112080	5.9	4
97	Relative utility of agronomic, phenological, and morphological traits for assessing genotype-by-environment interaction in maize inbreds. <i>Crop Science</i> , <b>2020</b> , 60, 62-81	2.4	7
96	Divergence of defensive cucurbitacins in independent Cucurbita pepo domestication events leads to differences in specialist herbivore preference. <i>Plant, Cell and Environment</i> , <b>2020</b> , 43, 2812-2825	8.4	6
95	Aerial high-throughput phenotyping enables indirect selection for grain yield at the early generation, seed-limited stages in breeding programs. <i>Crop Science</i> , <b>2020</b> , 60, 3096-3114	2.4	14
94	A maize LIPID TRANSFER PROTEIN may bridge the gap between PHYTOCHROME-mediated light signaling and cuticle biosynthesis. <i>Plant Signaling and Behavior</i> , <b>2020</b> , 15, 1790824	2.5	3
93	Structure-function analysis of the maize bulliform cell cuticle and its potential role in dehydration and leaf rolling. <i>Plant Direct</i> , <b>2020</b> , 4, e00282	3.3	5
92	Novel Bayesian Networks for Genomic Prediction of Developmental Traits in Biomass Sorghum. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 769-781	3.2	10
91	Random forest regression for optimizing variable planting rates for corn and soybean using topographical and soil data. <i>Agronomy Journal</i> , <b>2020</b> , 112, 5045-5066	2.2	0
90	Temporal covariance structure of multi-spectral phenotypes and their predictive ability for end-of-season traits in maize. <i>Theoretical and Applied Genetics</i> , <b>2020</b> , 133, 2853-2868	6	6
89	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> , <b>2020</b> , 11, 592769	4.5	11
88	Quantitative Phenotyping of Northern Leaf Blight in UAV Images Using Deep Learning. <i>Remote Sensing</i> , <b>2019</b> , 11, 2209	5	34
87	Genomic characterization of the Native Seeds/SEARCH common bean (Phaseolus vulgaris L.) collection and its seed coat patterns. <i>Genetic Resources and Crop Evolution</i> , <b>2019</b> , 66, 1469-1482	2	3
86	Genotypic evaluation of twenty-eight high- and low-cyanide cassava in low-land tropics, southeast Nigeria. <i>Heliyon</i> , <b>2019</b> , 5, e01855	3.6	3
85	The Germ Fraction Inhibits Iron Bioavailability of Maize: Identification of an Approach to Enhance Maize Nutritional Quality via Processing and Breeding. <i>Nutrients</i> , <b>2019</b> , 11,	6.7	6
84	Genome-Wide Association Study and Pathway-Level Analysis of Kernel Color in Maize. <i>G3: Genes, Genomes, Genetics</i> , <b>2019</b> , 9, 1945-1955	3.2	10
83	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat. <i>G3: Genes, Genomes, Genetics</i> , <b>2019</b> , 9, 1231-1247	3.2	44

82	Science-graphic art partnerships to increase research impact. <i>Communications Biology</i> , <b>2019</b> , 2, 295	6.7	13
81	Millimeter-Level Plant Disease Detection From Aerial Photographs Deep Learning and Crowdsourced Data. <i>Frontiers in Plant Science</i> , <b>2019</b> , 10, 1550	6.2	31
80	Machine Learning Enables High-Throughput Phenotyping for Analyses of the Genetic Architecture of Bulliform Cell Patterning in Maize. <i>G3: Genes, Genomes, Genetics</i> , <b>2019</b> , 9, 4235-4243	3.2	6
79	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> , <b>2019</b> , 234, 119-128	5.5	12
78	Transcriptome-Wide Association Supplements Genome-Wide Association in. <i>G3: Genes, Genomes, Genetics</i> , <b>2019</b> , 9, 3023-3033	3.2	28
77	Multivariate Genome-Wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat (L.). <i>G3: Genes, Genomes, Genetics</i> , <b>2019</b> , 9, 2963-2975	3.2	20
76	In-Field Whole-Plant Maize Architecture Characterized by Subcanopy Rovers and Latent Space Phenotyping. <i>The Plant Phenome Journal</i> , <b>2019</b> , 2, 1-11	5	11
75	Autonomous Detection of Plant Disease Symptoms Directly from Aerial Imagery. <i>The Plant Phenome Journal</i> , <b>2019</b> , 2, 1-9	5	28
74	Deleterious Mutation Burden and Its Association with Complex Traits in Sorghum (). <i>Genetics</i> , <b>2019</b> , 211, 1075-1087	4	27
73	Genome-Wide Association and Genomic Prediction Models of Tocochromanols in Fresh Sweet Corn Kernels. <i>Plant Genome</i> , <b>2019</b> , 12, 180038	4.4	20
72	Multivariate Analysis of the Cotton Seed Ionome Reveals a Shared Genetic Architecture. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 1147-1160	3.2	8
71	Image set for deep learning: field images of maize annotated with disease symptoms. <i>BMC Research Notes</i> , <b>2018</b> , 11, 440	2.3	43
70	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. <i>BMC Research Notes</i> , <b>2018</b> , 11, 452	2.3	16
69	A Low-Cost Automated System for High-Throughput Phenotyping of Single Oat Seeds. <i>The Plant Phenome Journal</i> , <b>2018</b> , 1, 1-13	5	5
68	Sustaining the Future of Plant Breeding: The Critical Role of the USDA-ARS National Plant Germplasm System. <i>Crop Science</i> , <b>2018</b> , 58, 451-468	2.4	55
67	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> , <b>2017</b> , 213, 1	2.1	6
66	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> , <b>2017</b> , 100, 153-162	5.9	11
65	Nucleotide diversity in the two co-resident genomes of allopolyploid cotton. <i>Plant Systematics and Evolution</i> , <b>2017</b> , 303, 1021-1042	1.3	3

64	A community resource for exploring and utilizing genetic diversity in the USDA pea single plant plus collection. <i>Horticulture Research</i> , <b>2017</b> , 4, 17017	7.7	23
63	NLR locus-mediated trade-off between abiotic and biotic stress adaptation in Arabidopsis. <i>Nature Plants</i> , <b>2017</b> , 3, 17072	11.5	30
62	Network-Guided GWAS Improves Identification of Genes Affecting Free Amino Acids. <i>Plant Physiology</i> , <b>2017</b> , 173, 872-886	6.6	36
61	A century of guayule: Comprehensive genetic characterization of the US national guayule (Parthenium argentatum A. Gray) germplasm collection. <i>Industrial Crops and Products</i> , <b>2017</b> , 109, 300-305	5.9	20
60	Novel Loci Underlie Natural Variation in Vitamin E Levels in Maize Grain. <i>Plant Cell</i> , <b>2017</b> , 29, 2374-2392	11.6	57
59	Automated Identification of Northern Leaf Blight-Infected Maize Plants from Field Imagery Using Deep Learning. <i>Phytopathology</i> , <b>2017</b> , 107, 1426-1432	3.8	136
58	Population Structure and Phylogenetic Relationships in a Diverse Panel of L. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 321	6.2	26
57	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> , <b>2017</b> , 8, 1405	6.2	10
56	Temporal Genetic Dynamics of an Experimental, Biparental Field Population of. <i>Frontiers in Genetics</i> , <b>2017</b> , 8, 26	4.5	10
55	ZEAXANTHIN EPOXIDASE Activity Potentiates Carotenoid Degradation in Maturing Seed. <i>Plant Physiology</i> , <b>2016</b> , 171, 1837-51	6.6	31
54	Identification of haplotypes at the Rsv4 genomic region in soybean associated with durable resistance to soybean mosaic virus. <i>Theoretical and Applied Genetics</i> , <b>2016</b> , 129, 453-68	6	28
53	Chemical variation for leaf cuticular waxes and their levels revealed in a diverse panel of Brassica napus L.. <i>Industrial Crops and Products</i> , <b>2016</b> , 79, 77-83	5.9	19
52	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> , <b>2016</b> , 6, 865-79	3.3	63
51	Genetic Diversity of the Two Commercial Tetraploid Cotton Species in the Gossypium Diversity Reference Set. <i>Journal of Heredity</i> , <b>2016</b> , 107, 274-86	2.4	30
50	Population Genomic Analysis Reveals Differential Evolutionary Histories and Patterns of Diversity across Subgenomes and Subpopulations of Brassica napus L. <i>Frontiers in Plant Science</i> , <b>2016</b> , 7, 525	6.2	20
49	The Quest for Understanding Phenotypic Variation via Integrated Approaches in the Field Environment. <i>Plant Physiology</i> , <b>2016</b> , 172, 622-634	6.6	75
48	Cotton phenotyping with lidar from a track-mounted platform <b>2016</b> ,		4
47	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of Gossypium spp. <i>G3: Genes, Genomes, Genetics</i> , <b>2015</b> , 5, 1187-209	3.2	117

46	From association to prediction: statistical methods for the dissection and selection of complex traits in plants. <i>Current Opinion in Plant Biology</i> , <b>2015</b> , 24, 110-8	9.9	94
45	Proximal hyperspectral sensing and data analysis approaches for field-based plant phenomics. <i>Computers and Electronics in Agriculture</i> , <b>2015</b> , 118, 225-236	6.5	40
44	Genomic diversity and phylogenetic relationships in the genus <i>Parthenium</i> (Asteraceae). <i>Industrial Crops and Products</i> , <b>2015</b> , 76, 920-929	5.9	14
43	Molecular characterization of the Gossypium Diversity Reference Set of the US National Cotton Germplasm Collection. <i>Theoretical and Applied Genetics</i> , <b>2015</b> , 128, 313-27	6	27
42	Closing the Divide between Human Nutrition and Plant Breeding. <i>Crop Science</i> , <b>2015</b> , 55, 1437-1448	2.4	26
41	Re-evaluating the phylogeny of allopolyploid <i>Gossypium</i> L. <i>Molecular Phylogenetics and Evolution</i> , <b>2015</b> , 92, 45-52	4.1	63
40	Effects of temperature and salinity on germination of non-pelleted and pelleted guayule ( <i>Parthenium argentatum</i> A. Gray) seeds. <i>Industrial Crops and Products</i> , <b>2014</b> , 55, 90-96	5.9	9
39	Genetic diversity and population structure in the US Upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Theoretical and Applied Genetics</i> , <b>2014</b> , 127, 283-95	6	107
38	Quantitative trait locus analysis of <i>Verticillium</i> wilt resistance in an introgressed recombinant inbred population of Upland cotton. <i>Molecular Breeding</i> , <b>2014</b> , 33, 709-720	3.4	30
37	A foundation for provitamin A biofortification of maize: genome-wide association and genomic prediction models of carotenoid levels. <i>Genetics</i> , <b>2014</b> , 198, 1699-716	4	129
36	Genome size variation in guayule and mariola: Fundamental descriptors for polyploid plant taxa. <i>Industrial Crops and Products</i> , <b>2014</b> , 54, 1-5	5.9	7
35	Linkage Map Construction and Quantitative Trait Locus Analysis of Agronomic and Fiber Quality Traits in Cotton. <i>Plant Genome</i> , <b>2014</b> , 7, plantgenome2013.07.0023	4.4	48
34	Genome-wide analysis of the omega-3 fatty acid desaturase gene family in <i>Gossypium</i> . <i>BMC Plant Biology</i> , <b>2014</b> , 14, 312	5.3	33
33	The genetic architecture of maize height. <i>Genetics</i> , <b>2014</b> , 196, 1337-56	4	211
32	Genome-wide analysis of branched-chain amino acid levels in <i>Arabidopsis</i> seeds. <i>Plant Cell</i> , <b>2013</b> , 25, 4827-43	11.6	93
31	Carotenoid cleavage dioxygenase4 is a negative regulator of $\beta$ -carotene content in <i>Arabidopsis</i> seeds. <i>Plant Cell</i> , <b>2013</b> , 25, 4812-26	11.6	139
30	Development and evaluation of a field-based high-throughput phenotyping platform. <i>Functional Plant Biology</i> , <b>2013</b> , 41, 68-79	2.7	225
29	Genome-wide association study and pathway-level analysis of tocopherol levels in maize grain. <i>G3: Genes, Genomes, Genetics</i> , <b>2013</b> , 3, 1287-99	3.2	111



28	Genetic Analysis of Visually Scored Orange Kernel Color in Maize. <i>Crop Science</i> , <b>2013</b> , 53, 189-200	2.4	49
27	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> , <b>2012</b> , 83, 1-11	5.9	148
26	GAPIT: genome association and prediction integrated tool. <i>Bioinformatics</i> , <b>2012</b> , 28, 2397-9	7.2	1135
25	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , <b>2012</b> , 44, 803-7	36.3	470
24	Field-based phenomics for plant genetics research. <i>Field Crops Research</i> , <b>2012</b> , 133, 101-112	5.5	404
23	Registration of the TM-1/NM24016 Cotton Recombinant Inbred Mapping Population. <i>Journal of Plant Registrations</i> , <b>2012</b> , 6, 124-127	0.7	19
22	Complex Ploidy Level Variation in Guayule Breeding Programs. <i>Crop Science</i> , <b>2011</b> , 51, 210-216	2.4	11
21	Mixed linear model approach adapted for genome-wide association studies. <i>Nature Genetics</i> , <b>2010</b> , 42, 355-60	36.3	1259
20	A first-generation haplotype map of maize. <i>Science</i> , <b>2009</b> , 326, 1115-7	33.3	613
19	Large-Scale Discovery of Gene-Enriched SNPs. <i>Plant Genome</i> , <b>2009</b> , 2,	4.4	48
18	Status and Prospects of Association Mapping in Plants. <i>Plant Genome</i> , <b>2008</b> , 1,	4.4	818
17	Evaluation of Target Preparation Methods for Single-Feature Polymorphism Detection in Large Complex Plant Genomes. <i>Crop Science</i> , <b>2007</b> , 47, S-135	2.4	32
16	Wild relatives of potato may bolster its adaptation to new niches under future climate scenarios. <i>Food and Energy Security</i> , 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	rAmpSeq: Using repetitive sequences for robust genotyping		26
13	Elemental Accumulation in Kernels of the Maize Nested Association Mapping Panel Reveals Signals of Gene by Environment Interactions		2
12	Structure-function analysis of the maize bulliform cell cuticle and its role in dehydration and leaf rolling		1
11	Random Forest Regression for Optimizing Variable Planting Rates for Corn and Soybean Using High-Resolution Topographical and Soil Data		1



10	Eleven biosynthetic genes explain the majority of natural variation for carotenoid levels in maize grain	2
9	Machine learning enabled phenotyping for GWAS and TWAS of WUE traits in 869 field-grown sorghum accessions	1
8	Leveraging mutational burden for complex trait prediction in sorghum	3
7	Transcriptome-wide association supplements genome-wide association in Zea mays	3
6	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat	5
5	Multivariate Genome-wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat ( <i>Avena sativa</i> L.)	1
4	Genetic analysis of the transition from wild to domesticated cotton ( <i>G. hirsutum</i> L.)	2
3	In-field whole plant maize architecture characterized by Latent Space Phenotyping	3
2	Comparative evolutionary analysis and prediction of deleterious mutation patterns between sorghum and maize	1
1	Temporal Genetic Dynamics of an Experimental, Biparental Field Population of <i>Phytophthora capsici</i>	1