

Melaku A Gedil

List of Publications by Year in descending order

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77
papers

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citations

304743

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docs citations

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times ranked

2392
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#	ARTICLE	IF	CITATIONS
1	Genotype by environment interaction and grain yield stability of drought tolerant cowpea landraces in Ethiopia. <i>Euphytica</i> , 2022, 218, 1.	1.2	5
2	Optimizing use of U.S. Ex-PVP inbred lines for enhancing agronomic performance of tropical Striga resistant maize inbred lines. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	3
3	Short communication: Finetuning molecular markers for efficient selection of vitamin A-rich tropical maize lines in a molecular breeding scheme. <i>Journal of Cereal Science</i> , 2021, 97, 103149.	3.7	1
4	Heterotic grouping of tropical maize inbred lines and their hybrid performance under stem borer infestation and low soil nitrogen condition in West and Central Africa. <i>Euphytica</i> , 2021, 217, 1.	1.2	7
5	Validation of Diagnostic Markers for Streak Virus Disease Resistance in Maize. <i>Agriculture (Switzerland)</i> , 2021, 11, 130.	3.1	6
6	Assessment of diversity in tropical soybean (<i>Glycine max</i> (L.) Merr.) varieties and elite breeding lines using single nucleotide polymorphism markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2021, 19, 20-28.	0.8	5
7	Genetic diversity and population structure of early and extra-early maturing maize germplasm adapted to sub-Saharan Africa. <i>BMC Plant Biology</i> , 2021, 21, 96.	3.6	20
8	Breeding maize (<i>Zea mays</i>) for Striga resistance: Past, current and prospects in sub-Saharan africa. <i>Plant Breeding</i> , 2021, 140, 195-210.	1.9	23
9	Genetic Diversity and Population Structure of Soybean Lines Adapted to Sub-Saharan Africa Using Single Nucleotide Polymorphism (SNP) Markers. <i>Agronomy</i> , 2021, 11, 604.	3.0	17
10	Development of Extra-Early Provitamin A Quality Protein Maize Inbreds with Resistance/Tolerance to Striga hermonthica and Soil Nitrogen Stress. <i>Agronomy</i> , 2021, 11, 891.	3.0	3
11	Identifying suitable tester for evaluating Striga resistant lines using DArTseq markers and agronomic traits. <i>PLoS ONE</i> , 2021, 16, e0253481.	2.5	5
12	Marker based enrichment of provitamin A content in two tropical maize synthetics. <i>Scientific Reports</i> , 2021, 11, 14998.	3.3	7
13	Assessing performance of white endosperm testers with varying resistance reactions to Striga () Tj ETQq1 1 0.784314 rgBT /Overlock 786.	1.9	3
14	Combining Ability and Heterosis for Endosperm Carotenoids and Agronomic Traits in Tropical Maize Lines. <i>Frontiers in Plant Science</i> , 2021, 12, 674089.	3.6	4
15	Comparative Assessment of Effectiveness of Alternative Genotyping Assays for Characterizing Carotenoids Accumulation in Tropical Maize Inbred Lines. <i>Agronomy</i> , 2021, 11, 2022.	3.0	5
16	Association analysis for resistance to Striga hermonthica in diverse tropical maize inbred lines. <i>Scientific Reports</i> , 2021, 11, 24193.	3.3	15
17	Assessment of heterotic patterns of tropical low-nitrogen-tolerant maize (<i>Zea mays</i> L.) inbred lines using testcross performance, morphological traits and SNP markers. <i>Plant Breeding</i> , 2020, 139, 1113-1124.	1.9	4
18	Genomic Analysis of Selected Maize Landraces from Sahel and Coastal West Africa Reveals Their Variability and Potential for Genetic Enhancement. <i>Genes</i> , 2020, 11, 1054.	2.4	5

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19	Identification of QTLs Controlling Resistance/Tolerance to <i>Striga hermonthica</i> in an Extra-Early Maturing Yellow Maize Population. <i>Agronomy</i> , 2020, 10, 1168.	3.0	22
20	Genetic Diversity and Inter-Trait Relationships among Maize Inbreds Containing Genes from <i>Zea diploperennis</i> and Hybrid Performance under Contrasting Environments. <i>Agronomy</i> , 2020, 10, 1478.	3.0	3
21	Genetic Diversity and Population Structure of Maize Inbred Lines with Varying Levels of Resistance to <i>Striga Hermonthica</i> Using Agronomic Trait-Based and SNP Markers. <i>Plants</i> , 2020, 9, 1223.	3.5	8
22	Effectiveness of Yellow Maize Testers with Varying Resistance Reactions to <i>Striga hermonthica</i> for Evaluating the Combining Ability of Maize Inbred Lines. <i>Agronomy</i> , 2020, 10, 1276.	3.0	11
23	Identification of QTLs for grain yield and other traits in tropical maize under <i>Striga</i> infestation. <i>PLoS ONE</i> , 2020, 15, e0239205.	2.5	14
24	Contrasting Response Mechanisms of Maize Lines to <i>Striga hermonthica</i> . <i>Agriculture (Switzerland)</i> , 2020, 10, 485.	3.1	1
25	Assessing Effect of Marker-Based Improvement of Maize Synthetics on Agronomic Performance, Carotenoid Content, Combining Ability and Heterosis. <i>Agronomy</i> , 2020, 10, 1625.	3.0	6
26	Genome-wide association study of <i>Striga</i> resistance in early maturing white tropical maize inbred lines. <i>BMC Plant Biology</i> , 2020, 20, 203.	3.6	29
27	Genetic dissection of yield associated traits in a cross between cowpea and yard-long bean (<i>Vigna</i>) Tj ETQq1 1 0.784314 rgBT ₁₁ /Overlo 0.7	0.7	11
28	Quantitative trait loci mapping for resistance to maize streak virus in F2:3 population of tropical maize. <i>Cereal Research Communications</i> , 2020, 48, 195-202.	1.6	3
29	Identification of candidate flowering and sex genes in white Guinea yam (<i>D. rotundata</i> Poir.) by SuperSAGE transcriptome profiling. <i>PLoS ONE</i> , 2019, 14, e0216912.	2.5	16
30	Genetic diversity and population structure of early-maturing tropical maize inbred lines using SNP markers. <i>PLoS ONE</i> , 2019, 14, e0214810.	2.5	45
31	Yield gains and associated changes in an early yellow bi-parental maize population following genomic selection for <i>Striga</i> resistance and drought tolerance. <i>BMC Plant Biology</i> , 2019, 19, 129.	3.6	19
32	Assessment of genetic diversity among low-nitrogen-tolerant early generation maize inbred lines using SNP markers. <i>South African Journal of Plant and Soil</i> , 2019, 36, 181-188.	1.1	8
33	Public sector soybean (<i>Glycine max</i>) breeding: Advances in cultivar development in the African tropics. <i>Plant Breeding</i> , 2019, 138, 455-464.	1.9	11
34	An Integrated Molecular and Conventional Breeding Scheme for Enhancing Genetic Gain in Maize in Africa. <i>Frontiers in Plant Science</i> , 2019, 10, 1430.	3.6	40
35	Genetic Loci Controlling Carotenoid Biosynthesis in Diverse Tropical Maize Lines. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1049-1065.	1.8	26
36	Effectiveness of predictive markers for marker assisted selection of pro-vitamin A carotenoids in medium-late maturing maize (<i>Zea mays</i> L.) inbred lines. <i>Journal of Cereal Science</i> , 2018, 79, 27-34.	3.7	26

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37	Optimizing sample size for molecular characterization of open-pollinated maize (<i>Zea mays</i> L.) varieties using simple sequence repeat markers. <i>Cereal Research Communications</i> , 2018, 46, 569-579.	1.6	1
38	Genetic diversity and population structure of a mini-core subset from the world cowpea (<i>Vigna</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70	3.3	63
39	Mapping of QTLs associated with recovery resistance to streak virus disease in maize. <i>Annals of Agricultural Sciences</i> , 2018, 63, 115-121.	2.9	7
40	Genetic Basis and Breeding Perspectives of Grain Iron and Zinc Enrichment in Cereals. <i>Frontiers in Plant Science</i> , 2018, 9, 937.	3.6	117
41	Identification of Quantitative Trait Loci for Grain Yield and Other Traits in Tropical Maize Under High and Low Soil Nitrogen Environments. <i>Crop Science</i> , 2018, 58, 321-331.	1.8	25
42	Correlation and Path Coefficient Analyses of Cowpea (&i>Vigna) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 547 Td (unguicular 2794-2812.	0.8	5
43	Morphological, SSR and ploidy analysis of water yam (<i>Dioscorea alata</i> L.) accessions for utilization of aerial tubers as planting materials. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 291-305.	1.6	16
44	Genetic divergence in two tropical maize composites after four cycles of reciprocal recurrent selection. <i>Plant Breeding</i> , 2017, 136, 41-49.	1.9	12
45	Genetic diversity of tropical maize inbred lines combining resistance to <i>Striga hermonthica</i> with drought tolerance using SNP markers. <i>Plant Breeding</i> , 2017, 136, 338-343.	1.9	24
46	Candidate gene sequencing and validation of SNP markers linked to carotenoid content in cassava (<i>Manihot esculenta</i> Crantz). <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	15
47	Genetic diversity and population structure of <i>Striga hermonthica</i> populations from Kenya and Nigeria. <i>Weed Research</i> , 2017, 57, 293-302.	1.7	23
48	Genetic Gains in Yield and Yield Related Traits under Drought Stress and Favorable Environments in a Maize Population Improved Using Marker Assisted Recurrent Selection. <i>Frontiers in Plant Science</i> , 2017, 8, 808.	3.6	45
49	Genetic Gains in Grain Yield of a Maize Population Improved through Marker Assisted Recurrent Selection under Stress and Non-stress Conditions in West Africa. <i>Frontiers in Plant Science</i> , 2017, 8, 841.	3.6	32
50	Genome Wide Association Mapping of Correlated Traits in Cassava: Dry Matter and Total Carotenoid Content. <i>Plant Genome</i> , 2017, 10, plantgenome2016.09.0094.	2.8	63
51	Genome sequencing of the staple food crop white Guinea yam enables the development of a molecular marker for sex determination. <i>BMC Biology</i> , 2017, 15, 86.	3.8	114
52	Heterotic Patterns of IITA and CIMMYT Early Maturing Yellow Maize Inbreds under Contrasting Environments. <i>Agronomy Journal</i> , 2016, 108, 1321-1336.	1.8	27
53	DNA barcoding of the main cultivated yams and selected wild species in the genus <i>Dioscorea</i> . <i>Journal of Systematics and Evolution</i> , 2016, 54, 228-237.	3.1	15
54	Tracking crop varieties using genotyping-by-sequencing markers: a case study using cassava (<i>Manihot</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70	2.7	83

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55	Heterotic responses among crosses of IITA and CIMMYT early white maize inbred lines under multiple stress environments. <i>Euphytica</i> , 2015, 206, 245-262.	1.2	24
56	Diversity assessment of drought tolerant exotic and adapted maize (<i>Zea mays</i> L.) inbred lines with microsatellite markers. <i>Journal of Crop Science and Biotechnology</i> , 2015, 18, 147-154.	1.5	11
57	Biotechnology Success Stories by the Consultative Group on International Agriculture Research (CGIAR) System. <i>Science Policy Reports</i> , 2014, , 95-114.	0.1	4
58	High-resolution mapping of resistance to cassava mosaic geminiviruses in cassava using genotyping-by-sequencing and its implications for breeding. <i>Virus Research</i> , 2014, 186, 87-96.	2.2	143
59	Next-generation sequencing based genotyping, cytometry and phenotyping for understanding diversity and evolution of guinea yams. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1783-1794.	3.6	59
60	Carotenoid accumulation and agronomic performance of maize hybrids involving parental combinations from different marker-based groups. <i>Food Chemistry</i> , 2014, 148, 131-137.	8.2	34
61	Genetic Mapping Using Genotyping-by-sequencing in the Clonally Propagated Cassava. <i>Crop Science</i> , 2014, 54, 1384-1396.	1.8	50
62	Marker-trait association analysis of functional gene markers for provitamin A levels across diverse tropical yellow maize inbred lines. <i>BMC Plant Biology</i> , 2013, 13, 227.	3.6	93
63	Molecular Markers and Their Application to Cassava Breeding: Past, Present and Future. <i>Tropical Plant Biology</i> , 2012, 5, 95-109.	1.9	34
64	<i>Dioscorea</i> . , 2011, , 71-96.		15
65	Draft genome sequence of the oilseed species <i>Ricinus communis</i> . <i>Nature Biotechnology</i> , 2010, 28, 951-956.	17.5	449
66	Relationship of Genetic Diversity of Inbred Lines with Different Reactions to <i>Striga hermonthica</i> (Del.) Benth and the Performance of Their Crosses. <i>Crop Science</i> , 2010, 50, 602-611.	1.8	36
67	Genetic differentiation analysis of African cassava (<i>Manihot esculenta</i>) landraces and elite germplasm using amplified fragment length polymorphism and simple sequence repeat markers. <i>Annals of Applied Biology</i> , 2009, 155, 187-199.	2.5	21
68	KIR3DL2: diversity in a hematopoietic stem cell transplant population. <i>Tissue Antigens</i> , 2007, 70, 228-232.	1.0	12
69	Genomic characterization of KIR2DL4 in families and unrelated individuals reveals extensive diversity in exon and intron sequences including a common frameshift variation occurring in several alleles. <i>Tissue Antigens</i> , 2005, 65, 402-418.	1.0	22
70	Candidate disease resistance genes in sunflower cloned using conserved nucleotide-binding site motifs: Genetic mapping and linkage to the downy mildew resistance gene <i>Pl1</i> . <i>Genome</i> , 2001, 44, 205-212.	2.0	16
71	An integrated restriction fragment length polymorphism - amplified fragment length polymorphism linkage map for cultivated sunflower. <i>Genome</i> , 2001, 44, 213-221.	2.0	22
72	Perspectives on the Application of Next-generation Sequencing to the Improvement of Africa's Staple Food Crops. , 0, , .		1

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73	Effects of drought stress on grain yield, agronomic performance, and heterosis of marker-based improved provitamin-A maize synthetics and their hybrids. <i>Journal of Crop Improvement</i> , 0, , 1-21.	1.7	1
74	Efficacy of maize inbred testers with varying levels of resistance to Striga for classifying Striga-resistant yellow-maize lines into heterotic groups. <i>Journal of Crop Improvement</i> , 0, , 1-21.	1.7	2
75	Mutagen Identification and Molecular Analysis of Pro-vitamin A Carotenoid Genes in Cassava (<i>Manihot esculenta</i> Crantz). <i>Molecular Plant Breeding</i> , 0, , .	0.0	1
76	Developing and deploying an efficient genotyping workflow for accelerating maize improvement in developing countries. <i>Gates Open Research</i> , 0, 6, 3.	1.1	0
77	Developing and deploying an efficient genotyping workflow for accelerating maize improvement in developing countries. <i>Gates Open Research</i> , 0, 6, 3.	1.1	0