

# CITATION REPORT

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**Maize inbreds exhibit high levels of copy number variation (CNV) and presence/absence variation (PAV) in genome content**

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#	Paper	IF	Citations
458	Detailed analysis of a contiguous 22-Mb region of the maize genome. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000728	6	34
457	Copy number variation shapes genome diversity in Arabidopsis over immediate family generational scales. <b>2010</b> , 2, 441-53		117
456	Divergence of gene regulation through chromosomal rearrangements. <i>BMC Genomics</i> , <b>2010</b> , 11, 678	4.5	15
455	Structure and expression of the maize ( <i>Zea mays</i> L.) SUN-domain protein gene family: evidence for the existence of two divergent classes of SUN proteins in plants. <b>2010</b> , 10, 269		66
454	Genetically modified myths and realities. <b>2010</b> , 27, 545-51		22
453	Repeat subtraction-mediated sequence capture from a complex genome. <i>Plant Journal</i> , <b>2010</b> , 62, 898-909	4.9	73
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451	Rice structural variation: a comparative analysis of structural variation between rice and three of its closest relatives in the genus <i>Oryza</i> . <i>Plant Journal</i> , <b>2010</b> , 63, 990-1003	6.9	38
450	Genome-wide patterns of genetic variation among elite maize inbred lines. <b>2010</b> , 42, 1027-30		365
449	Gene copy-number polymorphism in nature. <b>2010</b> , 277, 3213-21		106
448	High-throughput genetic mapping of mutants via quantitative single nucleotide polymorphism typing. <i>Genetics</i> , <b>2010</b> , 184, 19-26	4	56
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170	Variational Inference for Coupled Hidden Markov Models Applied to the Joint Detection of Copy Number Variations. <b>2019</b> , 15,		3
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165	Connecting genome structural variation with complex traits in crop plants. <b>2019</b> , 132, 733-750		53
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162	Modeling copy number variation in the genomic prediction of maize hybrids. <b>2019</b> , 132, 273-288		7
161	An updated gene atlas for maize reveals organ-specific and stress-induced genes. <i>Plant Journal</i> , <b>2019</b> , 97, 1154-1167	6.9	54
160	Gene copy number variations involved in balsam poplar ( <i>Populus balsamifera</i> L.) adaptive variations. <b>2019</b> , 28, 1476-1490		12
159	Genomic sequence and copy number evolution during hybrid crop development in sunflowers. <b>2019</b> , 12, 54-65		18
158	A high-quality cucumber genome assembly enhances computational comparative genomics. <b>2020</b> , 295, 177-193		21
157	The pomegranate ( <i>Punica granatum</i> L.) draft genome dissects genetic divergence between soft- and hard-seeded cultivars. <b>2020</b> , 18, 955-968		29
156	Genes and gene models, an important distinction. <b>2020</b> , 228, 50-55		6
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154	The hybrid protein interactome contributes to rice heterosis as epistatic effects. <i>Plant Journal</i> , <b>2020</b> , 102, 116-128	6.9	6

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152	Haplotype structure in commercial maize breeding programs in relation to key founder lines. <b>2020</b> , 133, 547-561		7
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150	Prospects of next generation sequencing in lentil breeding. <b>2020</b> , 47, 9043-9053		3
149	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. <b>2020</b> , 21, 275		42
148	Improved Brassica oleracea JZS assembly reveals significant changing of LTR-RT dynamics in different morphotypes. <b>2020</b> , 133, 3187-3199		14
147	European maize genomes highlight intraspecies variation in repeat and gene content. <b>2020</b> , 52, 950-957		34
146	Pangenomics in Crop Plants. <b>2020</b> , 1		1
145	Genome-wide variations analysis of sorghum cultivar Hongyingzi for brewing Moutai liquor. <b>2020</b> , 157, 19		3
144	High-quality chromosome-scale assembly of the walnut ( <i>Juglans regia</i> L.) reference genome. <b>2020</b> , 9,		33
143	CNVmap: A Method and Software To Detect and Map Copy Number Variants from Segregation Data. <i>Genetics</i> , <b>2020</b> , 214, 561-576	4	1
142	A 62K genic-SNP chip array for genetic studies and breeding applications in pigeonpea ( <i>Cajanus cajan</i> L. Millsp.). <b>2020</b> , 10, 4960		11
141	Low Long Terminal Repeat (LTR)-Retrotransposon Expression in Leaves of the Marine Phanerogam L. <b>2020</b> , 10,		2
140	Presence-absence polymorphisms of single-copy genes in the stony coral <i>Acropora digitifera</i> . <i>BMC Genomics</i> , <b>2020</b> , 21, 158	4.5	3
139	A computational genome-wide analysis of long terminal repeats retrotransposon expression in sunflower roots ( <i>Helianthus annuus</i> L.). <b>2020</b> , 148, 13-23		7
138	Segmental duplications are hot spots of copy number variants affecting barley gene content. <i>Plant Journal</i> , <b>2020</b> , 103, 1073-1088	6.9	3
137	Patterns of presence-absence variants in Upland cotton. <b>2020</b> , 63, 1600-1603		1
136	Pan-genomics of plants and its applications. <b>2020</b> , 285-306		1

135	AthCNV: A Map of DNA Copy Number Variations in the Arabidopsis Genome. <b>2020</b> , 32, 1797-1819		13
134	Assembly of Transcriptomes From a B73 Maize Line Introgressed With a QTL for Resistance to Gray Leaf Spot Disease Reveals a Candidate Allele of a Lectin Receptor-Like Kinase. <b>2020</b> , 11, 191		2
133	Fungal evolution: cellular, genomic and metabolic complexity. <b>2020</b> , 95, 1198-1232		27
132	New resources for genetic studies in maize ( <i>Zea mays</i> L.): a genome-wide Maize6H-60K single nucleotide polymorphism array and its application. <i>Plant Journal</i> , <b>2021</b> , 105, 1113-1122	6.9	2
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130	Single-parent expression drives dynamic gene expression complementation in maize hybrids. <i>Plant Journal</i> , <b>2021</b> , 105, 93-107	6.9	5
129	A copy number variant at the HPDA-D12 locus confers compact plant architecture in cotton. <b>2021</b> , 229, 2091-2103		8
128	Genetic Variation and Unintended Risk in the Context of Old and New Breeding Techniques. <b>2021</b> , 40, 68-108		5
127	Induced Mutagenesis in Date Palm ( <i>Phoenix dactylifera</i> L.) Breeding. <b>2021</b> , 121-154		
126	How the pan-genome is changing crop genomics and improvement. <b>2021</b> , 22, 3		43
125	Transcriptome-wide analysis of epitranscriptome and translational efficiency associated with heterosis in maize. <b>2021</b> , 72, 2933-2946		7
124	Reference-based QUantification Of gene Dispensability (QUOD). <b>2021</b> , 17, 18		2
123	Large-scale reconstruction of chromatin structures of maize temperate and tropical inbred lines. <b>2021</b> , 72, 3582-3596		0
122	Crop pangenomes.. <b>2021</b> , 25, 57-63		5
121	Genome assembly of the maize inbred line A188 provides a new reference genome for functional genomics.		
120	Stability of DNA methylation and chromatin accessibility in structurally diverse maize genomes.		
119	Oxford Nanopore and Bionano Genomics technologies evaluation for plant structural variation detection.		0
118	A heterochromatic knob reducing the flowering time in maize.		2

117	Widespread imprinting of transposable elements and variable genes in the maize endosperm. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009491	6	2
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114	Heterosis in Genomic Era: Advances in the Molecular Understanding and Techniques for Rapid Exploitation. <b>2021</b> , 40, 218-242		0
113	Genomic variation within the maize stiff-stalk heterotic germplasm pool. <b>2021</b> , 14, e20114		1
112	Shaping the biology of citrus: I. Genomic determinants of evolution. <b>2021</b> , 14, e20104		2
111	Quantitative resistance loci to southern rust mapped in a temperate maize diversity panel. <b>2021</b> ,		2
110	Stimulatory Effects of Androgens on Eel Primary Ovarian Development - from Phenotypes to Genotypes.		
109	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <b>2021</b> , 373, 655-662		40
108	Genome assembly of the maize inbred line A188 provides a new reference genome for functional genomics. <b>2021</b> , 10, 47-47		3
107	Megabase-scale presence-absence variation with <i>Tripsacum</i> origin was under selection during maize domestication and adaptation. <b>2021</b> , 22, 237		6
106	In silico analysis enabling informed design for genome editing in medicinal cannabis; gene families and variant characterisation. <i>PLoS ONE</i> , <b>2021</b> , 16, e0257413	3-7	3
105	GWAS for genetics of complex quantitative traits: Genome to pangenome and SNPs to SVs and k-mers. <b>2021</b> , 43, e2100109		1
104	Resistance to Biotic Stress: Theory and Applications in Maize Breeding. <b>2021</b> , 129-175		1
103	Calling large indels in 1047 Arabidopsis with IndelEnsembler. <b>2021</b> , 49, 10879-10894		1
102	Genomics of Long- and Short-Term Adaptation in Maize and Teosintes. <b>2020</b> , 2090, 289-311		3
101	Genome Evolution and Polyploidy. <b>2016</b> , 233-269		1
100	Rapid, Affordable, and Scalable Genotyping for Germplasm Exploration in Maize. <b>2018</b> , 31-46		3

99	Association Mapping of Genetic Resources: Achievements and Future Perspectives. <b>2014</b> , 207-235		21
98	Maize genome mapped.		3
97	Chromosome-scale genome assembly provides insights into rye biology, evolution, and agronomic potential.		10
96	Tandem Duplicate Genes in Maize are Abundant and Date to Two Distinct Periods of Time.		1
95	Genotyping-by-sequencing and SNP-arrays are complementary for detecting quantitative trait loci by tagging different haplotypes in association studies.		1
94	Genome wide analysis of Ga1-s modifiers in maize.		1
93	Transposable elements contribute to dynamic genome content in maize.		5
92	Non-Homology-Based Prediction of Gene Functions.		2
91	European maize genomes unveil pan-genomic dynamics of repeats and genes.		3
90	CNVmap: a method and software to detect and map copy number variants from segregation data.		1
89	High-quality chromosome-scale assembly of the walnut ( <i>Juglans regia</i> L) reference genome.		2
88	Maize nested introgression library provides evidence for the involvement of <i>flguleless1</i> in resistance to northern leaf blight.		1
87	Maize ( <i>Zea mays</i> L.) Genome Diversity as Revealed by RNA-Sequencing. <b>2014</b> , 329-356		1
86	Whole-genome resequencing: Current status and future prospects in genomics-assisted crop improvement. <b>2016</b> , 187-211		2
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84	Independent introductions and admixtures have contributed to adaptation of European maize and its American counterparts. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006666	6	45
83	High-resolution genotyping via whole genome hybridizations to microarrays containing long oligonucleotide probes. <i>PLoS ONE</i> , <b>2010</b> , 5, e14178	3.7	10
82	A large maize ( <i>Zea mays</i> L.) SNP genotyping array: development and germplasm genotyping, and genetic mapping to compare with the B73 reference genome. <i>PLoS ONE</i> , <b>2011</b> , 6, e28334	3.7	422

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