

Genome sequencing of adzuki bean (*Vigna angularis*)
starch and low fat accumulation and domestication

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Proteomics and Metabolomics: Two Emerging Areas for Legume Improvement. <i>Frontiers in Plant Science</i> , 2015, 6, 1116.	1.7	112
2	Development of a high-density genetic linkage map and identification of flowering time QTLs in adzuki bean (<i>Vigna angularis</i>). <i>Scientific Reports</i> , 2016, 6, 39523.	1.6	20
3	Comprehensive analysis and discovery of drought-related NAC transcription factors in common bean. <i>BMC Plant Biology</i> , 2016, 16, 193.	1.6	36
4	Integrated "omics" approaches to sustain global productivity of major grain legumes under heat stress. <i>Plant Breeding</i> , 2017, 136, 437-459.	1.0	36
5	Genome resources for climate-resilient cowpea, an essential crop for food security. <i>Plant Journal</i> , 2017, 89, 1042-1054.	2.8	199
6	Phylogenomics: The Evolution of Common Bean as Seen from the Perspective of All of Its Genes. <i>Compendium of Plant Genomes</i> , 2017, , 263-287.	0.3	0
8	Identification of QTL and Qualitative Trait Loci for Agronomic Traits Using SNP Markers in the Adzuki Bean. <i>Frontiers in Plant Science</i> , 2017, 8, 840.	1.7	26
9	Genome-Wide Association Study Identifies NBS-LRR-Encoding Genes Related with Anthracnose and Common Bacterial Blight in the Common Bean. <i>Frontiers in Plant Science</i> , 2017, 8, 1398.	1.7	56
10	Food Legumes and Rising Temperatures: Effects, Adaptive Functional Mechanisms Specific to Reproductive Growth Stage and Strategies to Improve Heat Tolerance. <i>Frontiers in Plant Science</i> , 2017, 8, 1658.	1.7	146
11	De novo transcriptomic analysis of cowpea (<i>Vigna unguiculata</i> L. Walp.) for genic SSR marker development. <i>BMC Genetics</i> , 2017, 18, 65.	2.7	28
12	Salt and drought stress and ABA responses related to bZIP genes from <i>V. radiata</i> and <i>V. angularis</i> . <i>Gene</i> , 2018, 651, 152-160.	1.0	43
13	Accelerating genetic gains in legumes for the development of prosperous smallholder agriculture: integrating genomics, phenotyping, systems modelling and agronomy. <i>Journal of Experimental Botany</i> , 2018, 69, 3293-3312.	2.4	87
14	Legume Cytosolic and Plastid Acetyl-Coenzyme A Carboxylase Genes Differ by Evolutionary Patterns and Selection Pressure Schemes Acting before and after Whole-Genome Duplications. <i>Genes</i> , 2018, 9, 563.	1.0	10
15	WRKY transcription factors in legumes. <i>BMC Plant Biology</i> , 2018, 18, 243.	1.6	66
16	Sequencing Plant Genomes. <i>Progress in Botany Fortschritte Der Botanik</i> , 2018, , 109-193.	0.1	4
17	Trends in herbgonomics. <i>Science China Life Sciences</i> , 2019, 62, 288-308.	2.3	46
18	OUP accepted manuscript. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	9
19	Insight Into the Prospects for the Improvement of Seed Starch in Legume" A Review. <i>Frontiers in Plant Science</i> , 2019, 10, 1213.	1.7	29

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20	Construction of a high density linkage map and genome dissection of bruchid resistance in zombi pea (<i>Vigna vexillata</i> (L.) A. Rich). <i>Scientific Reports</i> , 2019, 9, 11719.	1.6	15
21	Neglected treasures in the wild " legume wild relatives in food security and human health. <i>Current Opinion in Plant Biology</i> , 2019, 49, 17-26.	3.5	45
22	The characteristic of <i>Arachis duranensis</i> -specific genes and their potential function. <i>Gene</i> , 2019, 705, 60-66.	1.0	2
23	The genome of cowpea (<i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	2.8	264
24	Herbgenomics: A stepping stone for research into herbal medicine. <i>Science China Life Sciences</i> , 2019, 62, 913-920.	2.3	22
26	Effects of multiple N, P, and K fertilizer combinations on adzuki bean (<i>Vigna angularis</i>) yield in a semi-arid region of northeastern China. <i>Scientific Reports</i> , 2019, 9, 19408.	1.6	16
27	The future of legume genetic data resources: Challenges, opportunities, and priorities. , 2019, 1, e16.		30
28	The draft genomes of five agriculturally important African orphan crops. <i>GigaScience</i> , 2019, 8, .	3.3	108
29	Computational identification of receptor-like kinases "RLK" and receptor-like proteins "RLP" in legumes. <i>BMC Genomics</i> , 2020, 21, 459.	1.2	16
30	Breaks of macrosynteny and collinearity among moth bean (<i>Vigna aconitifolia</i>), cowpea (<i>V. Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS</i>)	2.0	10
31	Characterization of Drought-Responsive Transcriptome During Seed Germination in Adzuki Bean (<i>Vigna angularis</i> L.) by PacBio SMRT and Illumina Sequencing. <i>Frontiers in Genetics</i> , 2020, 11, 996.	1.1	16
32	Genomic interventions for sustainable agriculture. <i>Plant Biotechnology Journal</i> , 2020, 18, 2388-2405.	4.1	71
33	Identification and Validation of Reference Genes in the Adzuki Bean (<i>Vigna angularis</i>) Under Iron Deficiency Using Quantitative Real-Time PCR. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 250-261.	1.0	2
34	Polyploidization events shaped the transcription factor repertoires in legumes (Fabaceae). <i>Plant Journal</i> , 2020, 103, 726-741.	2.8	17
35	A chromosome-scale assembly of the black gram (<i>Vigna mungo</i>) genome. <i>Molecular Ecology Resources</i> , 2021, 21, 238-250.	2.2	33
36	Orthology and syntenic analysis of receptor-like kinases "RLK" and receptor-like proteins "RLP" in legumes. <i>BMC Genomics</i> , 2021, 22, 113.	1.2	4
37	Genetic analysis of seed coat colour in adzuki bean (<i>Vigna angularis</i> L.). <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2021, 19, 67-73.	0.4	7
38	Genomic resources for lupins are coming of age. , 2021, 3, e77.		5

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39	Comprehensive analysis and identification of drought-responsive candidate NAC genes in three semi-arid tropics (SAT) legume crops. <i>BMC Genomics</i> , 2021, 22, 289.	1.2	11
40	Draft genome sequence of the pulse crop blackgram [<i>Vigna mungo</i> (L.) Hepper] reveals potential R-genes. <i>Scientific Reports</i> , 2021, 11, 11247.	1.6	20
41	Recent developments in <i>Lablab purpureus</i> genomics: A focus on drought stress tolerance and use of genomic resources to develop stress-resilient varieties. , 2021, 3, e99.		16
42	Construction of a high-density adzuki bean genetic map and evaluation of its utility based on a QTL analysis of seed size. <i>Journal of Integrative Agriculture</i> , 2021, 20, 1753-1761.	1.7	2
43	VaSDC1 Is Involved in Modulation of Flavonoid Metabolic Pathways in Black and Red Seed Coats in Adzuki Bean (<i>Vigna angularis</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 679892.	1.7	10
44	Adzuki Bean (<i>Vigna angularis</i> (Willd.) Ohwi & Ohashi) Breeding. , 2019, , 1-23.		4
45	GWAS and Genomic Approaches in Legumes, an Expanding Toolkit for Examining Responses to Abiotic Stresses. , 2020, , 161-180.		3
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49	Genome, Transcriptome, and Germplasm Sequencing Uncovers Functional Variation in the Warm-Season Grain Legume Horsegram <i>Macrotyloma uniflorum</i> (Lam.) Verdc.. <i>Frontiers in Plant Science</i> , 2021, 12, 758119.	1.7	7
51	Updates on Legume Genome Sequencing. <i>Methods in Molecular Biology</i> , 2020, 2107, 1-18.	0.4	6
52	The chromosome-level genome assembly of <i>Astragalus sinicus</i> and comparative genomic analyses provide new resources and insights for understanding legume-rhizobial interactions. <i>Plant Communications</i> , 2022, 3, 100263.	3.6	11
54	<i>Flowering Date1</i>, a major photoperiod sensitivity gene in adzuki bean, is a soybean floral repressor <i>E1</i> ortholog. <i>Breeding Science</i> , 2022, 72, 132-140.	0.9	2
55	Bioinformatics characterization of patatin-related phospholipase A (pPLA) gene family in agriculturally important crops viz <i>Vigna radiata</i> , <i>Vigna angularis</i> , and <i>Glycine max</i> . <i>Biologia (Poland)</i> , 2022, 77, 1429.	0.8	0
56	Beyond a reference genome: pangenomes and population genomics of underutilized and orphan crops for future food and nutrition security. <i>New Phytologist</i> , 2022, 234, 1583-1597.	3.5	23
57	Progress of Genomics-Driven Approaches for Sustaining Underutilized Legume Crops in the Post-Genomic Era. <i>Frontiers in Genetics</i> , 2022, 13, 831656.	1.1	8
58	iTRAQ based protein profile analysis revealed key proteins involved in regulation of drought-tolerance during seed germination in Adzuki bean. <i>Scientific Reports</i> , 2021, 11, 23725.	1.6	5
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63	Orphan legumes: harnessing their potential for food, nutritional and health security through genetic approaches. <i>Planta</i> , 2022, 256, .	1.6	6
64	A pan-genome and chromosome-length reference genome of narrow-leaved lupin (<i>Lupinus</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Journal</i> , 0, , .	2.8	9
65	Genome-wide analyses of the mung bean NAC gene family reveals orthologs, co-expression networking and expression profiling under abiotic and biotic stresses. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	15
66	Genetic Improvement of Minor Crop Legumes: Prospects of <i>De Novo</i> Domestication. , 0, , .		1
67	Microscopic and ultramicroscopic anatomical characteristics of root nodules in <i>Podocarpus macrophyllus</i> during development. <i>Nordic Journal of Botany</i> , 2022, 2022, .	0.2	1
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70	Genomic analyses of rice bean landraces reveal adaptation and yield related loci to accelerate breeding. <i>Nature Communications</i> , 2022, 13, .	5.8	13
71	The Bambara Groundnut Genome. <i>Compendium of Plant Genomes</i> , 2022, , 189-215.	0.3	1
72	Histological and molecular responses of <i>Vigna angularis</i> to <i>Uromyces vignae</i> infection. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5
74	Vignette of <i>Vigna</i> domestication: From archives to genomics. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
75	Genome-wide comparative and evolutionary analysis of transposable elements in eight different legume plants. , 2020, 90, 1025-1031.		0
77	Investigate large gaps and improve genetic map in narrow-leaved lupin (<i>Lupinus angustifolius</i> L.). <i>Euphytica</i> , 2023, 219, .	0.6	0
78	<i>Plant Genomics</i> . , 2022, , 1-9.		0
79	Genome-Wide Identification of Aquaporin Genes in Adzuki Bean (<i>Vigna angularis</i>) and Expression Analysis under Drought Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 16189.	1.8	3
80	Vegetable biology and breeding in the genomics era. <i>Science China Life Sciences</i> , 2023, 66, 226-250.	2.3	10
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83	Legume-wide comparative analysis of pod shatter locus <i>PDH1</i> reveals phaseoloid specificity, high cowpea expression, and stress responsive genomic context. <i>Plant Journal</i> , 2023, 115, 68-80.	2.8	5
84	Plant domestication: setting biological clocks. <i>Trends in Plant Science</i> , 2023, 28, 597-608.	4.3	3
86	Comprehensive genomic analyses of <i>Vigna unguiculata</i> provide insights into population differentiation and the genetic basis of key agricultural traits. <i>Plant Biotechnology Journal</i> , 2023, 21, 1426-1439.	4.1	2
87	Divergent contributions of coding and noncoding sequences to initial high-altitude adaptation in passerine birds endemic to the Qinghai-Tibet Plateau. <i>Molecular Ecology</i> , 2023, 32, 3524-3540.	2.0	3
88	Genome-wide analysis of key gene families in RNA silencing and their responses to biotic and drought stresses in adzuki bean. <i>BMC Genomics</i> , 2023, 24, .	1.2	0
89	Unique Salt-Tolerance-Related QTLs, Evolved in <i>Vigna riukuensis</i> (Na ⁺ Includer) and <i>V. nakashimae</i> (Na ⁺) Tj ETQq0 0 0 rgBT /Overlock 15 Plants, 2023, 12, 1680.	1.6	0
90	Identification and expression analysis of SQUAMOSA-promoter-binding protein (SBP) genes in mungbean. <i>Plant Biotechnology Reports</i> , 0, , .	0.9	0