

Genomic Insights from Chickpea Super-Pangenome

SHENZHEN, CHINA, June 28, 2024 /EINPresswire.com/ -- A comprehensive super-pangenome of chickpea (Cicer arietinum) has been assembled, providing a detailed view of the species' genetic diversity. This genomic resource, published in *Nature Genetics*, offers valuable insights into the evolution and agronomic trait loci of chickpea, which is a major legume crop. The study identifies numerous genes and regulatory elements associated with important traits such as yield, drought tolerance, and disease resistance. The super-pangenome consists of 17 chromosomes and contains over 100,000 genes, including many previously unannotated ones. This resource will be instrumental in breeding improved chickpea varieties and understanding the genetic architecture of this important crop.

The study, led by researchers from BGI-Research, involved sequencing and assembling genomes from eight wild chickpea accessions. The resulting super-pangenome provides a comprehensive view of the chickpea genome, including regions that were previously missing from reference genomes. Key findings include the identification of novel genes and regulatory elements, as well as the discovery of structural variants and copy number variations. The researchers also identified several genes that are highly conserved across the accessions, suggesting their importance in chickpea biology. The super-pangenome will be a valuable resource for researchers and breeders alike, enabling a better understanding of chickpea genetics and the development of improved crop varieties. The study was published in *Nature Genetics* on May 23, 2024.

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Cicer super-pangenome provides insights into species evolution and agronomic trait loci for crop improvement in chickpea

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Table 1 | Statistical features of eight wild *Cicer* genomes

Assembly	<i>C. reticulatum</i>	<i>C. echinospermum</i>	<i>C. bijugum</i>	<i>C. judaicum</i>	<i>C. pinnatifidum</i>	<i>C. yamashitae</i>	<i>C. chorassanicum</i>	<i>C. cuneatum</i>
Total assembly size (Mb)	895.25	734.27	434.97	466.6	643.91	545.79	566.76	565.22
Number of scaffolds	33,080	3,445	1,832	1,324	30,683	22,096	11,728	2,038
Longest scaffold (Mb)	109.19	107.65	26.36	30.7	78.63	68.6	75.74	82.85
Number of scaffolds >10 Mb	8	8	11	12	8	9	8	8
N50 scaffold length (Mb)	60.33	92.71	6.76	9.24	53.1	54.71	59.62	75.06
Assembly anchored in pseudomolecules (%)	65.23	88.32	-	-	71	83.85	83.22	99.32
Total transposable element ratio (%)	58.9	51.37	49.64	52.02	56.21	44.12	47.89	56.6
GC content (%)	32.89	32.29	30.05	30.84	32.04	31.75	31.86	32.55
Number of genes	28,627	276,49	23,911	23,516	24,716	25,579	26,993	23,890
Mean gene length (bp)	4,293.5	4,362.46	4,582.07	4,578.58	4,551.47	4,593.59	4,671.78	4,435.23
Number of annotated genes	28,047	27,323	23,730	23,314	24,490	25,113	26,515	23,630
Number of miRNA genes	106	101	87	87	98	87	95	86
Number of tRNA genes	865	696	644	600	791	687	643	701
Number of rRNA genes	3,878	4,532	1,391	1,576	2,827	69,699	7,663	1,151
Number of snoRNA genes	813	776	682	603	824	592	636	666
Number of pseudogenes	1,297	1,252	700	811	881	920	1,141	1,173

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