

Genotypic and Phenotypic Variation in the Global Collection of Chickpea (*Cicer aritenum* L.)

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ABOUT CHICKPEA

Worldwide chickpea is the 4th largest grain-legume crop – area 11.2 million ha, production 9.2 million tons, and productivity 0.82 t ha⁻¹ (FAO 2005). Chickpea is grown in 40 countries (with area exceeding 10,000 ha). Chickpea productivity consistently increased in India and Mexico while it declined in many other countries. Two types of chickpeas – *desi* – widely grown in South Asia and Africa and *Kabuli* – widely grown in Mediterranean region are known. Large variation in chickpea germplasm has been noted for most of the morphological/agronomic traits and for resistance to biotic and abiotic stresses. However, careful assessment of genetic resources is a key to enhance utilization of genetically diverse accessions with beneficial traits in breeding programs.



Category	# Accessions	# Alleles	PIC Value
Global collection	3000	1160	0.839 (0.472-0.962)
Desi type	1711	328 (28%)	0.815 (0.382-0.954)
Kabuli type	71	306 (26%)	0.806 (0.459-0.938)
Pea-shaped type	1197	219 (19%)	0.815 (0.243-0.954)
Wild <i>Cicer</i>	20	179 (15%)	0.826 (0.540-0.924)

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MOLECULAR DIVERSITY

Fifty polymorphic SSRs, mostly with di- and tri-nucleotide repeat motifs, were selected to genotype global chickpea collection using high throughput assay: 35 markers and ABI3700 at ICRISAT and 15 marker and ABI1000 at ICARDA (Huttel et al. 1999; Winter et al. 1999; Niroj et al. 2003).

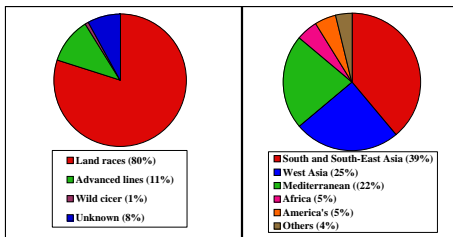
SSR Marker	Quality Index (Allelic Drift)	# Alleles	PIC Value
<i>Huttel et al. 1999 Markers</i>			
CaSTMS 2	0.39 (0.00)	20	0.929
CaSTMS 15	0.19 (0.00)	31	0.905
CaSTMS 21	0.42 (0.00)	21	0.472
<i>Niroj et al. 2003 Markers</i>			
NCPGR 4	0.25 (0.00)	16	0.608
NCPGR 6	0.20 (-0.10)	24	0.562
NCPGR 7	0.15 (0.00)	15	0.551
NCPGR 12	0.23 (0.00)	28	0.816
NCPGR 19	0.26 (0.00)	29	0.597
<i>Winter et al. 1999 Markers</i>			
TA 14	0.27 (0.00)	42	0.905
TA 21	0.44 (-0.13)	42	0.938
TA 22	0.34 (0.08)	53	0.962
TA 27	0.32 (0.00)	32	0.891
TA 28	0.53 (-0.08)	58	0.958
TA 46	0.33 (0.01)	24	0.844
TA 64	0.21 (0.00)	37	0.943
TA 71	0.16 (0.00)	41	0.918
TA 72	0.22 (0.00)	50	0.876
TA 76s	0.22 (0.00)	35	0.814
TA 113	0.14 (0.00)	23	0.853
TA 116	0.23 (0.00)	35	0.837
TA 117	0.20 (0.00)	37	0.930
TA 118	0.18 (0.00)	43	0.950
TA 130	0.15 (0.00)	24	0.824
TA 135	0.16 (0.00)	21	0.851
TA 142	0.37 (0.00)	25	0.760
TA 200	0.41 (0.00)	40	0.917
TA 206	0.33 (0.00)	33	0.899
TAA58	0.41 (0.11)	47	0.956
TaaSH	0.20 (0.07)	41	0.931
TR 2	0.43 (0.00)	53	0.953
TR 7	0.42 (0.00)	28	0.893
TR 29	0.12 (0.00)	34	0.917
TR 31	0.16 (0.00)	18	0.843
TR 43	0.41 (0.00)	55	0.956
TS 84	0.15 (0.00)	17	0.601

ASSESSING CHICKPEA GENETIC STRUCTURE AND DIVERSITY

Global composite collection

A composite collection of 3000 accessions were formed that consists of core collection, cultivars/breeding lines, trait-based unique germplasm, and wild *Cicer* species compatible with *Cicer aritenum* (Upadhyaya et al. 2005). All accessions are FAO designated and available on request to chickpea researchers via an appropriate Material Transfer Agreement.

Germplasm/Trait	# of Accessions	Germplasm/Trait	# of Accessions	Germplasm/Trait	# of Accessions
ICRISAT Core Collection	1956	Cultivars/Breeding lines	39	Ascochyta blight	13
Botrytis grey mold	8	Stunt	8	Fusarium wilt	50
Collar rot	9	Black root rot	8	Dry root rot	6
Helicoverpa	16	Leaf minor	5	Nematode	8
Cold	12	High temperature lines	4	Drought	10
Salinity	4	Early maturity	25	High protein	10
Multi-seeded	7	Seed size	18	Input responsive	4
Double podded	8	Nodulating	8	Morphological diversity	35
ICARDA Core Collection	699	Agroclimatalogical diversity	110	<i>Cicer echinospermum</i>	7
		<i>Cicer reticulatum</i>	13		



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SUMMARY OF THE PROGRESS TO DATE

- Except for TA21, TA28, and TAA58, all other markers detected allele size expected on the basis of SSR repeat motif

- 35 SSR loci detected 1160 alleles (ranging from 15 to 58 alleles per locus) with an average of 33.14 alleles per SSR locus and mean PIC value of 0.839 (ranging from 0.472 to 0.962)

- Few SSR loci detected greater number of alleles than others indicating wide genetic variation captured in the composite collection

- Although the average gene diversity remains the same among different cultigens (desi, kabuli and pea-shaped chickpea's) and wild *Cicer* types, the kabuli's were more genetically diverse than other types

- Shared allele frequency-based UPGMA dendrogram detected clear differentiation of cultigens from the wild species accessions. Desi chickpea's were distinct from the kabuli and pea-shaped chickpea's that clustered together.

- Further analysis is in progress to detect genetic structure and genetic diversity in the composite collection (50 marker data on 3000 accessions) using STRUCTURE program

FUTURE OUTLOOK

A reference collection of 300 accessions (10% of the composite collection), representing the maximum allelic diversity from the composite collection, will be evaluated for the traits associated with drought and salinity tolerance as well for agronomic traits. The breeders will have opportunity to use trait-based genetically diverse accessions for enhancing the genetic potential of chickpea. The genetically diverse accessions will be valuable resource for structural and functional genomics in chickpea.

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