



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 (area exceeding 10,000 ha in each country). 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.



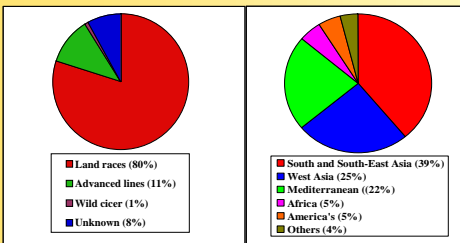
ASSESSING CHICKPEA GENETIC STRUCTURE AND DIVERSITY

Global composite collection

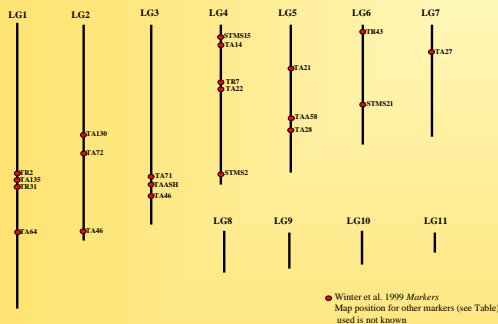
A composite collection of 3000 accessions were formed that consists of core collection, cultivars/breeding lines, trait-based unique germplasm, and wild *Cicer* species compatible with *Cicer aritenum* (Upadhyaya et al. 2005). All accessions are FAO designated and available on request to chickpea researchers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

Global chickpea composite collection.

Germplasm/Trait	Number of Accessions	Germplasm/Trait	Number of Accessions	Germplasm/Trait	Number of Accessions
ICRISAT Core Collection	1956	Cultivars/Breeding lines	39	Ascochyta blight	13
Botrytis grey mold	8	Shunt	8	Fusarium wilt	50
Collar rot	9	Black root rot	8	Dry root rot	6
Helicoverpa	16	Leaf miner	5	Nematode	8
Cold	12	High temperature	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	Agroclimatology diversity	110	<i>Cicer echinospermum</i>	7
		<i>Cicer reticulatum</i>	13		



Distribution of chickpea genotypes analyzed for molecular diversity



Winter et al. 1999 Markers
Map position of other markers (see Table) used is not known

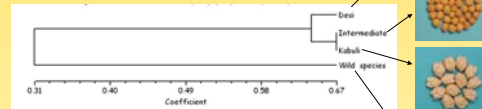
Distribution of microsatellite or simple sequence repeat (SSR) markers in chickpea genome.

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 Winter P, Pfaff T, Udupa SM, Hüttel B, Sharma PC, Sahi S, Arreguin-Espinosa R, Weigand F, Muehlbauer FJ, and Kahl G. 1999. Mol. Gen. Genet. 262:90–101.

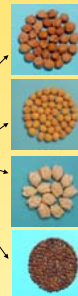
Genetic diversity in four groups of chickpea genotypes.

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)



Classification of four groups of chickpea genotypes

Genetic distances using Shared Allele Frequencies (SAF) for four land types were obtained using Power Marker v3.25. These genetic distances were used to prepare the UPGMA based dendrogram using NTSYSp2.2.



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 ABI3100 at ICARDA (Hüttel et al. 1999; Winter et al. 1999; Niroj et al. 2003).

Genetic diversity in the global collection of chickpea.

SSR Marker	Quality Index (Allelic Drift)	# Alleles	PIC Value
Hüttel et al. 1999 Markers			
CaSTMS 2	0.39 (0.00)	30	0.929
CaSTMS 15	0.19 (0.00)	31	0.905
CaSTMS 21	0.42 (0.00)	21	0.472
Niroj et al. 2003 Markers			
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
Winter et al. 1999 Markers			
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	0.93
TA 118	0.18 (0.00)	43	0.95
TA 130	0.15 (0.00)	24	0.824
TA 135	0.16 (0.00)	21	0.851

SUMMARY OF THE PROGRESS TO DATE

- Except for TA21, TA28, and TAA58, all other markers detected expected allele size 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

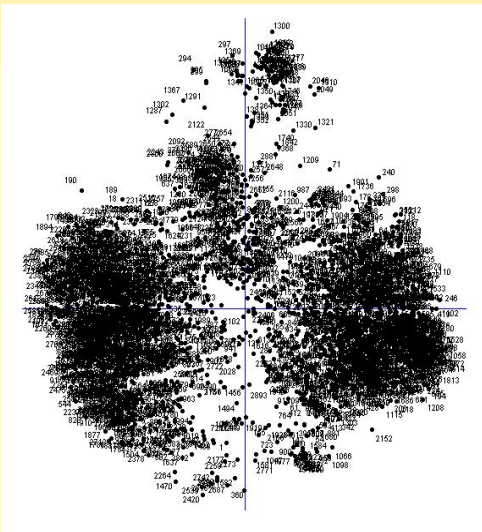
- Although the average gene diversity remains the same among different cultivars (desi, kabuli and pea-shaped chickpea's) and wild *Cicer* types, the kabuli's were more genetically diverse than other types

- Shared allele frequency-based UPGMA dendrogram detected clear differentiation of cultivars 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 diversity and genetic diversity in the composite collection (50 marker data on 3000 accessions) using STRUCTURE program

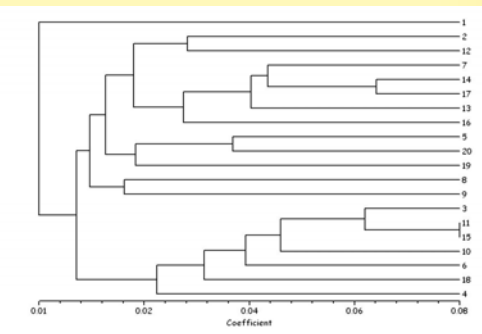
FUTURE OUTLOOK

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 an opportunity to use trait-based genetically diverse accessions to enhancing the genetic potential of chickpea. The genetically diverse accessions will be a valuable resource for structural and functional genomics in chickpea.



Genetic structure of the global composite collection

Principal component analysis (PCA) was done by using DARWIN programme after employing the genotyping data of the composite collection



Genetic relationships among 20 clusters (the value of K used in STRUCTURE)

Structure analysis was performed on 3000 accessions for different values of K. From the scatter plot of K vs log-likelihood values, the optimum value of K was 20. The individual membership (individual Q-matrix) for all the 20 clusters was obtained based on the maximum likelihood value of each genotype for a given K. i.e., P(X|K). Subsequently for each population, the membership coefficient for each cluster was averaged across individuals to form a population Q-matrix, which was used to plot the UPGMA based dendrogram.