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Section of the sectio

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ABOUT CHICKPEA

Worldwide chickpea is the 4^{sth} largest grain-legume crop – area 11.2 million ha, production 9.2 million tons, and productivity 0.82 t ha¹ (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 – des¹—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.



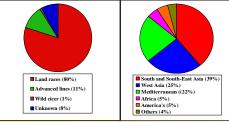
ASSESSING CHICKPEA GENETIC STRUCTURE AND DIVERSITY

Global composite collection

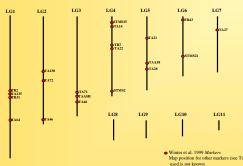
A composite collection of 3000 accessions were formed that consists of core collection, cultivars/breeding lines, trait-based unique germplasm, and wild *Cicer* species compatible with *Cicer aritienum* (Upadhyaya et al. 2005). All accessions are FAO designated and available on request to chickpea researchers 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	Stunt	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	Agroclimatological diversity	110	Cicer echinospermum	7
		C:	12		



Distribution of chickpea genotypes analyzed for molecular diversity



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

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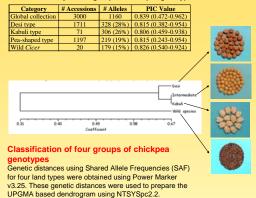
Niroj KS, Shokeen B, and Bhatia S. 2003. Mol. Ecol. Notes 34:28–430.

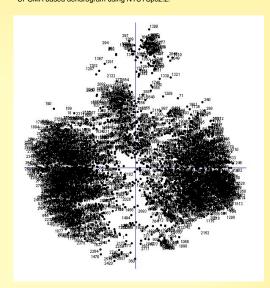
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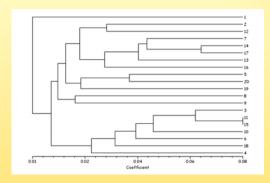
Genetic diversity in four groups of chickpea genotypes.





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 O-matrix) for all the 20 clusters was obtained based on the maximum likelihood value of each genotype for a given K. ie., 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.

MOLECULAR DIVERSITY

Fifty polymorphic SSRs, mostly with di- and trinucleotide 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 (Huttel et al. 1999; Winter et al. 1999; Niroj et al. 2003).

Genetic diversity in the global collection of chickpea.

SSR Marker (Allelic Drift) # Alleles PIC Value Huttel et al. 1999 Markers 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 12 0.23 (0.00) 28 0.816 NCPGR 19 0.26 (0.00) 29 0.597 Winter et al. 1999 Markers 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 75 0.22 (0.00) 50 0.876 TA 76s 0.22 (0.00) <		Quality Index						
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	TA 76s	0.22 (0.00)	35	0.814				
TA 113 0.14 (0.00) 23 0.853	TA 113	0.14 (0.00)	23	0.853				
TA 116 0.23 (0.00) 35 0.837	TA 116	0.23 (0.00)	35	0.837				
TA 117 0.20 (0.00) 37 0.93	TA 117	0.20 (0.00)	37	0.93				
TA 118 0.18 (0.00) 43 0.95	TA 118	0.18 (0.00)	43	0.95				
TA 130 0.15 (0.00) 24 0.824	TA 130	0.15 (0.00)	24	0.824				
TA 135 0.16 (0.00) 21 0.851	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 cultigens (desi, kabuli and peashaped chickpea's) and wild *Cicer* types, the kabuli's were more genetically diverse than other types
- Shared allele frequency-based UPGMA dendogram 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 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.