



Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

2008

Project abstracts



Generation Challenge Programme

Project abstracts

July 2008

Generation Challenge Programme (GCP)

Hosted by CIMMYT

(Centro Internacional de Mejoramiento de Maíz y Trigo;
the International Maize and Wheat Improvement Center)

Mailing address:
Apdo Postal 6641
06600 Mexico, DF Mexico

Physical address:
Km 45 Carretera México-Veracruz
El Batán, Texcoco, México, CP 56130

Tel: +52 55 5804 2004
Fax: +52 55 5804 7558

Email: generationcp@cgiar.org or info@generationcp.org www.generationcp.org

based on geographic origin and this was further characterised within racial groups (five basic races and ten hybrid races). Race kafir (largely from Southern Africa) was distinct. Accessions of the durra, caudatum and guinea races each formed distinct geographic subgroups. Race bicolor was more structured than in the original analysis, with two clusters of East African origin, one of which grouped with bicolor accessions having passport data indicating a North American origin (which in turn suggests that the latter are originally from East Africa).

This additional marker genotyping has doubled the density of SSR marker genotyping of the GCP sorghum reference germplasm set, and largely validated the population structure of this set. The combined results will benefit sorghum research programmes globally, and ultimately sorghum producers and consumers around the world. The implications of this work are that the GCP sorghum reference germplasm set is sufficiently diverse that it can serve as a suitable panel for linkage disequilibrium mapping, and/or as an entry to global sorghum germplasm collections when seeking variation in any trait of interest, provided that the phenological diversity present in this germplasm set is not so great that it interferes with phenotyping of other traits of interest.

Work remaining: Submitting the final project report and drafting journal article manuscripts for publication.

24. G4005.01.04 (1d): Completing genotyping of composite germplasm set of chickpea

January 2005–December 2005; no-cost extension to October 2007

Principal Investigator

Hari Upadhyaya, ICRISAT, h.upadhyaya@cgiar.org

ICRISAT, Patancheru, 502324, India; Phone: 91-040-30713071

Collaborating institutions and scientists

- ICRISAT: SL Dwivedi; DA Hoisington; PM Gaur; CLL Gowda; RK Varshney; S Chandra
- ICARDA: SM Udupa; BJ Furman; M Baum

Composite collection

ICRISAT and ICARDA jointly developed a composite collection of 3000 accessions (Upadhyaya et al. 2006), which consists of 1956 accessions of the ICRISAT core collection (Upadhyaya et al. 2001), 709 accessions from ICARDA, 39 advanced lines/cultivars, 35 accession with distinct morphological variants, 20 accessions from wild *Cicer* species (*C. reticulatum* and *C. echinospermum*), and 241 trait-specific (resistance to biotic and abiotic stresses, early maturity, multi-seeded pods, double podded, large-seed, high seed protein, nodulation and responsive to high input conditions) accessions. Biologically, it represents 80% land races, 11% advanced lines/cultivars, 1% wild species, and 8% accessions of unknown biological status or geographic origin. This composite collection has been molecularly profiled using 50 SSRs in high throughput assay (ABI3700).

Genetic structure of composite collection

The 48 SSR markers data on 2915 accessions were analyzed using PowerMarker V3.0 (Liu and Muse 2005) and DARwin 5.0 version (Perrier et al. 2003). This composite collection showed rich allelic diversity (1683 alleles, 35 alleles per locus, 748 most common alleles and 935 rare alleles at 1%), group-specific unique alleles, and common alleles sharing between the species and geographical groups.

Unique alleles are those detected in a group of accessions but absent in other groups. Group-specific unique alleles were 104 in Kabuli, 297 in desi, and 69 in wild *Cicer*; 114 each in Mediterranean and West Asia (WA), 117 in South and South East Asia (SSEA), and 10 in African region accessions. Desi and kabuli shared 436 alleles while wild *Cicer* with desi and kabuli, respectively, shared 17 and 16 alleles. The accessions from SSEA and WA shared 74 alleles while those from Mediterranean with WA and SSEA, respectively, 38 and 33 alleles. Desi's detected higher proportion of rare alleles (53%) than kabuli's (46%), while wild *Cicer* accessions were devoid of rare alleles.

Reference set

A reference set consisting of 300 genetically most diverse accessions have been formed. This reference set captured 1315 (78%) of the 1683 composite collection alleles, representing diversity from the entire spectrum of composite collection (Figure). The usefulness of this reference set in genomics and breeding of chickpea needs to be investigated.

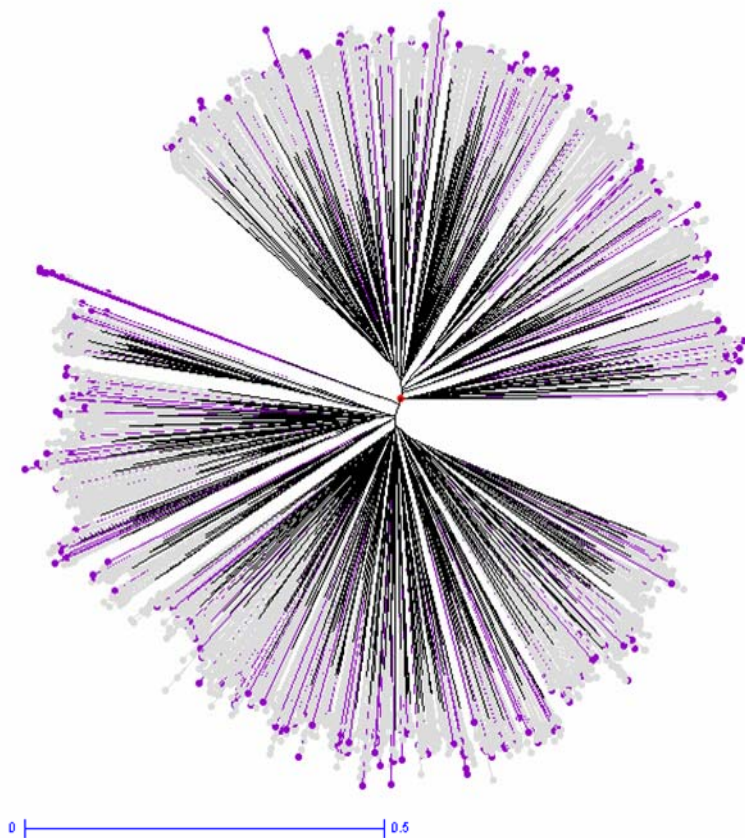


Figure. Un-weighted neighbour-joining tree based on the simple matching dissimilarity matrix of 48 SSR markers across the 2915 accessions of chickpea composite collection (Grey colour) with proposed reference set (300 accessions) in purple colour

References

- Liu K, Muse SV (2005). Power marker: Integrated analysis environment for genetic marker data. *Bioinformatics* 21:2128-2129.
- Perrier X, Flori A, Bonnot F (2003). Data analysis methods. In P Hamon, M Seguin, X.Perrier, and JC Glaszmann (eds), *Genetic diversity of cultivated tropical plants*. Enfield, Science Publishers. Montpellier. pp 43-76.
- Upadhyaya HD, Bramel PJ, Singh S (2001). Development of a chickpea core subset using geographical distribution and quantitative traits. *Crop Sci* 41:206-210.
- Upadhyaya HD, Furman BJ, Dwivedi SL, Udupa SM, Gowda CLL, Baum M, Crouch JH, Buhariwalla HK, Singh S (2006). Development of a composite collection for mining germplasm possessing allelic variation for beneficial traits in chickpea. *Plant Genet Resour* 4:13-19.

25. G4005.03.02 (3b): Molecular characterisation of pigeonpea (*Cajanus cajan*) composite collection

January 2005–December 2006; no-cost extension to December 2007

Principal Investigator

Hari Upadhyaya, ICRISAT, h.upadhyaya@cgiar.org
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT),
Patancheru, 502324, India; Phone: 91-040-30713071 (extension 2333)

Collaborating Institution and Scientist

ICRISAT: R Bhattacharjee; DA Hoisington; S Chandra; RK Varshney; KB Saxena

Composite Collection

ICRISAT developed a composite collection of 1000 accessions, which consists of 146 mini core subset accessions (Upadhyaya et al. 2006), another 146 comparator mini core accessions, 236 of the 1290 core collection accessions (Reddy et al. 2005), 389 trait-based accessions (resistance to biotic and abiotic stresses and those with superior morpho-agronomic traits), 20 advanced lines/cultivars, and 63 accessions from seven wild *Cajanus* species. Geographically, it consists of 73% accessions from Asia, 13% from Africa, 5% from Caribbean, 3% each from America's and Oceania, and remaining 3% from other regions. This composite collection has been molecularly profiled using 20 SSRs in high throughput assay (ABI3700).

Genetic structure of composite collection

The 20 SSR markers data on 952 accessions were analyzed using PowerMarker V3.0 (Liu and Muse 2005) and DARwin 5.0 version (Perrier et al. 2003). This composite collection showed rich allelic diversity (197 alleles, 10 alleles per locus, 82 most common alleles and 115 rare alleles at 1%), group-specific unique alleles, and common alleles sharing between the species and geographical groups.

Unique alleles are those detected in a group of accessions but absent in other groups. Group-specific unique alleles were 60 in wild types and 64 in cultivated types. Accessions from Asia had 48 unique alleles while those from Africa had only two unique alleles. Non-determinate type (NDT) cultivated pigeonpea accessions were represented by 37 unique alleles while determinate types (DT) only one allele. Wild and cultivated