



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

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

types shared 73 alleles, DT and NDT 10 alleles, DT and wild types 4 alleles, and NDT and wild types 20 alleles. A tree diagram using DARwin 5.0 revealed wild types as a group genetically more diverse than cultivated types, while NDT were more diverse than DT.

Reference set

A reference set consisting of 300 genetically most diverse accessions have been formed. This reference set captured 187 (95%) of the 197 composite collection alleles, representing diversity from the entire spectrum of composite collection (Figure). The usefulness of this reference set in genomics and breeding of pigeonpea needs to be investigated.

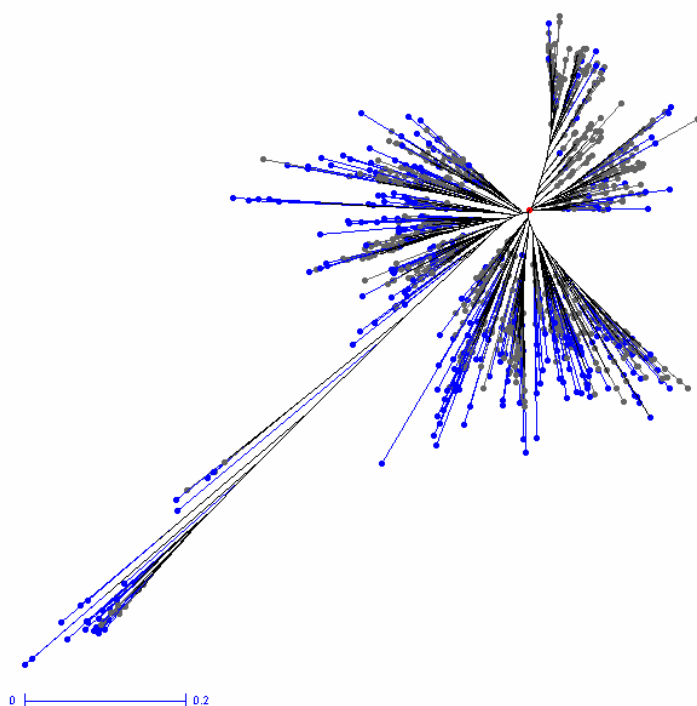


Figure. Un-weighted neighbour-joining tree based on the simple matching dissimilarity matrix of 20 SSR markers across the 952 accessions of pigeonpea composite collection (Grey colour) with proposed reference set (300 accessions) in blue colour

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.
- Reddy LJ, Upadhyaya HD, Gowda CLL, Singh S (2005). Development of core collection in pigeonpea [*Cajanus cajan* (L.) Millspaugh]] using geographic and qualitative morphological descriptors. *Genet Resour Crop Evol* 52:1049-1056.
- Upadhyaya HD, Reddy LJ, Gowda CLL, Reddy KN, Singh S (2006). Development of a mini core subset for enhanced and diversified utilisation of pigeonpea germplasm resources. *Crop Sci* 46:2127-2132.