Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

2008 Project abstracts

Generation
Cultivating Plant Diversity for the Resource-Poor

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July 2008

Generation Challenge Programme (GCP)
Hosted by CIMMYT
(Centro Internacional de Mejoramiento de Maíz y Trigo;
the International Maize and Wheat Improvement Center)

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26. G4005.03.06 (3f): Molecular characterisation of groundnut (*Arachis hypogaea L.*) composite collection

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

Principal Investigator

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Collaborating institutions and scientists

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- UCB: D Bertioli

Composite collection

ICRISAT and EMBRAPA jointly developed a global composite collection, consisting of 1000 diverse groundnut accessions, which included 184 groundnut mini core subset (Upadhyaya et al. 2002), another 184 mini core comparator, 110 accessions from Asia core and mini core, 408 elite germplasm/cultivars and trait-specific (resistance to biotic and abiotic stresses, early maturity and/or fresh seed dormancy, large-seed, high shelling percentage, high oil and/or protein content, and interspecific derivatives) accessions, and 114 wild *Arachis* accessions. This composite collection has been molecularly profiled using 21 SSRs in high throughput assay (ABI3700).

Genetic structure of composite collection

Twenty-one SSR markers data on 852 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 (490 alleles, 23 alleles per locus, 246 common alleles and 244 rare alleles at 1%), group-specific unique alleles, and common alleles sharing between subspecies and geographical regions.

Unique alleles are those detected in a group of accessions but absent in other groups. Group-specific unique alleles were 101 in wild *Arachis*, 50 in subsp. *fastigiata*, and only 11 in subsp. *hypogaea*. Accessions from America's revealed highest number of unique alleles (109) while Africa and Asia, respectively, had only six and nine unique alleles. The two subsp. *hypogaea* and *fastigiata* shared 70 alleles. The wild *Arachis* in contrast shared only 15 alleles with *hypogaea* and 32 alleles with *fastigiata*. A tree-diagram using DARwin 5.0 separated majority of the *hypogaea* from *fastigiata* accessions while wild *Arachis* accessions clustered with *hypogaea*.

Reference set

A reference set consisting of 300 genetically most diverse accessions have been formed. This reference set captured 466 (95%) of the 490 composite collection alleles, representing diversity from the entire spectrum of composite collection (Figure). The usefulness of this reference set in genomics and breeding of groundnut needs to be investigated.

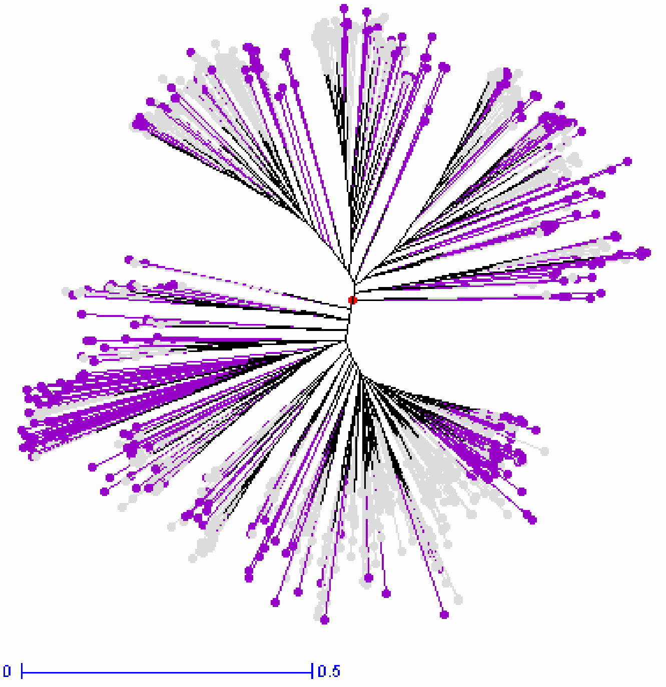

Figure. Un-weighted neighbour-joining tree based on the simple matching dissimilarity matrix of 21 SSR markers across the 852 accessions of groundnut composite collection (Grey colour) with proposed reference set (300 accessions) in purple colour

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, Cox PJB, Ortiz R, Singh S (2002). Developing a mini core of peanut for utilisation of genetic resources. Crop Sci 42:2150-2156.

27. G4005.05 Assessing Eco-tilling as a methodology for targeted genotyping and SNP discovery

January 2005– May 2007; no cost extension – May 2008

Principle Investigator

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Collaborating institutions and scientists

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1. Research activities and developments at IRRI

1.1 EcoTILLING of selected *Oryza* germplasm for drought candidate genes

EcoTILLING, a tool that detects polymorphism in the form of SNPs or indels in natural populations, was employed to survey variation in a panel of *Oryza* germplasm consists of a mini-core collection of 1536 *O. sativa* accessions, 190 accessions of *O. glaberrima*, and