



Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

2008

Project abstracts



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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)

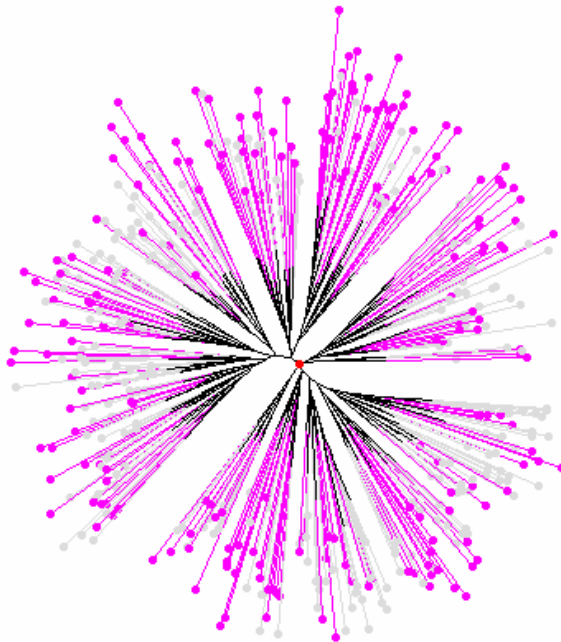
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**Figure. Un-weighted neighbour-joining tree based on the simple matching dissimilarity matrix of 19 SSR markers across the 452 accessions of foxtail millet composite collection (Grey colour) with proposed reference set (200 accessions) in pink colour**

0 |—————| 0.2

## References

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## **36. G4006.31: Development and genotyping of composite collection of pearl millet (*Pennisetum glaucum* (L.)R. Br.)**

*January 2006–December 2006; no-cost extension to Dec 2008*

### Principal Investigator

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### Collaborating institutions and scientists

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### Composite collection

A composite collection of pearl millet, consisting of 1021 accessions, has been developed from the world collection of 21,594 pearl millet germplasm held at ICRISAT genebank. This composite collection consists of 710 landraces, 251 advanced breeding lines, and 60

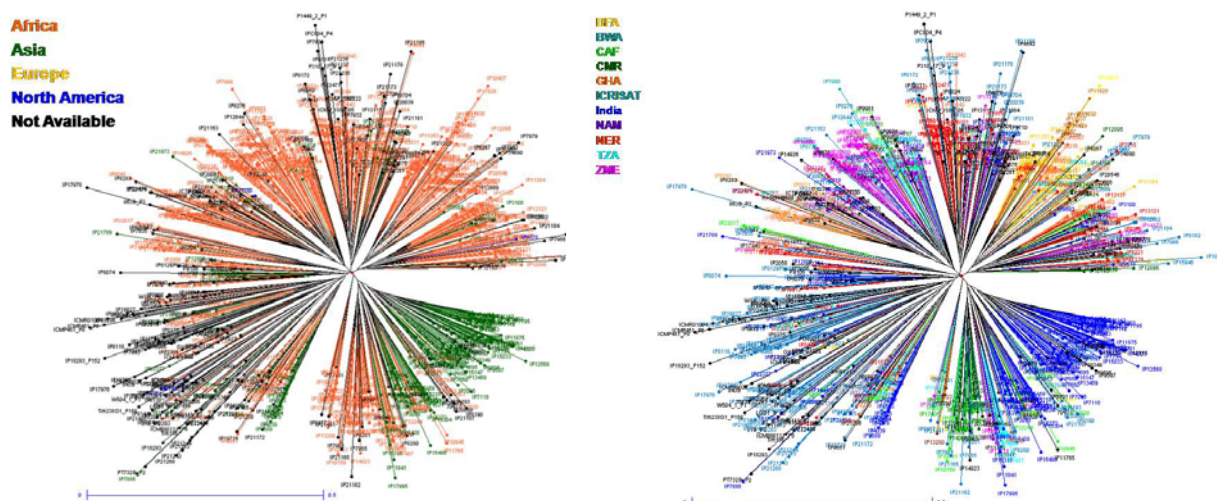
accessions from the seven wild species. Geographically, 441 accessions belong to Asia, 315 to West Africa, 147 to Southern Africa, 56 each to Eastern and Central Africa, five to America's, and one to Europe.

### Genetic structure of composite collection

Nineteen SSR markers (Allouis et al. 2001; Qi et al. 2001, 2004; Senthilvel et al. 2004) data on 1021 accessions were analyzed using PowerMarker V3.0 (Liu and Muse 2005) and DARwin 5.0 version (Perrier et al. 2003). This composite collection showed a total of 230 alleles, averaged 12 alleles per locus and 102 of them were rare alleles at 1%. The accessions were highly heterogeneous and up to 7 alleles were detected per locus. The accessions were grouped by geographical locations but not by biological status (Figure). Only seven alleles were unique to wild species whereas none were unique in landraces. The released cultivars and advanced lines were scattered across different groups. The allelic data of 19 SSR loci for 1021 accessions will be made available to the GCP central repository.

### Reference set

A reference set consisting of 300 accessions were chosen using 'max length subtree' option of DARwin5.0 which creates the subset of units minimizing the redundancy between units and limiting the loss of diversity. This reference set has captured 95% of the composite collection alleles (230), representing diversity from the entire spectrum of composite collection. The usefulness of this reference set in genomics and breeding of pearl millet needs to be investigated.



**Figure: Neighbour joining tree of composite collection based on Euclidean distance**

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### **37. G4007.01: Genotyping validation of the GCP reference sets**

*January 2008–December 2008*

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The scientific community involved in the SP1 sub-programme of the Generation Challenge Programme is about to deliver one of the biggest efforts of characterisation of genetic diversity on 21 crop species. This characterisation was based on the utilisation of microsatellite markers, which constitute a powerful marker system for such a purpose. However, this work was by nature composite, involving different species and different partners using different technologies.

For each crop, one of the main products of this exercise is a reference set of representative germplasm to serve as a material for international coordination in the future.

The present project proposes to assess the different microsatellite datasets produced in SP1 by having a subsample of germplasm accessions re-genotyped by an external genotyping facility (service provider). This subsample will be the reference set, so that the new data will also serve to validate and certify the genotypic information attached to the reference set.

This genotyping validation project will be connected to the management of the genetic material constituting the reference sets. As an output, stabilised materials specifically handled as genetic stocks by gene bank curators and associated to validated genetic diversity data will be available.