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
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35. G4006.30: Genotyping of composite collection of foxtail millet [Setaria italica (L). P. Beauv.]

January 2006 –December 2006; no-cost extension to June 2008

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Composite collection

Not much information is available about the usefulness of foxtail millet germplasm in breeding programmes. A composite collection of 500 accessions has been developed and molecularly profiled using 19 SSRs (Xia et al. 2007; Dida et al. 2007; ICRISAT unpublished data) in high throughput assay (ABI3700).

Genetic structure of composite collection

Nineteen SSR markers data on 452 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 (362 alleles, 19 alleles per locus, 196 common alleles and 166 rare alleles at 1%), group-specific unique alleles, and common alleles sharing between the races and geographical groups. Markers UGEP53, UGEP81, UGEP15, UGEP90, and UGEP33 detected large number of alleles (28-35).

Unique alleles are those detected in a group of accessions but absent in other groups. Group-specific unique alleles observed among the races were 40 in Indica, 21 in Moharia, 10 in Pumila, and 8 in Maxima, while region-wise unique alleles were 57 in South Asia, 17 in West Asia, 14 in East Asia, and 3 in Africa. The common alleles shared by two races were 28 between Moharia and Indica, 16 between Maxima and Indica, 9 between Maxima and Moharia, 4 between Moharia and Pumila, 3 each between Italica and Indica, and Pumila and Indica and one between Moharia and Italica. Region-wise shared alleles were 43 between East Asia and South Asia, 24 between South Asia and West Asia, 4 between Africa and South Asia, 3 each between East Asia and West Asia and Africa and West Asia, 2 between Africa and East Asia, and 1 between Europe and South Asia.

Reference set

A reference set consisting of 200 genetically most diverse accessions have been formed. This reference set captured 316 (87%) of the 362 composite collection alleles, representing diversity from the entire spectrum of composite collection (Figure). The usefulness of this reference set in genomics and breeding of foxtail millet needs to be investigated.

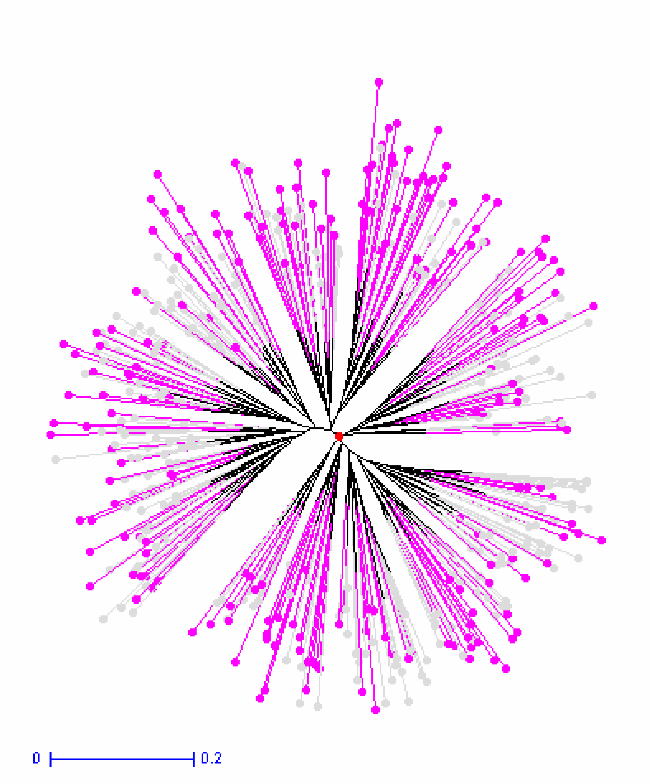

Figure. Un-weighted neighbour-joining tree based on the simple matching dissimilarity matrix of 19 SSR markers across the 452 accessions of foxtail millet composite collection (Grey colour) with proposed reference set (200 accessions) in pink colour

References

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Xia PJ, Yun SS, Yan CS, Wan GY, Wan TY, Li Y (2007). Development of EST-SSR in foxtail millet (Steria italica). Genet Resour Crop Evol 54:233-236.

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

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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 germpasm held at ICRISAT genebank. This composite collection consists of 710 landraces, 251 advanced breeding lines, and 60