



Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

2008

Project abstracts



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#### **Generation Challenge Programme (GCP)**

Hosted by CIMMYT

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the International Maize and Wheat Improvement Center)

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**Table 2: Summary of genotyping 1000 faba bean accessions with 18 microsatellite primers.**

<b>Primer name</b>	<b>% Missing</b>	<b>Max (bp.)</b>	<b>Min (bp.)</b>	<b>Range (bp.)</b>	<b>% Heterozygosity</b>
A110-1	16.7	245	117	129	8.28
F112-1	18.2	308	250	57	2.12
E115-1	43.4	300	211	89	8.92
E114-1	44.4	306	219	86	14.12
C7-1	48.1	250	204	46	12.10
O25-JF1-AG2	48.7	217	145	71	28.13
A105-1	48.9	329	248	81	16.77
G114-1	49.8	137	92	44	11.15
A102-1	51.6	254	146	108	27.28
A9	51.9	301	250	60	17.3
O23-GA1154	52.1	252	176	76	12.21
O13-GA3	55.5	237	150	87	11.57
F117-1	62.0	250	197	53	9.98
F11-1	62.7	307	266	40	2.34
E109-1	64.9	282	194	88	7.01
A117-1	69.7	214	171	44	6.37
A116-1	71.5	300	239	61	2.76
O3-GATA2	79.3	198	128	70	6.48
A109-1	79.7	240	176	64	2.76
<b>Average</b>	<b>53.7</b>	<b>256.9</b>	<b>185.0</b>	<b>72.0</b>	<b>10.6</b>

### **34. G4006.06: Genotyping of composite collection of finger millet [Eleusine coracana (L.) Gaertn]**

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

#### **Principal Investigator**

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#### **Collaborating institutions and scientists**

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#### **Composite collection**

Finger millet germplasm pool remains largely uncharacterised, thus a constraint to finding genetically diverse germplasm with beneficial traits for use in breeding programmes. A composite collection of 1000 accessions, which also consists of 622 core collection accessions (Upadhyaya et al. 2006), has been developed and molecularly profiled using 20 SSRs (Dida et al. 2007) in high throughput assay (ABI3700).

#### **Genetic structure of composite collection**

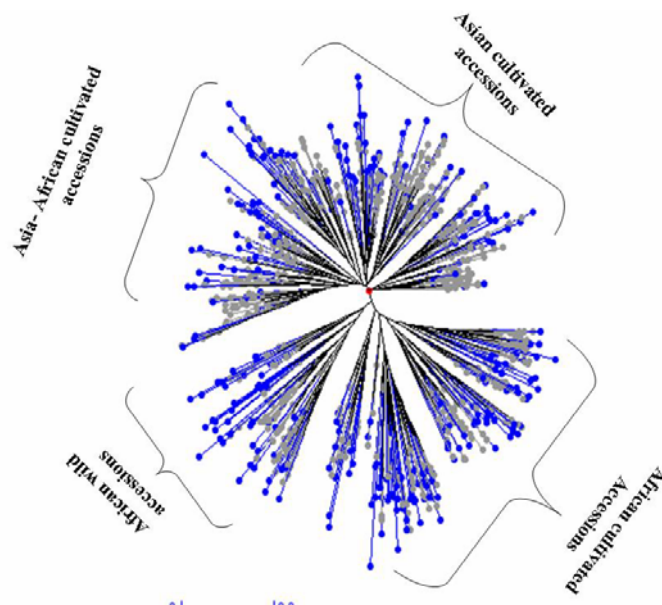
Twenty SSR markers data on 959 accessions were analyzed using PowerMarker V3.0 (Liu and Muse 2005) and DARwin 5.0 version (Perrier et al. 2003). This composite collection showed rich allelic diversity (231 alleles, 11.6 alleles per locus, 121 common

alleles and 110 rare alleles at 1%), group-specific unique alleles, and common alleles sharing between the races and geographical groups. Markers UGEP 81, UGEP 10, UGEP 102, UGEP 26, and UGEP 77 detected the large number of alleles (10-21).

Unique alleles are those detected in a group of accessions but absent in other groups. Race-specific unique alleles were 37 in Vulgaris, 5 in Plana, 4 in Africana, and 2 in Compacta while region-specific alleles were 29 in the accessions originating from East Africa, 12 in the accessions originating from South Asia, 11 in the accessions originating from Southern Africa, and one each in the accessions originating from Central Africa and Europe. The common alleles shared by two groups were 15 for East Africa and South Asia, 5 for East Africa and Southern Africa, and 3 for South Asia and Southern Africa.

### Reference set

A reference set consisting of 300 genetically most diverse accessions have been formed. This reference set captured 206 (89.2%) of the 231 composite collection alleles, representing diversity from the entire spectrum of composite collection (Figure). The usefulness of this reference set in genomics and breeding of finger millet needs to be investigated.



**Figure: Un-weighted neighbour-joining tree based on the simple matching dissimilarity matrix of 20 SSR markers across the 959 accessions of finger millet composite collection (Grey colour) with proposed reference set (300 accessions) in blue colour.**

### References

- Dida MM, Srinivasachary, Ramakrishna S, Bennetzen JL, Gale MD, Devos KM (2007). The genetic map of finger millet (*Eleusine coracana*). *Theor Appl Genet* 114:321-332.
- 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, Gowda CLL, Pundir RPS, Reddy VG, Singh S (2006). Development of core subset of finger millet germplasm using geographical origin and data on 14 quantitative traits. *Genet Resour Crop Evol* 53:679-685.