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## Marker Assisted Heterotic Grouping of Sudanese Landraces

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### Abstract

Sorghum [*Sorghum bicolor* (L.) Monech] is the most important grain crop in the Sudanese economy and diet. In Sudan sorghum ranks first in terms of cultivated area (6 million hectares) and production (2.6 million metric tons) (FAO, 2005). However, yield per unit area is very low (250 kg/ha) in comparison to the world average (1390 kg/ha). The aim of this study therefore is to characterise the pattern of molecular genetic diversity in a representative samples of Sudanese sorghum landraces and to determine genetically distinct pools which shall serve as base materials for hybrid breeding.

The pattern of genetic diversity was assessed among 40 sorghum landraces from Sudan along with 27 cultivars from ICRISAT. Thirty-one simple sequence repeat markers (SSRs) were used. Fifteen of them were used as individual primers while the other 16 were combined into sets suitable for triplex PCR loaded on a 3% metaphor gel.

In total 193 alleles (different fragment sizes) were observed in the Sudanese landraces and in the world collection. The number of alleles per locus ranged from 4 for primer Sb5–256 to 19 for Sb5–206 & Sb6–84 with an average of 12.9 alleles per locus. In the triplex PCR, the number of alleles per locus ranged from 2–8 averaging to 2.8.

A dendogram was constructed from Modified Rogres, Distance (MRD) measures. The accessions clustered into eight major groups. No major clustering by race was observed.

Based on the cluster analysis, 31 landraces and inbred lines were selected for production of testcrosses with 2 cytoplasmic male sterile (ms) lines derived from different gene pools. In addition, diallel crosses among representatives of different clusters were produced. The landraces, inbred lines, and testcrosses were evaluated in regular yield trials at two test sites in Sudan (Wad Medani and Damazin) in 2005 while the diallel crosses (in generation F<sub>2</sub>) were evaluated at Wad Medani only. The evaluation will be repeated in the 2007 season. Final clustering will be based on both molecular-marker and field data.

**Keywords:** Sorghum, Diversity