

Isozyme variation in *Sorghum bicolor* sub sp. *arundinaceum* in Zimbabwe

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Abstract

Patterns of isozyme variation were analysed in 17 wild *S. bicolor* sub sp. *arundinaceum* accessions collected from different parts of the country, a male sterile line, a cultivated sorghum variety, a landrace and a sorghum crop-wild hybrid. Three enzyme systems were assayed; esterase (EST), peroxidase (PER) and alcohol dehydrogenase (ADH) using native polyacrylamide gel electrophoresis (native PAGE). Nine loci were resolved four for EST, three for PER and two for ADH with two alleles each for EST and PER and three for ADH. For EST the hybrid and Bindura accessions exhibited the highest variation exhibiting the highest heterozygous frequencies for all alleles. Peroxidase produced the only monomorphic loci *Per-C*, the other loci *Per-A* and *Per-B* produced a total of seven heterozygotes. ADH was the least variable system exhibiting the lowest heterozygote frequencies for its alleles. This system produced three heterozygotes; the Bindura and Hybrid accessions were heterozygous at both loci while the Avondale accession was heterozygous at the *Adh-B* loci. The non-wild sorghums were found to have a low genetic diversity compared to their wild counterparts, all their alleles were represented in every wild sorghum accession supporting the theory that domestication may have resulted in a genetic bottleneck. The findings from this study do not dispute the fact that wild sorghum from southern Africa may not have been active in the domestication process. A rare allele *Adh-B* (2) was observed in the wild Avondale accession. Such accessions must be prioritised for conservation purposes as they may be harbouring alleles that may be exploited for breeding purposes. Cluster analysis clustered three Harare accessions Avondale, UZ and Crowborough together this group was found to be genetically similar and distinct from the other Harare accessions. For the Bulawayo accessions the Thokozani and Hillside were found to be more genetically similar to each other than the Tradefare accession. Variation was also found among the closely clustering accessions this variation may be attributed to the predominantly self-pollinating nature of sorghum. The Bindura accession shared 66 % of its alleles with the hybrid pointing to a possibility of gene flow from the cultivated sorghum. These results were supported by the clustering results which clustered the two accessions closely together. In light of these findings it is recommended that steps be taken to conserve wild sorghum as it is in danger of genetic erosion due to gene flow. Before taking these steps there is need to assess the extent of gene flow in Zimbabwe. It is recommended that studies be undertaken using DNA markers to confirm findings from this study.