

## **Genetic diversity evaluation among fifty sugarcane accessions from the Zimbabwe Sugar Industry using DNA-SSR markers and qualitative traits.**

Mugehu E Mpofu L.T. and Manjeru P

### **Abstract**

Due to the increasingly diverse needs of the Zimbabwe Sugar Industry, the need for developing improved varieties of sugarcane cannot be overemphasized. Since the establishment of experiment station in 1966, the Zimbabwe Sugar Industry (ZSI) has always been dependent on importation of crosses from other countries for development and release. However, the ZSI is now planning on developing its own crossing facilities. The ZSI's gene bank has up to 746 imported varieties which can be used as potential parents in a breeding program. With the impending establishment of Zimbabwe's own crossing facilities, morphological and molecular characterization of the available germplasm is essential to identify parental lines which can be used during crossing. The main objective of this study was to determine the genetic and phenotypic diversity of fifty ZSAES gene bank sugarcane varieties (accessions) and assess how the existing diversity can be utilized in a breeding program in parental selection and variety identification. Fifty sugarcane accessions were chosen based on country of origin and availability of seed and evaluated for qualitative morphological traits followed by molecular evaluation using DNA-SSR markers in a PCR based protocol. Fifty 'one eyed' setts were planted in the greenhouse and transplanted into labeled asbestos pots with ZSAES media. Fresh leaf samples were collected from the plants for DNA extraction using a modified CTAB method. Field trials for morphological assessment were laid out in a completely randomized design in a 1.5 x 4m plot. Agglomerative, hierarchical UPGMA clustering based on morphological traits with SAS® (9.3) categorized the fifty accessions into two main groups. The morphological traits managed to classify the accessions according to pedigree data, source of origin and similarities in traits like internode waxiness and adherence of leaf sheath. Contrastingly, molecular UPGMA cluster analysis by DarWin® (6.0) grouped the accessions into three main clusters. The three clusters were aligned according to time of release of varieties with the latter varieties in cluster III and the older ones in cluster I. The groups also showed clustering according to similarities in pedigree and source of origin. The molecular and morphological phylogenetic clusters suggest horizontal gene transfer through parallel and convergent evolution. Similarity trends observed also highlight similarities in breeding goals in different parts of the world. The information obtained from the study justifies the need for more importation of varieties from across the world to broaden the genetic base of the germplasm pool in the ZSI's breeding program. Information from morphological data can be used for identification of released varieties in the ZSI using unique descriptors. More varieties should be analyzed and agronomic characterization should also be done to complement the results of this study and be incorporated into a database.