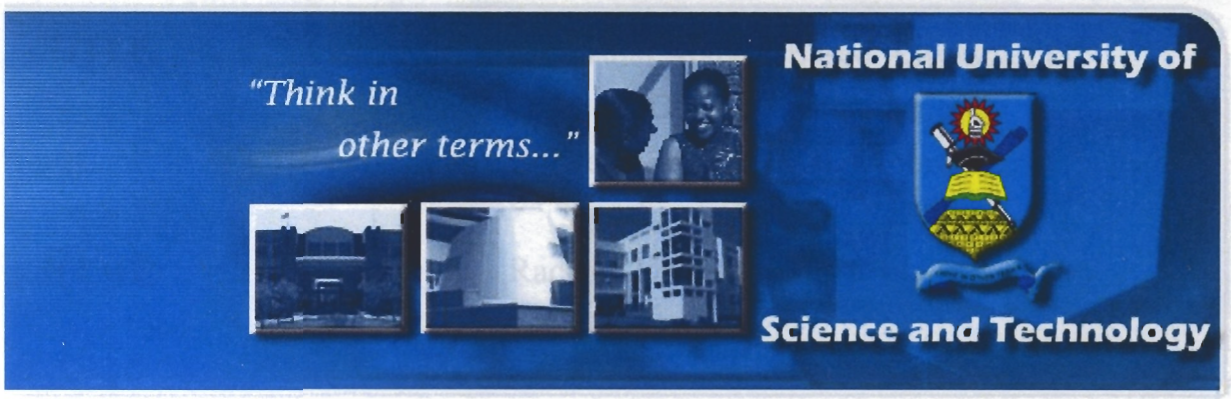

DEPARTMENT OF APPLIED BIOLOGY AND BIOCHEMISTRY

Molecular Marker-Based Assessment of Genetic Relationships between Selected Maize Inbred Lines

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ABSTRACT

Molecular markers have been used extensively in the identification and differentiation of cereal crops. The molecular marker-based determination of genetic diversity in inbred lines of maize is important for the development of hybrids which exhibit improved vigour and give better yields. In this study, 6 closely-related inbred lines were used to find molecular markers and molecular-marker based techniques methods that can employed in the differentiation of maize lines. DNA was extracted and it was amplified using PCR-based molecular markers which were chosen for their simplicity and requirement for any small quantities of sample DNA. Four SSR primers, 8 ISSR primers and 2 UP PCR primers were used and out of the 14 primers used, 5 could be used for differentiation and identification of selected inbred lines of maize. SSR primers Phi96100 and Umc 1555 were found to produce very reproducible results Phi96100 showed a 37 % similarity between the maize lines which it divided into 4 subgroups. Umc 1555 showed that lines were related with a 50 % similarity coefficient. From ISSR analyses, the primers SSR 1, SSR 17 and TCI-A could be used to amplify maize DNA but SSR 1 is the only one that gave clear reproducible fingerprints. The marker however did not differentiate lines significantly, giving a similarity coefficient of 88 % between lines. The fingerprints confirmed the presence of the ACTG repeat in the maize genome. UP PCR primers L 15/ L 45 gave unique fingerprints with high polymorphism. Using these primers, lines were shown to be 33 % different. The results showed that UP PCR can be used in differentiating maize inbred lines. Overally, SSR markers gave the highest number of bands though most were monomorphic using agarose gel electrophoresis stained with ethidium bromide.