GENETIC DIVERSITY ANALYSIS OF TRADITIONAL RICE VARIETY "KURULUTHUDA" USING SSR MARKERS

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by

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ABSTRACT

"Kuruluthuda" is a highly nutritious traditional red rice variety. Further crop improvement programs breeders have to identify true to type traditional rice varieties. Molecular characterization provides exact information about degree of genetic diversity and identity. Main objective of this study is to analyze genetic diversity of Kuruluthuda rice by molecular characterization based on SSR polymorphism. Nineteen Kuruluthuda accessions with two controls, Kaluheenati and BG 360 were used.DNA was extracted from tender leaves of 14 days old seedlings using modified CTAB method. Confirmation, quantification and dilution of raw DNA were done using0.8% Agarose gel electrophoresis. Thirty SSR markers were used in molecular analysis. Specific SSR regions of rice were amplified by Touchdown PCR. Amplified PCR products were confirmed using 1.5% Agarose gel electrophoresis and analyzed by 8% non-denaturing Polyacrylamide gel electrophoresis. DNA bands were scored. Cluster analysis was performed. Phylogeny tree was obtained by using Nei's genetic distance. The molecular analysis of all 21 accessions generated eleven clusters at a relative genetic distance of 0.179. Kaluheenati and BG360 were clustered in to two different clusters. Out of eleven clusters, two accessions in one cluster were closely related at Nei's relative distance zero, inferring those are duplicates. Heterozygosity value for many primers was zero because rice is highly self-pollinating crop. Out of nineteen accessions, three accessions were recognized as representative set of Kuruluthuda accessions. By grouping them in to nine different clusters, it shows that considerable higher genetic diversity exists within "Kuruluthuda" accessions collected from all over the country.

Key words: SSR, Accessions, Kuruluthuda, Genetic Diversity, Genetic Distance