ASSESSMENT OF GENETIC DIVERSITY IN SELECTED *CAPSICUM* SPP. CULTIVATED IN SRI LANKA

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ABSTRACT

Simple Sequence Repeat (SSR) markers are useful tools for evaluating genetic diversity and DNA fingerprinting. The purpose of this study was to evaluate the genetic diversity within 10 chilli accessions by using microsatellite markers and morphological markers. Over the last few decades, the use of molecular markers has played an increasing role in chilli breeding and genetics. This research was conducted at the Division of Plant Biotechnology, Field Crops Research and Development Institute (FCRDI), Mahailluppallama, Anuradhapura, Located at $8^{0}6'$ 0"N (latitude) and $80^{0}27'0"$ E (longitude).

A fingerprint was developed in this study for ten chilli accessions using six Simple Sequence Repeat primers. DNA was extracted using modified CTAB protocol. Polyacrylamide gel electrophoresis was done to identify polymorphism in different alleles of polymerase chain reaction products. Amplified products varied from 140 bp to 290 bp. The molecular data were subjected to statistical analysis using PopGene.S2 software and genetic distances were calculated. The differences and relationships of ten chilli accessions were identified from the clusters in the dendrogram.

Molecular cluster analysis indicated two distinct clusters and many sub clusters. The first group contained Hen miris, MICH-3, ICPN-18-7 line, Arunalu, MI-2 and MI green. The second group contains Waraniya purple, Hot beauty, Purple Nai Miris (*C. chinense*) and Acc.No.11642 (*C. frutescent*).

This study revealed the genetic similarity between the varieties of Arunalu and MI-2. The most distant phylogenetic relationship was observed between Hot beauty and MICH-3 followed by MICH-3 and Waraniya Purple. MICH-3 is a variety developed

by the Field Crops Research and Development Institute (FCRDI), Mahailuppallama using parents (MI-1 and Wonder hot). Hot beauty and Waraniya Purple have been developed through selections from local landraces. Purple Nai Miris (*C. chinense*) and Acc.No.11642 (*C. frutescens*) both formed another subcluster with more distance. These accessions show genetic difference from the improved varieties.

According to morphological classification, Most of the accessions had green colour stems and Intermediate type of plant habits. White colour corolla and pendent type of flower position were common among the accessions.

Higher genetic variability within varieties and significant difference between varieties indicated rich genetic material of a species. Thus, microsatellite markers offer a potential, simple, rapid and reliable DNA fingerprinting method to evaluate genetic variation among the chilli germplasm. The findings of the present study have the potential applications in future breeding programme for the genetic improvement of chilli.

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