THE VARIATION OF FRUIT COMPONENTS IN CONSERVED COCONUT GERMPLASM AT POTTUKULAMA FIELD GENEBANK IN SRI LANKA

K.N.S. Perera, H.M.N.B. Herath, S.A.C.N. Perera

Genetics and Plant Breeding Division, Coconut Research Institute, Lunuwila

chandrikaperera2003@yahoo.com

Characterization of conserved coconut germplasm has been undertaken globally for identification of important features of different accessions for them to be effectively used in coconut breeding. One hundred and fifty seven accessions comprising of local and exotic material have been conserved in *ex-situ* field genebanks of Coconut Research Institute. The objective of this paper is to quantitatively characterize fruit components by weight based analysis. Twenty local tall coconut accessions; Moorock, Palugaswewa, Pitiyakanda, Clovis, Namalwatta, St. Anne's, Margaret, Kasagala, Debarayaya, Razeena, Ambakelle special, Melsiripura, Mangalaeliya, Goyambokka, Goluwapokuna, Keenakelle, Maliboda, Horakelle, Walahapitiya, Wellawa conserved at Pottukulama Gene bank were characterized following Bioversity International descriptors for coconut. Sampled nuts were scored for weights of fresh nut, husked nut, split nut and kernel and the weights of husk, water, and shell of each nut were derived from the scored data. Analysis of variance by general linear models procedure and mean separation by Duncan's multiple range test were performed in SAS v8 and principal component analysis and cluster analysis using squared Euclidean distances were performed in Minitab V17. General linear models procedure revealed significant differences for all the components at 5% probability level. Clovis recorded the highest values for most of the parameters followed by the accession Margaret. The highest per nut kernel producer, Clovis, was followed by Margaret with statistically equal performances and this is important because kernel is the main economically important component followed by the husk. Principal Component (PC) Analysis was performed to describe the diversity among variables and the first three PCs accounted for 79.1%, 16.2% and 2.7% of the variation respectively accumulating to a total of 98% variability among the evaluated coconut accessions. The PC plots and the dendrogram revealed three major groups at 66.6% similarity level and four distinct accessions namely; Clovis, Namalwatta, Margaret and Goyambokka grouped together having higher values for fruit components. Results revealed diversity of fruit components among tall accessions indicating the potential of them to be utilized in breeding programmes. The study also unveiled the duplications among accessions with respect to fruit components which will help in formulating future conservation strategies.

Keywords: *Coconut, Germplasm, Fruit Component Analysis, Characterization, Multivariate Discrimination*