Characterization of Conserved Germplasm of Pungent Chilli Landraces *(Capsicum chinense* Jacq)

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Morphological and agronomical traits are widely used to study the diversity in *Capsicum* species, to determine the relationship between various species and to develop an identification key. *Capsicum chinense* Jacq ("Nai Miris") species are still not properly characterized as the attention has been directed to *Capsicum annum* species. Hence present study was undertaken to explore the morphological and agronomical diversity of *Capsicum chinense* Jacq at Regional Agricultural Research and Development Centre, Makandura, low country intermediate zone (IL,$_a$). Thirty three morphological traits and fourteen agronomical traits considered for 48 accessions germinated from 112 *Capsicum* accessions. Accessions were collected from Plant Genetic Resource Centre and chilli breeder, Mr. K.N. Kannangara. Characterization was based on descriptor for *Capsicum* produced by PGRC. Based on the results of48 *Capsicum* accessions, there were no duplicated accessions within the studied accessions. The traits that largely contributed to the variability within and between the accessions included corolla colour, anther colour, fruit colour at intermediate stage, fruit colour at mature stage, fruit shape, mature leaf length, mature leaf width, number of days for flowering, number of days for fruiting, fruit length, fruit wall thickness, fruit weight and 1000 seeds weight. Cluster analysis showed that there are three major clusters in germplasm collection of *Capsicum.* One major cluster consisted with 23 accessions of pungent chilli having useful and most common characteristics such as: annular constriction of calyx and clusters of flowers or fruits at node, which are exclusively found in the *Capsicum chinense* Jacq accessions. The twenty three accessions divided in to seven sub clusters and showed wide genetic diversity that exists in *Capsicum chinense* germplasm.

Keywords: Morphological traits, Agronomical traits, *Capsicum chinense* Jacq, Cluster analysis, Genetic diversity