Genebanking and Diversity Analysis of Sweetpotato (*Ipomoea batatas)* Collections in the Philippine Cordillera Administrative Region

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Abstract

Sweetpotato (*Ipomoea batatas* L.) is one of the staple food and a ritual food in the remote areas of the Philippine highlands. Being one of the survival crops of the rural people, it is also a potential and cheap source of vitamins. Being rich source of ascorbic acid and vitamin C. Not only being a source of food but also as animal feed. Because of its high nutritive value and versatility as food, fodder and as cover crop, a necessary step to avoid the loss of this production potential and disease resistant, crop germplasm is conservation and preservation.

Protocols in the conservation and preservation of germplasm in genebank are characterization and evaluation. Characterization is necessary to establish identity of each accession while evaluation is done to enhance the utilization of each accession in future crop improvement.

One hundred ninety five sweetpotato accessions from the cordillera region were characterized using the CIP's International Plant genetic Resources descriptors list to determine the phylogenetic relationship of the sweetpotato collections. Qualitative descriptors list to determine the phylogenetic relationship of the sweetpotato collections. Qualitative data includes predominant vine color, secondary vine color, vine tip pubescence, general outline of the leaf, leaf lobe type, leaf lobe number, shape of central leaf lobe, abaxial leaf vine pigmentation, mature leaf color, immature leaf color, petiole pigmentation, predominant skin color, intensity of predominant skin color, secondary skin color, predominant flesh color, secondary flesh color, distribution of secondary flesh color and maturity. Quantitative data includes; number and weight of marketable and non-marketable roots and total weight of roots.

The hierarchical clustering analysis particularly the Wards method was employed to easily determine the groupings were the accessions belong so that the sweetpotato strains in the same cluster are more or less alike than elements in different clusters. Thus, the resulting clusters shall exhibit high internal homogeneity (within cluster and high external heterogeneity between clusters). It showed that sweetpotato collections significantly differed on the quantitative data which includes the number of marketable roots, weight of marketable roots, number of non-marketable roots, weight of non-marketable roots and total weight of roots. Significant results for the qualitative data includes: the general outline of the leaf, predominant skin color, intensity of predominant skin color and secondary skin color. All other characters did not differ significantly.

Keywords: crop improvement, evaluation, predominant vine color