

### Abstract

Phenotypic traits qualitatively and quantitatively are helpful as a preliminary evaluation of maize genetic diversity and provided practical and critical information required characterizing genetic resources. To find out the varietal characterization and grouping with similarity, fifty maize genotypes including hybrids and inbreds were examined in this experiment. According to the results, diverse qualitative traits were observed among the tested genotypes and genotypes varied different qualitative traits with different frequencies.

### Introduction

The data collection according to UPOV TG is better for characterization of the genotypes which are used to set up reference varieties in TG preparation, and Distinctness, Uniformity and Stability (DUS) testing, rather than using International Board for Plant Genetic Resources (IBPGR) descriptor and International Union for the Protection of New Varieties of Plants (UPOV) Test Guide line (TG). Therefore this experiment was conducted to characterize qualitative characters of maize and to identify similarity among maize genotypes.

### Materials and Methods

This experiment was carried out in a randomized complete block design with three replications during wet season from June to October, 2019, at Maize and other Cereal Crops Section, Department of Agricultural Research (DAR), Yezin Nay Pyi Taw, Myanmar. The qualitative characters were recorded at different growing stages according UPOV Test Guide line (TG). The agglomerative cluster analysis was computed using Ward's hierarchical algorithm based of qualitative characters.

### Results and Discussion

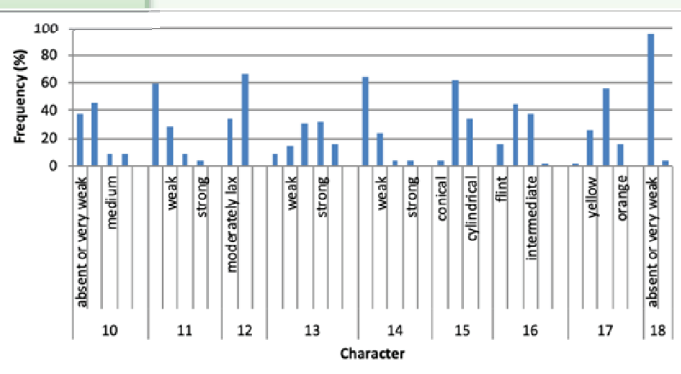
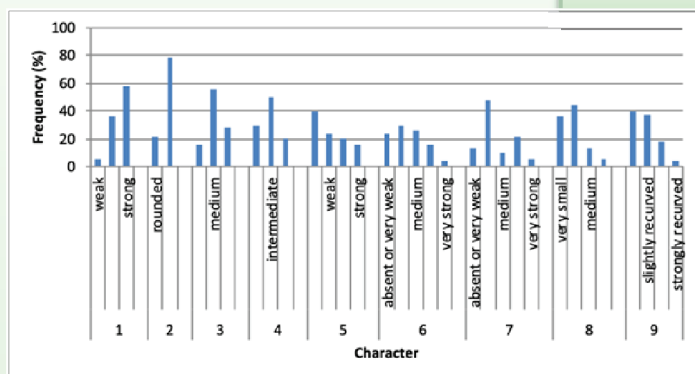


Fig. 1. Variation of different qualitative characters in Maize Genotypes

(note: 1-anthocyanin coloration of first leaf sheet, 2-apex shape of first leaf, 3-intensity of green in foliage, 4-undulation of leaf blade margin, 5-anthocyanin coloration at base of tassel glume, 6- anthocyanin coloration of tassel glumes, 7-anthocyanin coloration of anthers, 8-tassel angle between main axis and lateral branches, 9-curvature of lateral branches, 10-anthocyanin coloration of silks, 11-anthocyanin coloration of brace roots, 12-density of spikelets, 13-anthocyanin coloration of leaf sheath, 14-anthocyanin coloration of internodes, 15-ear shape, 16-type of grain, 17-grain color, and 18-anthocyanin coloration of glumes of cob)

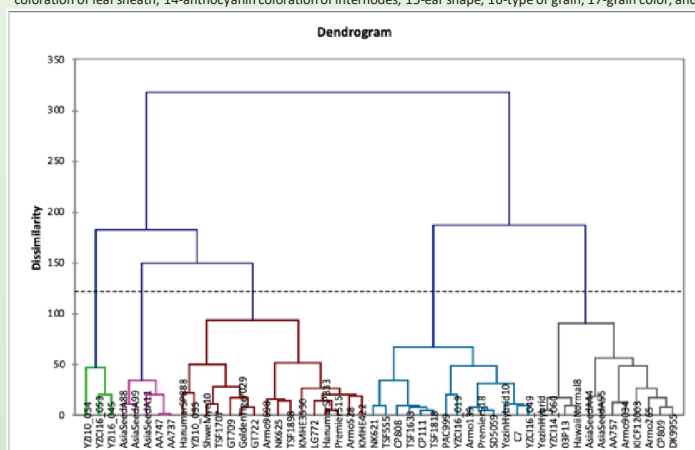


Fig. 2. Dendrogram of maize genotypes based on morphological distances by a visual assessment of the group of plants and single measurement of individual plants or part of plants

Cluster	No.	Name of genotype
I	12	03P13, AA-757, Armo 265, Armo 9034, Asia Seed A44, Asia Seed A55, CP 809, DK 9955, Hawaii Norma 18, KICF12003, Yezin Hybrid, YZCI 14-060
		AA 747, AA737, Asia Seed A11, Asia Seed A88, Asia Seed A99
III	16	Armo 528, Armo 9698, GoldenTiger 029, GT 709, GT 722, Hanumar SP333, Hanumar SP888, KMHE 3550, KMHE 422, LG 772, NK 625, Premier 515, Shwe Mye 10, TSF 1707, TSF 1898, YZ110-095
		Armo 139, C7, CP 111, CP 808, NK 621, PAC 999, Premier 518, SD 5059, TSF 1633, TSF 1818, TSF 555, Yezin Hybrid 10, YZCI 16-019, YZCI 16-049
V	3	YZCI16-053, YZ110-054, YZ16-045

COPHENETIC CORRELATION COEFFICIENT = 0.577

### Conclusion

The fifty maize genotypes, with the help of cluster analysis, were successfully characterized and accurately grouped into five clusters with distinct promising features. It should be noted that although some maize genotypes collected in an area are included in different groups because of the different characteristics they

pose. Thus the application of morphological markers according to UPOV descriptor could contribute to more efficient selection of parental pairs in the early generations of testing.