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Research article

Characterization and Diversity of Selected Maize (*Zea mays* L.) Genotypes Using Qualitative Traits

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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. 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 Research Section, Department of Agricultural Research (DAR), Yezin, Nay Pyi Taw, Myanmar. The qualitative characters were recorded at different growing stages according to the International Union for the Protection of New Varieties of Plants (UPOV) Test Guide line (TG). The agglomerative cluster analysis was computed using Ward's hierarchical algorithm based of qualitative characters. According to the results, diverse qualitative traits were observed among the tested genotypes and genotypes varied different qualitative traits with different frequencies. Thus, comparisons of qualitative traits were made to know the extent of variation among maize varieties under investigation to estimate the genetic diversity. The tested maize genotypes could be grouped five clusters based on qualitative traits. Although some maize genotypes collected in an area are included in different groups because of the different characteristics they pose. Since qualitative characters have less environmental influences, these traits could be used for Distinctness, Uniformity and Stability (DUS) test and Value for Cultivation and Use (VCU) testing of plant varieties. 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.

Keywords characters, cluster, maize genotypes, variation

INTRODUCTION

Maize (*Zea mays* L.) is the world's third most important cereal, widely used in poultry and food industries next to wheat and rice. As it has higher yield potential than any other cereals, it is referred to as "miracle crop" or the "queen" of cereals. Maize is grown both as food for human beings and fodder for animals (Malhotra, 2017). In Myanmar, maize is the second most important cereal after rice. In 2017-2018, maize growing area is 504,000 ha and production is 1940,000 MT. As demand for maize has increased annually since 2009, the maize growing area has expanded year by year (DoP, 2018). Most of cultivars grown in Myanmar are introduced hybrid varieties and these varieties are registered according to the Seed Law and Regulation. Although the registered varieties are increasing year by year, the procedure on clarification as a new variety is weak. Awareness of genetic diversity among elite breeding materials or adapted cultivars has an important role in the improvement of crop plants.

Many tools are now available to study the relationships among the cultivars, including various types of molecular markers; however, morphological characterization is the first step in the description and classification of germplasm (Smith and Smith, 1989). There is an important role of morphological data in the management of genetic resources that are conserved in *ex-situ* gene-banks. The characterization and grouping of lines helps the breeders to avoid duplication in sampling populations and to aid in the identification of varieties and hybrids (Madhukeshwara and Sajjan, 2015). Although there are the ways to collect the morphological character by 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), collection of the data 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. The inventory and agro-morphological characterization of these genetic resources (improved varieties and local's accessions) are essential to provide a sound database on the characteristics of the maize (Salami et al., 2015). Therefore, this experiment was conducted to characterize qualitative characters of maize and to identify similarity among maize genotypes.

METHODOLOGY

This experiment was carried out during the wet season from June to October, 2019, at Maize and other Cereal Crops Research Section, Department of Agricultural Research (DAR), Yezin Nay Pyi Taw, Myanmar which was located at 19° 49' 33″ N; 96° 16 44″ E; 102 m above sea level. In the present investigation, 38 hybrids (developed from DAR and imported by private companies) and 12 inbred lines and open pollinated varieties (OPVs) (developed from DAR, Yezin) were utilized. These genotypes are selected based on the most recommended for importation in 2018-19, as new varieties approved by 10th-14th National Seed Committee (NSC) and currently grown in Regions and Divisions.

All tested genotypes were evaluated in Randomized Completely Block Design with three replications. Each entry (genotype) was grown at a spacing of 75 cm × 25 cm, in a plot size of two rows with 4 m length. Two seeds were sown in each hill and thinning was done 14 days after sowing and single plant per hill was left. For fertilizer application, Urea, Triple Super Phosphate and Muriate of Potash were applied as basal at the rate of 123.5 kg ha^{-1}, 123.5 kg ha^{-1} and 61.75 kg ha^{-1}, respectively. Then, the first and second sides dressing of 61.75 kg ha^{-1} Urea, 30.86 kg ha^{-1} Muriate of Potash were applied three weeks after sowing and five weeks after sowing, respectively. Inter-cultivation was done two times; just before the fertilizer applications which control weeds and also improve soil aeration. The qualitative parameters were recorded on each tested genotype in each replication on five representative plants according to UPOV test guidelines. The qualitative characters were recorded at different growing stages following UPOV TG. The agglomerative cluster analysis was computed based on qualitative and morphological characters using Ward's hierarchical algorithm according to the procedure as described by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

Characterization of Maize Genotypes

The qualitative traits of tested maize genotypes were classified according to UPOV test guidelines. Variations of 18 qualitative characters in 50 maize genotypes are shown in Fig. 1. Some distinctive characteristics of tested maize genotypes are presented in Plate 1. The anthocyanin coloration of first leaf sheet possessed five groups such as absence, weak, medium, strong and very strong color anthocyanin. There were 29 genotypes (58%) having strong anthocyanin, 18 genotypes (36%) having medium and 3 genotypes (6%) having weak anthocyanin. There was no genotype with absence of anthocyanin and very strong anthocyanin coloration. In shape of first leaf apex, the maximum percentage of genotypes exhibited rounded to speculate type (78.00%) and the minimum accessions showed round apex type (22%) of leaf apex shape. The intensity of green color in foliage was classified into three groups such as light, medium and dark green for tested maize genotypes. Of the total, 28 genotypes showed medium green color foliage (56%), 14 genotypes (28%) had dark green foliage and other 8 genotypes were observed (16%) light green foliage. The undulation of margin in first leaf blade in tested genotypes was classified as absence, intermediate and strong. Among the genotypes, 25 genotypes possessed intermediate undulation of margin of leaf blade, 15 genotypes were absent and the rest 10 genotypes had strong undulation leaf blade margin.

Five characters regarding with tassel were examined in this study: tassel anthocyanin coloration at the base of glume, anthocyanin coloration of glume excluding base, anther anthocyanin coloration, the angle between main axis and lateral branches and curvature of lateral branches of tassel. In this result, different genotypes possessed different tassel characters. The types of spikelets density in tassel was classified into three types. Among the 50 genotypes, most were medium density of spikelets (66%) and the rest was moderately lax (34%), and there was no moderately dense density of spikelets. In, anthocyanin coloration of silk of ear, no anthocyanin (19 genotypes = 38%), weak anthocyanin (23 genotypes = 46%), medium anthocyanin (8%) and strong anthocyanin (8%) colors were found among the 50 genotypes. Among the maize genotypes studied, 30 genotypes (60 %) were found no purple anthocyanin in brace root, 14 genotypes (28%) had weak anthocyanin, 4 genotypes (8%) had medium color and 2 genotypes (4%) were noticed as strong anthocyanin.

Leaf sheath and stem (internode) anthocyanin color were classified five groups as absent or very weak anthocyanin, weak, medium, strong and very strong. Leaf sheath anthocyanin was dispersed at all groups as very strong anthocyanin color (16%), strong anthocyanin color (32%), medium anthocyanin color (30%), weak anthocyanin color (14%) and very weak or absence of anthocyanin color (8%). In stem color, absence of anthocyanin (68%), weak anthocyanin (24%), medium (4%) and light strong anthocyanin (4%) were observed among the genotypes. There was no genotype with strong anthocyanin color in internode color. The shape of maize ear was characterized as conical, conical-cylindrical and cylindrical. Most of the tested genotypes had conical-cylindrical type of ear (62%), followed by cylindrical type of ear (34%) and the rest (4%) had conical type of ear.

In types of grain, UPOC TG showed nine types: flint, flint like, intermediate, dent-like, dent, sweet, pop, waxy and flour. In this study, four types of grain were observed among the genotypes. Most of the genotypes possessed flint like grain showing about 44% of total. Nineteen out of 50 (38%) showed intermediate type of grain, 16% had flint of grain, and the rest genotype about 2% had dent type of grain. There were 10 types of color of grain top such as white, yellowish white, yellow, yellowish orange, orange, red orange, red, purple, brownish and blue black color. In this study, only four types of color of grain top were observed among the tested genotypes with the frequencies of 2%

in yellowish white, 26% in yellow, 56% in yellowish yellow and 16% in orange. No more color of grain top was examined. Although five types of anthocyanin coloration of glumes of cob were classified, only two distinct colors with distinct frequencies like absent anthocyanin (96%) and medium anthocyanin (4%) were observed among the tested maize genotypes. According to the results, comparisons of qualitative traits were made to know the extent of variation among maize varieties under investigation to estimate the genetic diversity.

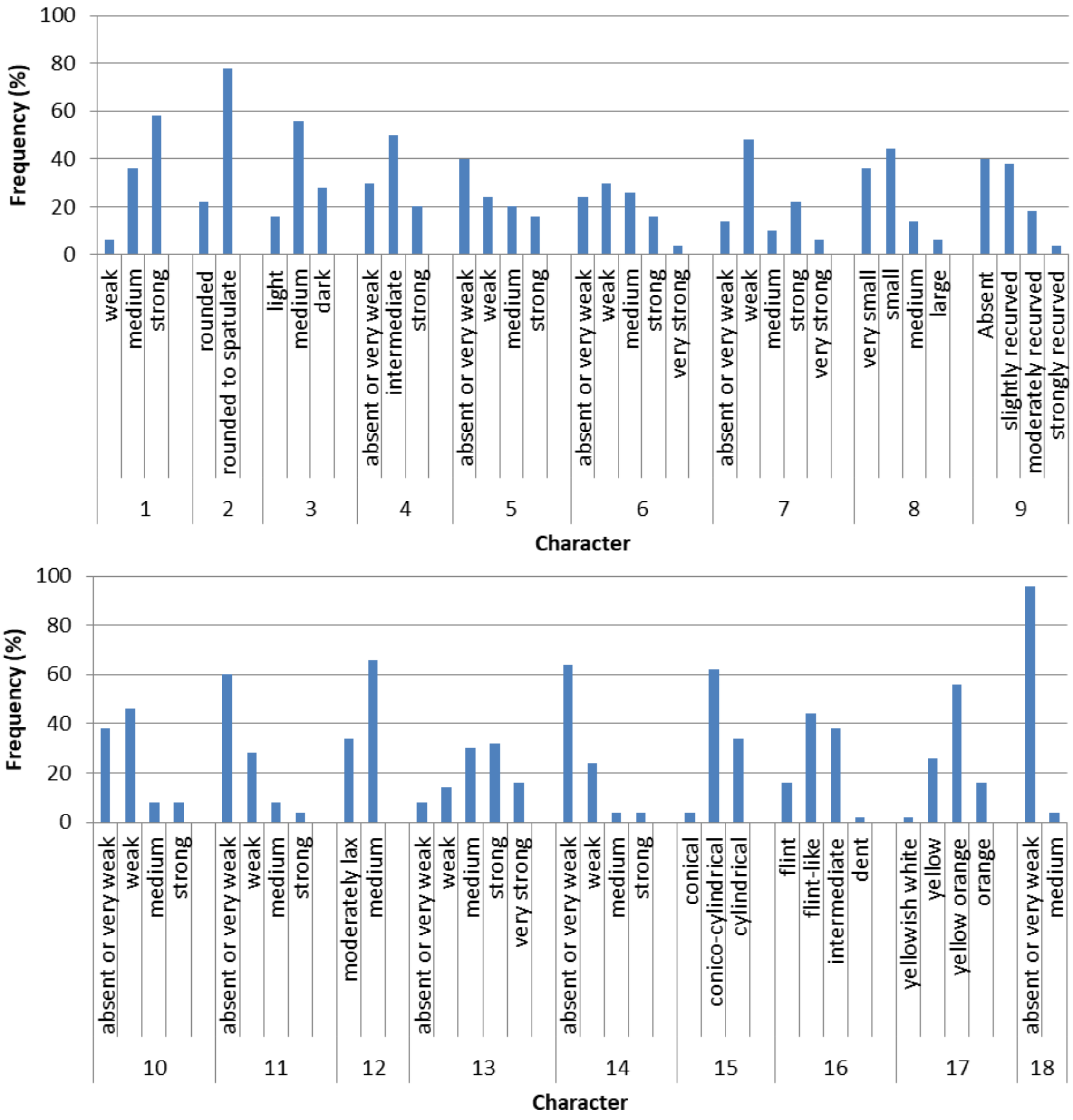

Fig. 1 Variation of different qualitative characters in maize genotypes

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

Cluster analysis of maize genotypes

The cluster analysis, using WARD method based on the squared Euclidean distance criteria, was conducted for measuring genetic diversity and relatedness among the studied genotypes by using qualitative characters (Fig. 2). The studied maize hybrids were grouped into five clusters, showing the existence of considerable genetic diversity among 50 maize genotypes. Some of the hybrids of the same geographical region (source) were observed in different groups. Maximum number of genotypes were grouped in Cluster III (16 genotypes), followed by cluster IV (14 genotypes) and Cluster I (12 genotypes) whereas cluster V contained the least number of genotypes (only three genotypes) followed by cluster II (five genotypes) (Table 1). It can be concluded that the genotypes present in the same region were genetically distinct from each other. These results are in accordance with previous findings of Babic et al. (2016) who concluded that the grouping of maize lines based on the scale-measured characteristics was not in accordance with the information of their origin and even related line pairs were not grouped in the same cluster.

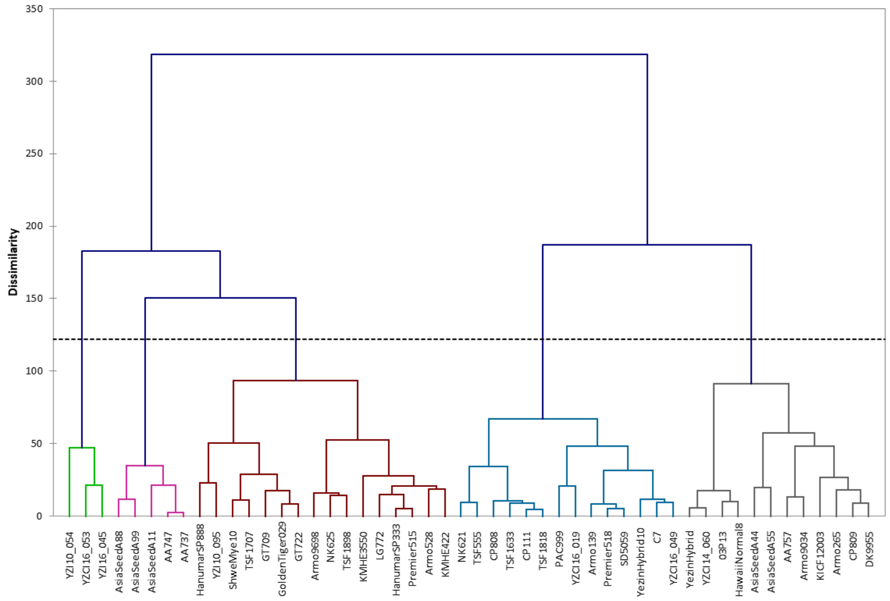

Fig. 2 Dendrogram of maize genotypes based on morphological distances by a visual assessment of the group of plants and single measurement of individual plants or part of plants

Table 1 Cluster based on qualitative characters

Cluster	No.	Name of genotypes
I	12	03P13, AA-757, Armo 265, Armo 9034, Asia Seed A44, Asia Seed A55, CP 809, DK 9955, Hawaii Norma l8, KICF12003, Yezin Hybrid, YZCI 14-060
II	5	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, YZI10-095
IV	14	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, YZI10-054, YZI16-045

Cophenetic correlation coefficient = 0.577

CONCLUSION

The total 50 maize genotypes (including hybrids and inbreds) were examined their qualitative characters. The results showed that genotypes varied different qualitative traits with different frequencies. 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 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.

APPENDIX

Some distinct qualitative traits of maize from this study were summarized below.

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