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Assessing diversity of Maize (*Zea mays* L.) genotypes based on multivariate analysis of the quantitative traits

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Abstract

Fourteen genotypes along with one standard check of maize were evaluated in Randomized Complete Block Design with three replications. Observations were taken for days to 50% germination, 50% tasselling, silking, tasselling silking interval, plant height, ear height, number of tassel branches, tassel length, leaves below cob, leaves above cob, ear length, ear girth with kernels, number of rows per ear, number of grains per row, thousand kernel weight and grain yield. Principal component analysis and cluster analysis were done on the observed data. Four principal components governing 83.3% of the variance and four distinct clusters having five, two, four and three genotypes in the respective clusters were identified. The genotypes of second cluster, COMPOZ-NIPB and SO3TEY/LN, represented the genotypes showing highest number of tassel branch, ear diameter, ear length, leaf below ear, leaf above ear, grain rows per ear, grains per row, thousand kernel weight and grain yield.The selection of genotypes from the second cluster, characterised by high value of traits like grain row per column, number of grains per row, thousand kernel weight and grain yield, could lead to a fruitful selection of better performing genotypes for future breeding activities and can be selected as promising parents for hybridization

Keywords: Cluster analysis, maize, multivariate analysis, PCA.

Introduction

The maize is one of the important cash crops cultivated globally and is among the top 3 in both cultivated area and demanded grain. Characterization of the crop comprises recording of the characters that are in general, highly heritable, easily observable through the naked eyes, and are expressed in all environments. The proper use of the adopted germplasm involves its characterization and evaluation.

The genetic relationship among them is an important step in germplasm utilization and

conservation. The analysis of the genetic diversity within and among the germplasm is especially important to both plant genetic resource management programs and breeding programs (Bretting & Widrlechner, 1995).

One of the important approaches to maize breeding is hybridization followed by subsequent selection. Choosing of parents is the first step in plant breeding program through hybridization. Genetic distance between parents is necessary in order to benefit transgressive segregation (Joshi et al., 2004). Higher the genetic distance between parents higher is the heterosis in progeny (Joshi and Dhawan, 1966; Anand and Murrty, 1968).Appropriate selection of the parents is imperative in crossing nurseries to enhance the genetic recombination for potential yield increase (Islam, 2004). Some of the appropriate methods currently available are cluster analysis, PCA and factor analysis, for genetic diversity identification, parental selection, tracing the pathway to evolution of crops, centre of origin and diversity, and study interaction between environments (Bhatt, 1970; Carves et al., 1987; Mohammadi and Prasanna, 2003; Eivazi et al., 2007).

Combined PCA along with other techniques or solitarily can be used for grouping (Mohammadi and Prasanna, 2003). The cluster analysis is an appropriate method to determine family relationships (Mellingers, 1972). The main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only (Mohammadi, 2002). One of the issues with breeding projects based on hybridization is estimating the relationship between parents before initiating the cross. Euclidean distance can theoretically estimate the genetic distance between parents so as to maximize the transgressive segregation (Hoque and Rahman, 2006). Through understanding the interrelationships existed between yield and its contributing components and the diversity in the performance of different genotypes, we can improve the efficiency of crop breeding programmes (Mohammadi et al., 2003).

This study was conducted with the objective to assess the diversity in the genotypes of maize in terms of different traits and identify the superior genotypes which can be further used in the breeding programs as promising superior parents and also for planning other breeding strategies. Determination of genetic diversity is useful for plant breeding and hence aids in production of more efficient plant species under different environmental conditions.

Material and Methodology

The present research was carried out during winter 2015 at the field of National Maize Research Programme (NMRP), Rampur, Chitwan, Nepal. The geographical location of the trial was $27^{o}37'$ N latitude, $84^{o}25'$ E longitude and at an altitude of 228 meter above sea level with sub-tropical climate (Thapa & Dangol, 1988). The material of experimentation wasobtained from National Maize Research Program (NMRP), Chitwan, which includes 14 genotypes including one standard check (Arun-4) variety of maize (Table 1). The experiment was laid out in randomized block design with three replications. The plot size was 5 m× 3 m = 15 m^2 each. The row spacing of each treatment for maize sowing was 75 cm and there were four rows per plot. Fertilizer was applied at the rate of 120:60:40 kg NPK per ha.

Sowing was done on 9^{th} October, 2015. Harvesting was done after complete maturity of the crop on 24^{th} March, 2016. The ears were harvested from sample plants and from two mid rows of treatment for yield estimation. The harvested ears were de-husked, air dried and kernels were threshed, cleaned and weighted,

then yield per plot was recorded at 15% moisture.

Observations were taken for days to 50% germination, 50% tasselling, silking, tasselling silkinginverval, plant height, ear height, number of tassel branches, tassel length, leaves below cob, leaves above cob, ear length, ear girth with kernels, number of rows per ear, number of grains per row, thousand kernel weight and grain yield (ton/ha).

Data entry and processing was done in Microsoft Excel 2017. Principal component analysis was done from all the observed data through Minitab 17. Similarly, cluster analysis and dendogram were also prepared with the help of Minitab 17.

Result and Discussion

Principal component analysis (PCA)

Twelve components were extracted from the 16 studied traits by PCA analysis. The first four components that explained 83.3% of total variation were used for clustering genotypes. In fact, with this method, 14 variables were reduced to four (Table 2) with the help of the PCA and the number of components shown by the scree plot (Fig 1).

The most effective trait in the first component were number of tassel branches, ear diameter, ear length, leaves below cob, leaves above cob and number of grains per row. Tasselling silking interval and days to silking were the most effective traits in the second component. The most effective traits in third component were tassel length, plant height, ear height and grain row per cob. Days to germination, leaves above cob, numbers of grains per row and grain yield were the most effective trait governing fourth component (Table 3). These were the major effective traits that governed the variation in these four components.

When the two first principal components account for high variation percentage, grouping according to these two components, can certainly be a useful method to find the clusters (Fotokian et al., 2002).

Cluster analysis

The cluster analysis of the studied quantitative traits of 14 maize genotypes is presented in the dendogram (Figure 2). The critical examination of dendrogram revealed four clusters. As this cluster analysis was based on quantitative traits, cluster was obtained on the basis of similarity percentage and related characters.

Five maize genotypes (ACROSS-99402, EEYC1, ZM-621/POOL-15, Early mid Katamani, ARUN-4 (StdChk)) were grouped in cluster 1 which represented 35% of total genotype. This cluster represented the genotypes that had moderate performance for all the traits.

Cluster 2 had 2 maize genotypes (COMPOZ-NIPB and SO3TEY/LN) which represent 14% of total genotypes. This cluster represented the genotypes showing highest number of tassel branch, ear diameter, ear length, leaf below ear, leaf above ear, grain rows per ear, grains per row, thousand kernel weight and grain yield. This cluster represented the genotype showing moderate tasseling silking interval and smallest tassel length.

Cluster 3 had 4 genotypes (FARMERS VARIETY, R.C./POOL-17, SO3TEY-LN/PP and SO3TEY-PO-BM) it represented 29% of the total genotypes. This cluster had the characteristics of high tassel length, plant height and ear height. This group also showed moderate yield, days to tasselling, tasselling silking interval, days to silking, thousand kernel weight and grain row per cob.

There are three genotypes (S97TEYGHAYB, Rajahar Local and POP-445/POP-446) in cluster

Table 1. List of plant material used in the experiment.

EN	Entry	EN	Entry
1	Across-99402	8	Rajahar Local
2	COMPOZ-NIPB	9	S97TEYGHAYB(3)
3	Earlymid Katamani	10	SO3TEY-LN/PP
4	EEYC1	11	SO3TEY-PO-BM
5	FARMERS VARIETY	12	SO3TEY/LN
6	POP-445/POP-446	13	ZM-621/POOL-15
7	R.C./POOL-17	14	ARUN-4 (Std Chk)

Table 2. Eigen analysis of the Correlation Matrix.

Eigen value	6.52	2.979	2.3789	1.4523	0.9557	0.5725	0.526
Proportion	0.407	0.186	0.149	0.091	0.06	0.036	0.033
Cumulative	0.407	0.594	0.742	0.833	0.893	0.929	0.962
Eigen value	0.2467	0.1712	0.1306	0.041	0.0225	0.0037	0
Proportion	0.015	0.011	0.008	0.003	0.001	0	0
Cumulative	0.977	0.988	0.996	0.998	1	1	1

Table 3. PCA analysis of 16 studied traits in maize genotypes.

Variable	PC1	PC2	PC3	PC4
Days to germination	-0.012	-0.256	-0.104	0.671
Days to tasseling	-0.048	-0.506	-0.166	0.118
Tasseling silking interval	-0.12	-0.419	0.08	-0.247
Days to silking	-0.057	-0.543	-0.111	0.042
Number of tassel branches	0.315	0.17	-0.106	0.074
Tassel length	-0.038	-0.179	0.547	0.088
Plant height	0.184	-0.126	0.521	0.051
Ear height	0.256	-0.021	0.437	-0.101
Ear girth/diameter	0.327	-0.192	-0.069	-0.095
Ear length	0.339	-0.153	-0.039	-0.108
Leaves below cob	0.348	0.048	-0.001	-0.165
Leaves above cob	0.305	-0.21	-0.078	-0.359
Grain row per cob	0.296	0.008	-0.306	0.07
Number of grains per row	0.301	0.025	0.158	0.398
Thousand kernel weight	0.288	-0.086	-0.197	-0.056
Grain yield	0.288	0.126	0.001	0.323

Table 4. Average value of the studied traits of two clusters formed from cluster analysis.

Variable	Cluster1	Cluster2	Cluster3	Cluster4	Grand Centroid
Days to germination	5.066	5.165	4.832	4.887	4.975
Days to tasseling	56.402	56.670	55.998	56.110	56.262
Tasseling silking interval	4.798	4.665	4.752	4.667	4.738
Days to silking	61.264	61.335	61.000	60.777	61.094
Number of tassel branches	13.594	15.200	11.585	9.977	12.474
Tassel length (cm)	35.652	32.035	37.275	33.747	35.191
Plant height (cm)	165.540	156.875	176.385	146.370	163.293
Ear height (cm)	50.166	48.040	56.313	35.790	48.538
Ear girth/diameter (cm)	3.980	4.405	4.110	3.590	3.994
Ear length (cm)	13.644	14.450	12.995	10.463	12.892
Leaves below cob	10.200	10.665	10.253	9.333	10.096
Leaves above cob	5.934	6.500	5.832	4.777	5.738
Grain row per cob	12.292	13.835	12.510	11.957	12.503
Number of grains per row	21.126	22.085	21.215	16.423	20.281
Thousand kernel weight (gm)	207.514	242.350	219.978	199.927	214.426
Grain yield (ton/ha)	2.036	2.595	2.245	1.823	2.130

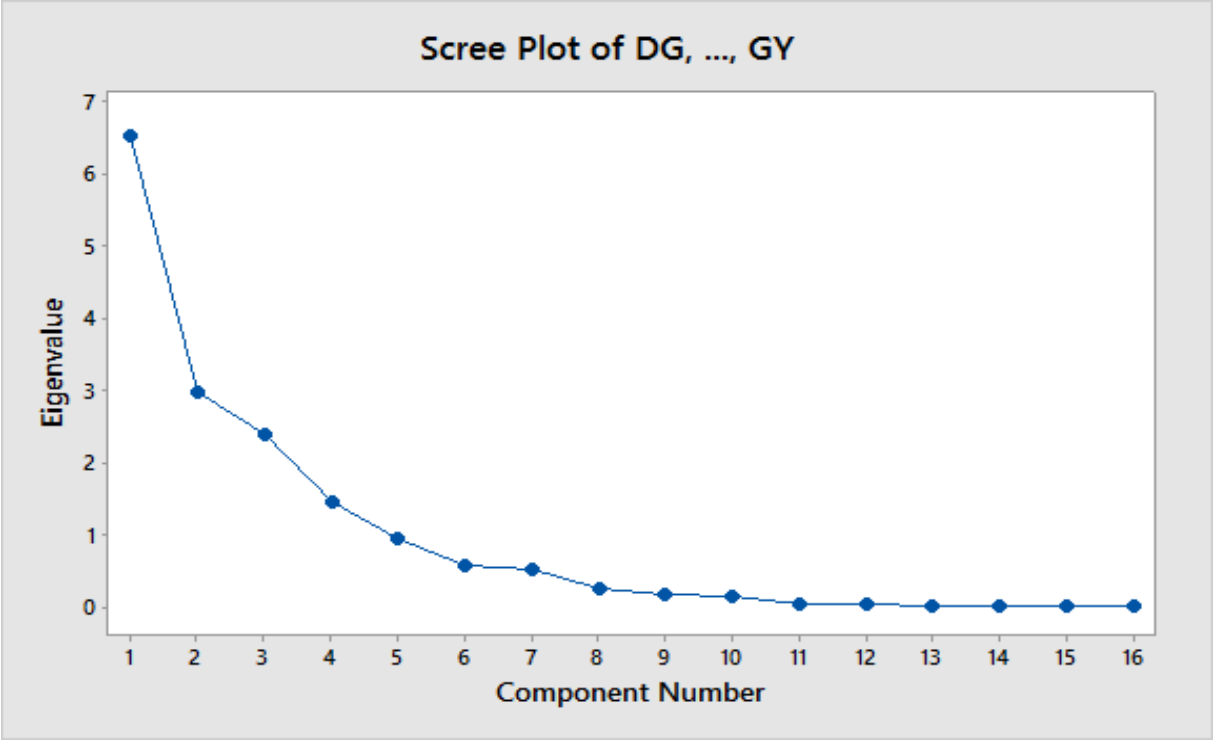

Figure 1. Scree plot for the determination of number of components in PCA.

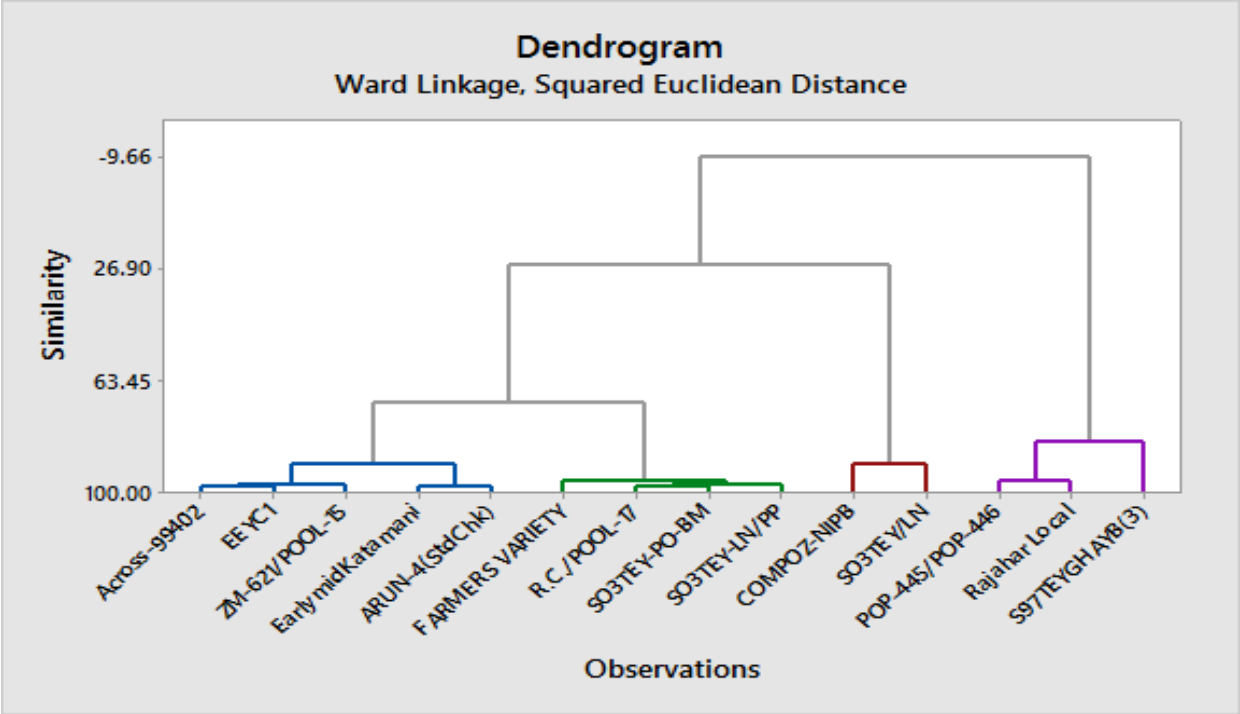

Figure 2. Dendogram of 14 genotypes for 16 studied variables using hierarchical cluster analysis (ward's method and squared Euclidean Distance).

which accounted for 21% of total genotypes. This cluster represented the genotype showing the least values of number of tassel branches, plant height, ear height, ear length, leaf below ear, leaf above ear, ear diameter, grain per row, thousand kernel weight and grain yield. Whereas the group shows moderate performance in terms of days to germination, tasselling, tasselling silking interval and tassel length.

Clustering these genotypes can be useful in identifying accessions with similar traits which can in turn be useful in breeding programs. Crossing genotypes belonging to different clusters could maximize the chances of transgressive segregation as there is higher probability that unrelated genotypes will contribute unique desirable alleles at different loci.

The observation of second cluster and the associations therein of high value for the traits like number of tassel branches, ear diameter, number of leaves below cob, grain row per cob, grain numbers per row, thousand kernel weight and grain yield hint that the selection of the varieties from the second cluster can be worthwhile for future breeding purpose and also for getting better performing genotypes.

Also, the high value traits that this cluster comprises are the traits that are also most effective in governing the variance in the major four principal components. The selection for the high value of traits other than yield is important as the above-mentioned traits. Selection of clusters with higher value of these traits will lead to selection of better yielding genotypes.

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