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Multivariate Analysis of Genetic Diversity among some Maize Genotypes under Maize-*Albizia* Cropping System in Indonesia

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ABSTRACT

Maize is one of the most important cereals in the world after wheat and rice. Now-a-days, the improvement of maize production is hindered by conversion of agricultural lands into industrial and residential areas. One of the suggested solutions is the production of maize cultivars that can be incorporated in agroforestry systems and can be grown with tree plants such as *Albizia.* The success of the improvement of new maize cultivars suited to this Maize-*Albizia* system depends on the availability of genetic variability. Research on the genetic diversity of maize inbred lines that is suited to the agroforestry system with *Albizia* were conducted in a real forests planted with *Albizia* tree plants that are around three years old in Cimalaka, Sumedang, West Java, Indonesia. The evaluation of inbred lines was laid on a split plot design with two replications. The main plot consisted of two cropping systems, namely; maize sole cropping system and Maize-*Albizia* agroforestry system. The subplots were having seventy five inbred lines of maize. The biometric characters included days to anthesis, days to silking, days to harvesting, plant height, length of nodes, plant diameter, chlorophyll content, leaf area index, ear length, ear diameter, number of rows, weight of 1000 seeds and ear weight per plant. Based on the analysis of the main components, in conditions maize sole cropping system, the results showed an Eigen value between 1.08-4.52 which contributes to 67.27% variability, whereas, in the condition Maize-*Albizia* cropping system, the Eigen value ranged from 1.16-5.37 which contributed to 71.85% variability. Cluster analysis of 75 maize genotypes showed a wide distribution obtaining nine clusters in the maize sole cropping system and five clusters in the Maize-*Albizia* cropping system. High genetic variability seen in both cropping system greatly supports the development of elite new cultivars of maize that can be utilized in agroforestry systems.

Key words: Agroforestry, genetic diversity, Maize-*Albizia* cropping system, multivariate analysis

INTRODUCTION

Maize, together with wheat and rice are the important cereal crops in the world (Rezaeieh and Eivazi, 2011). Indonesia is among the important world maize producer in South East Asia (Ruswandi *et al*., 2014). Some of the problems encountered in maize development in Indonesia are the conversion of fertile land under maize production into industrial and residential areas, drought due to global climate change, displacement of maize planting area to marginal land including forest and others. One of the possible solutions in responding to the land shortage is incorporating maize in an agroforestry system. In this manner, several needs of farmers can be met and auxiliary sources of food, fodder, fuel-wood can be obtained.

Agroforestry is a land management system, which is a combination of crop production with forestry technologies (De Foresta and Michon, 1996). *Albizia* is a popular leguminous tree grown for agroforestry in Indonesia. This tree can be found in a very broad distribution of climate and is among the fastest growing timber species. It is also used in pulp, paper, veneer and furniture (Chairomani and Suhaendi, 1994) aside from being environmentally friendly (Nemoto, 2002). The leguminous supply nitrogen, organic materials and recycle leached nutrients (Yamoah *et al*., 1986). Thus, it has the potential to be used in an agroforestry system with maize, which is called as Maize-*Albizia* cropping system.

The first step in the development of a Maize-*Albizia* cropping system is breeding of maize cultivars that are suitable for growth in such a system. In order to achieve this, maize plants should be screened for genetic diversity. The success in developing new high yield cultivars depends on the availability of genetically diverse germplasm (Buckler, 2009). The higher the genetic diversity possessed, the greater the chances of success for developing new superior cultivars. Germplasm improvement and genetic diversity is a key to reliable and sustainable production of the food crops through breeding.

Measuring the available genetic diversity is of utmost importance for effective evaluation and utilization of germplasm (Zubair *et al*., 2007). Some researchers emphasize the importance of the assessment of the levels and patterns of genetic diversity in crop breeding (Barrett and Kidwell, 1998; Cox *et al*., 1986; Franco *et al*., 2001; Habtamu and Milion 2013; Hallaur and Miranda, 1988; Mohammadi and Prasanna, 2003; Thompson *et al*., 1998). The diverse applications include: (1) Analysis of genetic variability in cultivars, (2) Identification of diverse parental combinations to create segregating progenies with maximum genetic variability for further selection, (3) Introgressing of desirable genes from diverse germplasm into the available genetic base, (4) Study of genetic relationships among inbred lines or pure lines for planning crosses, assigning lines to specific heterotic groups and for precise identification with respect to plant varietal protection, (5) Classification of accessions and identification of subsets of core accessions with possible utility for specific breeding purposes and (6) Identification groups with the same genetic background for preservation, evaluation and utilization of genetic resources.

Multivariate analysis is the most popular approach for genetic variability estimation to study the patterns of variation and their genetic relationships among germplasm collections (Ajmal *et al*., 2013; Malik *et al*., 2014). The PCA and cluster analysis are preferred tools for morphological characterization of genotypes and their grouping on similarity basis based on this approach (Mohammadi and Prasanna, 2003; Peeters and Martinelli, 1989). Multivariate analyses have been utilized in many countries for several crops such as wheat (Ajmal *et al*., 2013; Malik *et al*., 2014), sorghum (Ali *et al*., 2011) and maize (Lee *et al*., 2005; Babic *et al*., 2010; Azad *et al*., 2012).

We have previously developed a germplasm collection with more than 500 maize elite inbred lines representing the major tropical breeding programs of Indonesia. Some of the lines in the collection have been described in previous studies, viz. Ruswandi *et al*. (2014) reported some maize genotypes showing early maturity and also drought tolerance. Some maize hybrid formation showed high yield (Ruswandi *et al*., 2015a, b). Based on the information on maturity, drought tolerance and yield potential data obtained from the field experiments, 75 lines were chosen for the present study. The objective was to estimate genetic diversity of elite maize inbred collection that can potentially be used in a Maize-*Albizia* cropping system.

MATERIALS AND METHODS

Genetic materials: Genetic material evaluated in the research included 75 inbred lines of maize developed by Ruswandi, Laboratory of Plant Breeding, Faculty of Agriculture, University of Padjadjaran Indonesia and 2 inbred lines of ICERI (Indonesia Cereals Research Institute). These inbred lines were inbred lines series BR, DR, MBR and MDR. Evaluation of inbred lines in experimental trials was performed in rainy season of 2014 (April-July, 2014), in the community forests planted with 3 year old *Albizia* trees in 2×2 m. The forests are located in Cimalaka, West Java, Indonesia at 1100 m asl (above sea level), which represents climate type of C3 classified by Oldeman.

Field experimental details: The evaluation of inbred lines was laid on a split plot design with two replications. The main plot consisted of two cropping systems, namely; maize sole cropping system and Maize-*Albizia* agroforestry system. The subplots had 75 inbred lines of maize. The experimental plot consisted of single rows, 5 m long, with 0.75 m between rows and between plots and 0.20 m within rows. During the crop cultivation, the standard crop management practices were applied and the plots were manually harvested.

The characters included days to anthesis, days to silking, days to harvesting, plant height, length of nodes, plant diameter, chlorophyll content, leaf area index, ear length, ear diameter, number of rows, weight of 1000 seeds and ear weight per plant. The biometric characters (mentioned above) were recorded from 15 randomly chosen competitive plants in each replicate.

Data analysis: The average data were subjected to Analysis of Variance (ANOVA) using Microsoft Office Excel 2010. Principal Component Analysis (PCA) was used to classify maize genotypes and see how big contribution to the character of maize genotype appearance. Genetic diversity and distance based on the similarity between objects under study were analyzed using cluster analysis based on the "t" Euclidian coefficient. The XLSTAT 2012 computer software was used for cluster analysis and PCA.

RESULTS AND DISCUSSION

Analysis of variance: The results of Table 1 show that days to tasseling, days to silking, days to harvesting, node length, leaf area index, chlorophyll content and grain yield is influenced by

Table 1: ANOVA and coefficient of variance from 14 biometric characters observed

Parameters	MS cropping system (A)	MS genotypes (B)	MS A× B	CV (%)
UBB	**	**	**	1.20
UBJ	*	**	**	1.48
UP	**	**	**	2.07
TT		**	**	14.37
PR	*	**	**	13.81
DB		**	**	7.51
LD	**	**	**	5.86
ILD	**	**	**	5.86
KLO	*	**	**	14.18
DT		**	**	6.34
PT		**	*	12.17
JB		**		9.53
B1000		**	**	11.91
YIELD	*	**	**	14.03

**Significant at 0.01 probability level, UBB: Days to silking; UBJ: Days to tasseling, UP: Days to harvesting, TT: Plant height, PR: Node length, DB: Stem diameter, LD : Leaf area, ILD: Leaf area index, KLO: Chlorophyll content, DT: Ear diameter, PT : Ear length, JB: Rows number, B1000 =1000 seeds weight, Yield: Grain yield per ha

Table 2: Origin of 75 maize genotypes in the study

No.	Genotype	Origin	No.	Genotype	Origin
1	DR 1	Plant breeding Lab., UNPAD, Indonesia	39	M6DR 7.3.2	mutant line derived from DR 7
2	DR 3	Plant breeding Lab., UNPAD, Indonesia	40	M6DR 7.4.1	mutant line derived from DR 7
3	DR 4	Plant breeding Lab., UNPAD, Indonesia	41	M6DR 7.4.2	mutant line derived from DR 7
4	DR 5	Plant breeding Lab., UNPAD, Indonesia	42	M6DR 8.5.3	mutant line derived from DR 8
5	DR 6	Plant breeding Lab., UNPAD, Indonesia	43	M6DR 8.8.1	mutant line derived from DR 8
6	DR 7	Plant breeding Lab., UNPAD, Indonesia	44	M6DR 9.1.3	mutant line derived from DR 9
7	DR 8	Plant breeding Lab., UNPAD, Indonesia	45	M6DR 9.1.5	mutant line derived from DR 9
8	DR 9	Plant breeding Lab., UNPAD, Indonesia	46	M6DR 9.4.1	mutant line derived from DR 9
9	DR 10	Plant breeding Lab., UNPAD, Indonesia	47	M6DR 10.2.2	mutant line derived from DR 10
10	DR 11	Plant breeding Lab., UNPAD, Indonesia	48	M6DR 14.1.1	mutant line derived from DR 14
11	DR 12	Plant breeding Lab., UNPAD, Indonesia	49	M6DR 14.2.1	mutant line derived from DR 14
12	DR 14	Plant breeding Lab., UNPAD, Indonesia	50	M6DR 14.2.2	mutant line derived from DR 14
13	DR 15	Plant breeding Lab., UNPAD, Indonesia	51	M6DR 14.3.1	mutant line derived from DR 14
14	DR 16	Plant breeding Lab., UNPAD, Indonesia	52	M6DR 14.3.8	mutant line derived from DR 14
15	DR 17	Plant breeding Lab., UNPAD, Indonesia	53	M6DR14.3.11	mutant line derived from DR 14
16	DR 18	Plant breeding Lab., UNPAD, Indonesia	54	M6DR 14.5.1	mutant line derived from DR 14
17	DR 20	Plant breeding Lab., UNPAD, Indonesia	55	M6DR 16.1.1	mutant line derived from DR 16
18	BR 152	Plant breeding Lab., UNPAD, Indonesia	56	M6DR 16.2.1	mutant line derived from DR 16
19	BR 153	Plant breeding Lab., UNPAD, Indonesia	57	M6DR16.5.15	mutant line derived from DR 16
20	BR 154	Plant breeding Lab., UNPAD, Indonesia	58	M6DR16.6.14	mutant line derived from DR 16
21	BR 157	Plant breeding Lab., UNPAD, Indonesia	59	M6DR 16.7.1	mutant line derived from DR 16
22	M6DR 1.1.12	mutant line derived from DR 1	60	M6DR 18.2.1	mutant line derived from DR 18
23	M6DR 1.1.3	mutant line derived from DR 1	61	M6DR 18.3.1	mutant line derived from DR 18
24	M6DR 1.2.3	mutant line derived from DR 1	62	M6DR 18.4.1	mutant line derived from DR 18
25	M6DR 1.6.3	mutant line derived from DR 1	63	M6DR 18.5.1	mutant line derived from DR 18
26	M6DR 3.1.10	mutant line derived from DR 3	64	M6DR 18.6.1	mutant line derived from DR 18
27	M6DR 3.1.2	mutant line derived from DR 3	65	M6DR 18.8.1	mutant line derived from DR 18
28	M6DR 3.6.1	mutant line derived from DR 3	66	M6DR 12.3.1	mutant line derived from DR 12
29	M6DR 4.2.2	mutant line derived from DR 4	67	M6BR153.1.2	mutant line derived from BR 153
30	M6DR 4.7.2	mutant line derived from DR 4	68	M6BR153.2.2	mutant line derived from BR 153
31	M6DR 4.8.8	mutant line derived from DR 4	69	M6BR153.6.1	mutant line derived from BR 153
32	M6DR 5.4.1	mutant line derived from DR 5	70	M6BR153.7.1	mutant line derived from BR 153
33	M6DR 5.5.1	mutant line derived from DR 5	71	M6BR 153.10.2	mutant line derived from BR 153
34	M6DR 7.1.2	mutant line derived from DR 7	72	M6BR153.11.1	mutant line derived from BR 153
35	M6DR 7.1.7	mutant line derived from DR 7	73	M6BR153.13.1	mutant line derived from BR 153
36	M6DR 7.1.9	mutant line derived from DR 7	74	G-632	line derived from ICERI
37	M6DR 7.2.5	mutant line derived from DR 7	75	G-203-1	line derived from ICERI
38	M6DR 7.3.1	mutant line derived from DR 7			

cropping system, genotype and the interaction between cropping system and genotype. However, characters such as plant height, stem diameter, diameter of ear, length of ear, weight of 1000 seeds were found influenced by genotype and interaction between genotype and cropping system, whereas, the number of rows per ear was found influenced only by the genotype.

Fehr (1987) reported that the level of performance of different genotypes might not be the same if they are planted in different environments and will grow according to their genetic capability. The performance of one plant in one population varies with their genetic make up and the environment affecting it (Poehlman and Sleper, 1995).

The efficiency of one trial can be determined in terms of its Coefficient of Variation (CV). The greater the CV, the efficiency is lower. A higher CV shows a decrease in accuracy of the trial. The ideal CV should be less than 20%, which indicates a higher efficiency of the results. Table 2 shows that in all characters, the CV is less than 20%, which indicates the accuracy of the results.

Principal component analysis: Multivariate analysis is used to analyze a group of data with more than one variable. One of the multivariate analyses is Principal Component Analysis (PCA), which aims to reduce the dimension from a group of data with a higher number of variables that

Table 3: Principle component analysis of various morpho-physiological traits in maize under conditions maize sole cropping system and Maize-*Albizia* cropping system

Parameters	PC 1	PC 2	PC 3	PC 4
Eigenvalue				
Maize sole cropping system	4.523	2.361	1.446	1.088
Maize-*Albizia* cropping system	5.369	2.052	1.478	1.159
Variability (%)				
Maize sole cropping system	32.308	16.861	10.326	7.772
Maize-*Albizia* cropping system	38.349	14.660	10.557	8.281
Cumulative (%)				
Maize sole cropping	32.308	49.169	59.495	67.267
Maize-*Albizia* cropping system	38.349	53.009	63.566	71.847

Table 4: Factor loadings morpho-physiological trait markers contributed to variability in maize sole cropping system

Parameters	PC 1	PC 2	PC 3	PC 4
UBB	-0.190	0.822	-0.331	0.118
UBJ	-0.222	0.872	-0.244	0.046
UP	-0.119	-0.102	0.029	0.928
TT	0.589	-0.279	-0.318	0.303
PR	0.281	-0.514	-0.446	-0.043
DB	0.718	0.013	-0.078	0.220
LD	0.840	0.025	-0.327	-0.064
ILD	0.840	0.025	-0.327	-0.064
KLO	0.596	-0.266	-0.088	-0.146
DT	0.710	0.258	0.456	0.125
PT	0.450	0.346	-0.032	0.006
JB	0.414	-0.110	0.666	0.070
B1000	0.586	0.489	0.120	-0.025
YIELD	0.702	0.248	0.286	-0.132

UBB: Days to silking, UBJ: Days to tasseling, UP: Days to harvesting, TT: Plant height, PR: Node length, DB : Stem diameter, LD: Leaf area, ILD: Leaf area index, KLO: Chlorophyll content, DT: Ear diameter, PT: Ear length, JB: Rows number, B1000 =1000 seed weight, Yield: Grain yield per ha

Table 5: Factor loadings morphological trait markers contributed to variability in Maize-*Albizia* cropping system

Parameters	F1	F2	F3	F4
UBB	-0.520	0.676	0.399	-0.001
UBJ	-0.492	0.704	0.407	-0.011
UP	-0.355	0.326	0.016	0.705
TT	0.736	-0.115	-0.120	0.342
PR	0.711	0.083	-0.020	0.399
DB	0.705	0.416	-0.251	-0.041
LD	0.740	0.485	-0.072	-0.336
ILD	0.740	0.485	-0.072	-0.336
KLO	0.721	-0.059	-0.163	-0.033
DT	0.677	-0.122	0.539	-0.037
PT	0.572	0.150	0.353	0.279
JB	0.103	-0.435	0.688	-0.225
B1000	0.540	0.178	0.024	0.098
YIELD	0.695	-0.262	0.385	0.137

UBB: Days to silking, UBJ: Days to tasseling, UP: Days to harvesting, TT: Plant height, PR: Node length, DB: Stem diameter, LD: Leaf area, ILD: Leaf area index, KLO: Chlorophyll content, DT: Ear diameter, PT: Ear length, JB: Rows number, B1000 =1000 seeds weight, Yield: Grain yield per ha

are interrelated (Jolliffe, 2002). Main component analysis is a technique used to determine the contribution of one character on variability to easily determine the character that can represent a genotype (Afuape *et al*., 2011). The PCA is also used to describe a genotypic data to look for characters that have high contribution towards variability shown within the biplot.

Results of the PCA analysis showed four main axial components that have Eigen values more than 1.00 (Table 3). Table 4 and 5 shows the Principal Component (PC) that forms variability from 14 characters observed. The determination of the PC is based on an eigenvalue more than 1.00 (Jeffer, 1967) and a cumulative percentage more than 80% (Jolliffe, 2002). For each PC, characters are with PC values more than 0.70 (Jeffer, 1967).

In maize sole cropping system, the Eigen value ranged from 1.08-4.52 which contributed to 67.27% variability. Primary component 1 (PC 1) covers 32.31% of variability from a variation of 75 genotypes given the biometric characters namely; stem width, leaf width, leaf area, leaf area index, ear width and yield per hectare. The PC 2 covers 16.86% variability from variations in 75 genotypes given the characters days to tasseling and days to silking. PC 3 covers 10.32% variability given the character rows number. For PC 4, it covers 7.77% variability given the character days to harvesting.

Under Maize-*Albizia* cropping system, the Eigen value was between 1.16-5.37 which gives a variability of as high as 71.85%. The PC 1 covered 38.31% of variability from a variation of 75 genotypes given the characters plant height, node length, stem length, leaf area and chlorophyll content. The PC 2 showed 14.66% variability given the characters days to tasseling and for PC 4, variability was at 8.28% given the character days to harvesting. For both sets of cropping, maize sole cropping system and Maize-*Albizia* cropping system, the one that gave a variability contribution were stem diameter, leaf area, leaf area index, days to tasseling and days to harvesting.

The scatter plots are shown in a graphic biplot as determined by the PC values that give the highest contribution to variability. The PC 1 and PC 2 are the component values that give the highest contribution towards variability of a character. Under maize sole cropping system, the PC 1 and PC 2 values are 32.31 and 16.86%, respectively, whereas, under Maize-*Albizia* cropping system, the PC 1 and PC 2 values were 38.31 and 14.66%, respectively.

The variability values from the two components for each maize genotype are scattered within the biplot forming 4 quadrants (Fig. 1 and 2). The figures show that the different morpho-physiological and maize genotypes are found in four different quadrants. In the study by Worede *et al*. (2014), PC 1 and PC 2 that showed cumulative variabilities as high as 61.16% were used. This shows that there are characters in the PC that have relatively high variability and are important in separating genotypes. Under maize sole cropping system (Fig. 1), quadrant I has a positive value showing the biometric characters viz. leaf area index, leaf area, yield per hectare

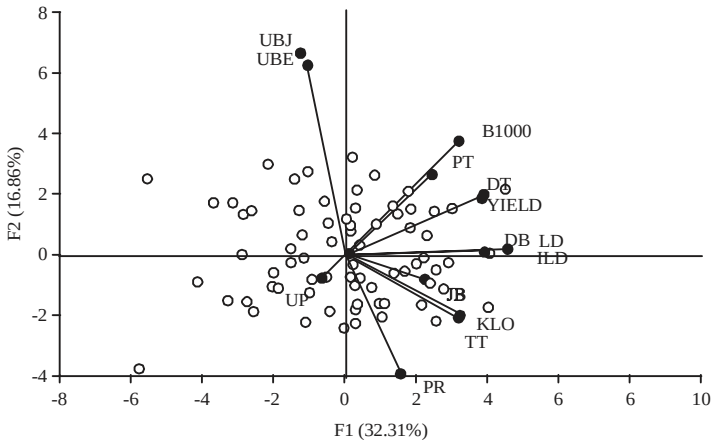

Fig. 1: Distribution pattern of 75 maize inbred in maize sole cropping system based on 14 morpho-physiological characters

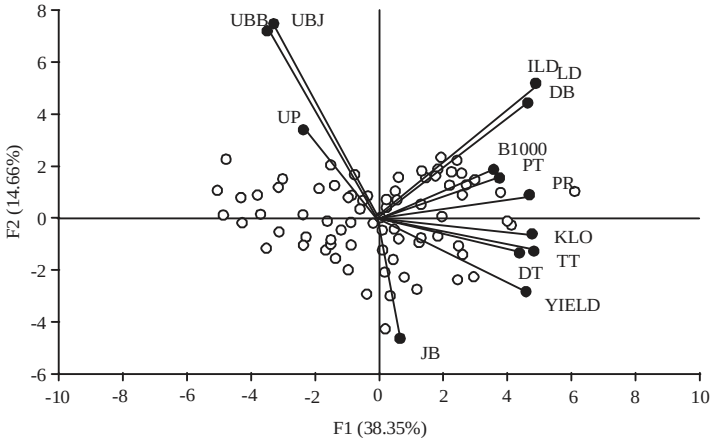

Fig. 2: Distribution pattern of 75 maize inbred in Maize-*Albizia* cropping system based on 14 morpho-physiological characters

and weight per 1000-seeds and ear length are tightly related or linked. Genotypes in quadrant I (DR 4, DR 6, DR 9, DR 10, DR 11, DR 12, DR 14, DR 16, DR 17, DR 18, DR 20, BR 154, M6DR 16.1.1, M6DR 18.5.1, M6DR 16.6.14, M6DR 3.1.10, M6BR 153.2.2, M6DR 1.1.3 and M6DR 1.1.12) are closely related and they have high level of similarities. For Maize-*Albizia* cropping system, (Fig. 2), characters with positive values are leaf area index, leaf area, stem diameter, weight per 1000 seeds, ear length and node length. Genotypes that have high similarities are M6DR 1.6.3, M6DR 8.5.3, M6DR 16.6.14, M6DR 3.1.10, M6DR 1.1.3, M6DR 7.3.1, M6DR 16.2.1, M6DR 14.5.1, M6DR 1.2.3, M6DR 14.2.2, M6DR 7.4.2, M6DR 16.1.1, DR 4, DR 6, DR 7, DR 9, DR 10, DR 11, DR 12, DR 20, BR 153. Different characters in the same quadrant mean that they are closely and positively related. The opposite is true if they are in different quadrants.

Agglomerative Hierarchical Clustering (AHC) analysis: Cluster analysis is a method used in grouping a set of characters into clusters. Genotypic clustering makes use of a procedure called Agglomerative Hierarchical Clustering (AHC) using Unweighted Pair Group Method with Arithmetic mean (UPGMA) mentioned by Mohammadi and Prasanna (2003). Cluster analysis is one of the statistical techniques aimed in grouping objects in clusters so that the objects in one cluster have high similarities than those in other clusters (Sharma, 1996). Euclidian distance values in the range of 0-1 indicates a small dissimilarity, whereas, its value more than 1 indicates a large dissimilarity coefficient. A small dissimilarity coefficient indicates that for each genotype one or the other characters have a narrow variability (Tairo *et al*., 2008). Cluster analysis for 75 genotypes using 14 morpho-physiological characters is presented in Fig. 3 (maize sole cropping system) and Fig. 4 (Maize-*Albizia* cropping system). Morphological traits have been successfully used for estimation of genetic diversity and cultivar development since they provide a simple way of quantifying genetic variation (Fufa *et al*., 2005).

In maize sole cropping system, clustering resulted in nine main clusters with a point Euclidian coefficient of 4.8, level of dissimilarity between genotypes is high in the dendogram with a genetic distance of 0-0.8. In Maize-*Albizia* cropping system, five main clusters were formed with a point

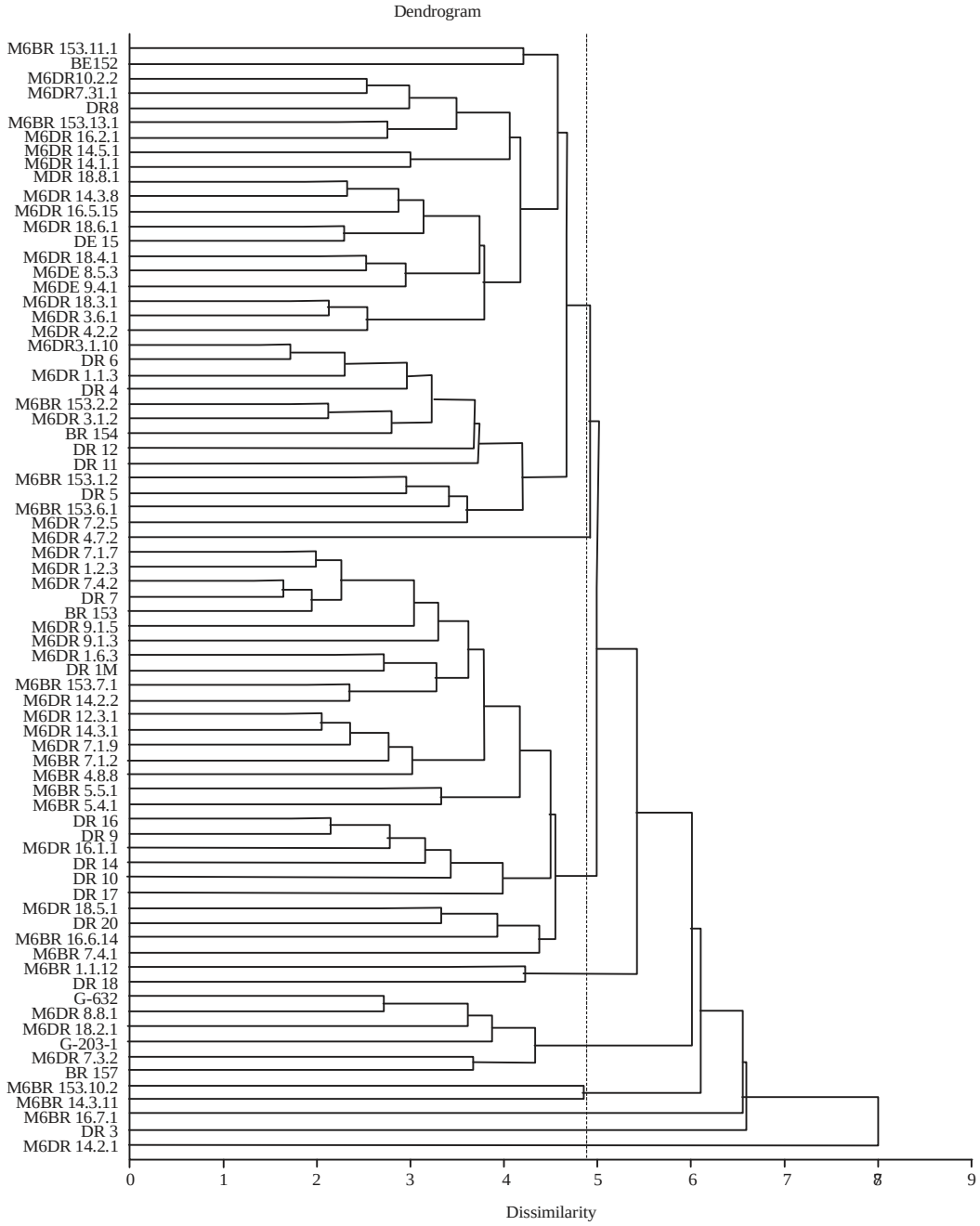

Fig. 3: Dendogram for 75 maize inbred based on morpho-physiological characters in maize sole cropping system

Euclidian coefficient of 5.1. The level of dissimilarity among genotypes in the dendogram has a distance of 0-6.4. From the dendogram results, the clustering of genotypes based on the morpho-physiological characters is as shown in Table 6. The dendogram shows that the distribution of the 75 genotypes is wide. Nine and five clusters were obtained in the dendogram forming a wide distance from its cluster. Morpho-physiological diversity in the materials studied is structured by

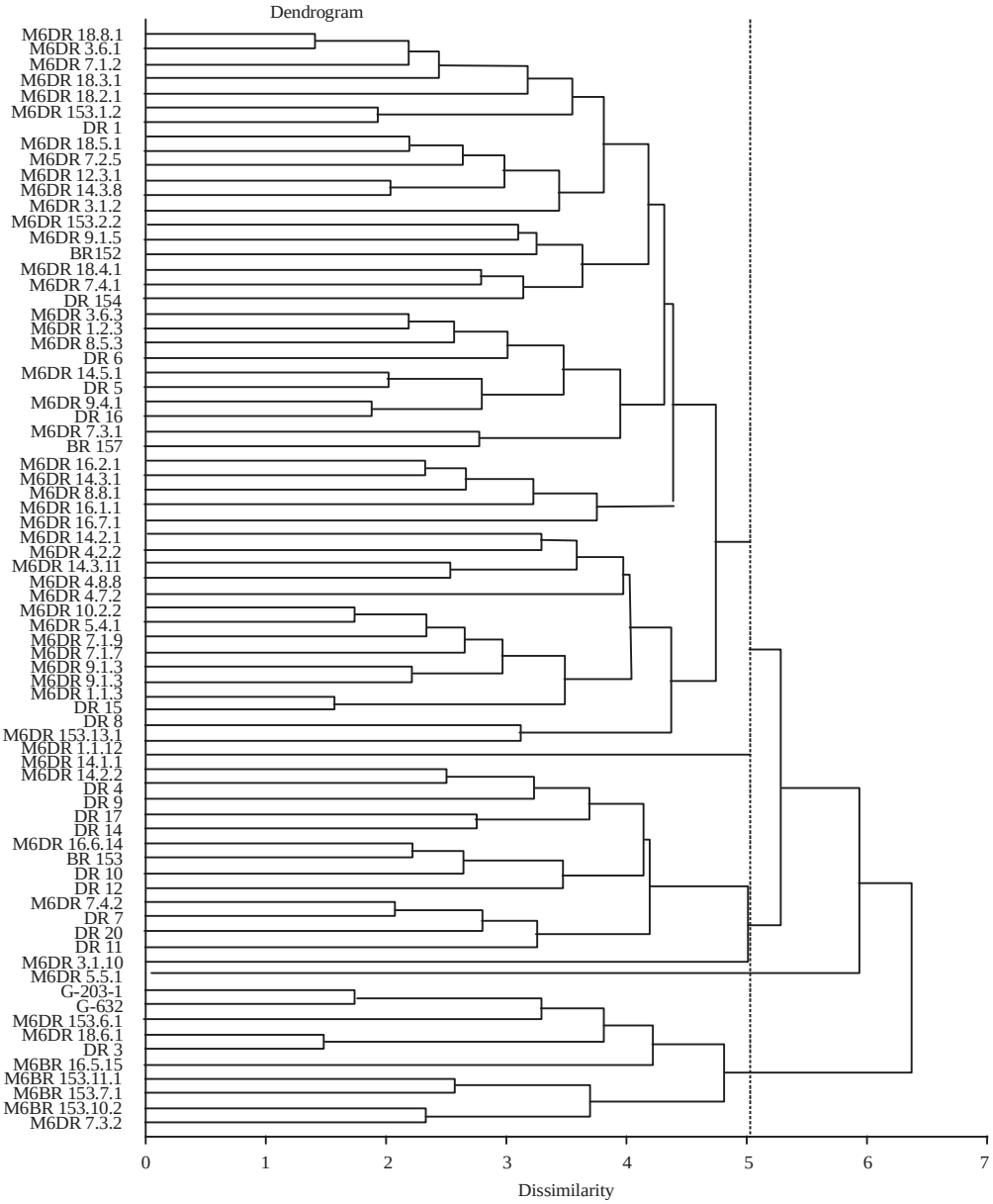

Fig. 4: Dendogram for 75 maize inbred based on morpho-physiological characters in Maize-*Albizia* cropping system

genotypes and this diversity could be utilized for cultivar breeding and germplasm conservation programs (Ali *et al*., 2011; De Jesus *et al*., 2013), particularly in breeding for Maize-*Albizia* cropping system.

CONCLUSION

Based on the results of the experiment, it can be concluded that there is a high variability in the morpho-physiology in the maize genotypes from UNPAD. This is found in almost all the characters observed in maize sole cropping system and Maize-*Albizia* cropping system. Multivariate analysis showed high genetic variability in all genotypes in both cropping system.

Table 6: Genotypes accessions related to various clusters based on various morpho-physiological traits

Clusters	Cropping system	Genotypes
I	Maize	DR 1; DR 7; DR 9; DR10; DR 14; DR 16; DR 17; DR 20; BR 153; M6DR 1.2.3; M6DR 1.6.3 ; M6DR 4.8.8; M6DR 5.4.1; M6DR 5.5.1; M6DR 7.1.2; M6DR 7.1.7; M6DR 7.1.9;M6DR 7.4.1; M6DR 7.4.2; M6DR 9.1.3; M6DR 9.1.5; M6DR 14.2.2; M6DR 14.3.1; M6DR 16.1.1; M6DR 16.6.14; M6DR 18.5.1; M6DR 12.3.1; and M6BR 153.7.1
I	Maize-*Albizia* cropping system	DR1; DR5; DR6; DR8; DR 15; DR 16; DR 18; BR 152; BR 154; BR 157; M6DR 1.1.2;M6DR 1.1.3; M6DR 1.2.3; M6DR 1.6.3; M6DR 3.1.2; M6DR 3.6.1; M6DR 4.2.2; M6DR 4.7.2; M6DR 4.8.8; M6DR 5.4.1; M6DR 7.1.2; M6DR 7.1.7; M6DR 7.1.9; M6DR 7.2.5; M6DR 7.3.1; M6DR 7.4.1; M6DR 8.5.3; M6DR 8.8.1; M6DR 9.1.3; M6DR 9.15; M6DR 9.4.1; M6DR 10.2.2; M6DR 14.2.1; M6DR 14.3.1; M6DR14.3.8; M6DR 14.3.11; M6DR 14.5.1; M6DR16.1.1; M6DR 16.2.1; M6DR16.7.1; M6DR 18.2.1; M6DR 18.3.1; M6DR18.4.1; M6DR18.5.1; M6DR 18.8.1; M6DR12.3.1; M6BR 153.1.2; M6BR 153.2.2; and M6BR 53.13.1
II	Maize	DR3
	Maize-*Albizia* cropping system	DR 3; M6DR 7.3.2; M6DR 16.5.15; M6DR 18.6.1; M6BR 153.6.1; M6BR 153.7.1; M6BR 153.10.2; M6BR 153.11.1; G-632 and G-203-1
III	Maize	DR4;DR 5;DR 6; DR 8; DR 11; DR 12; DR 15; BR 152; BR 154; M6DR 1.1.3; M6DR 3.1.10; M6DR 3.1.2; M6DR 3.6.1; M6DR 4.2.2; M6DR 7.2.5; M6DR 7.3.1; M6DR 8.5.3; M6DR 9.4.1; M6DR 10.2.2; M6DR 14.1.1; M6DR 14.3.8; M6DR 14.5.1; M6DR 16.2.1; M6DR16.5.15; M6DR 18.3.1; M6DR 18.4.1; M6DR 18.6.1; M6DR 18.8.1; M6BR 153.1.2; M6BR 153.2.2; M6BR 153.6.1; M6BR 153.11.1; M6BR 153.13.1;
	Maize-*Albizia* cropping system	DR 4; DR7; DR 9; DR 10; DR 11; DR 12; DR 14; DR 17; DR 20; BR 53; M6DR 3.1.10; M6DR 7.4.2; M6DR 14.2.2 and M6DR 16.6.14
IV	Maize	DR 18; MGDR 1.1.12
	Maize-*Albizia* cropping system	M6DR 5.5.1
V	Maize	BR 157; M6DR 7.3.2; M6DR 8.8.1; M6DR 18.2.1; G-632; G-203-1
	Maize-*Albizia* cropping system	M6DR 14.1.1
VI	Maize	M6DR 4.7.2
VII	Maize	M6DR 14.2.1
VIII	Maize	M6DR 14.3.11; M6BR 153.10.2
IX	Maize	M6DR 16.7.1

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