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## GENETIC DIVERSITY STUDIES IN ELITE MAIZE (*ZEA MAYS* L.) LINES

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### ABSTRACT

Analysis of variance (ANOVA) showed a significant difference among the 30 genotypes for all the eighteen characters studied, indicating the presence of enough genetic variability and diversity. Data recorded were subjected to Mahalanobis D<sup>2</sup> statistics and genotypes were grouped into seven different clusters. The cluster I comprised of 13 genotypes, cluster II with 11 genotypes, cluster VII consists of 2 genotypes and cluster III, IV, V, and VI each comprised of one genotype. Here the single genotype containing clusters denoting the higher degree of heterogeneity with rest of the genotypes. Intra cluster distance was recorded maximum in cluster VII (424.60) and least intra cluster distance was observed in clusters III, IV, V and VI. The highest inter cluster distance was between cluster V and VII (3406.10), followed by cluster II and VII (2816.39), cluster IV and VII (2596.46) and cluster III and VII (1674.17), implying that a wider genetic diversity between the genotypes evaluated. The genotypes falling in different clusters can be used as parents in hybridization program. The mean values of cluster IV had relatively high ear diameter, number of kernels/row, cob yield/plant, germination 1<sup>st</sup> count, germination 2<sup>nd</sup> count, SVI-1, SVI-2, speed of germination and grain yield/plant. Among all the traits studied, SVI-2 had the major contribution towards the genetic divergence followed by the speed of germination, SVI-1, ear height, 100-grain weight, germination final count and germination first count. Hence, these traits can be considered during genotype selection in segregating populations.

**Key words :** Maize, Inbreds, Genetic diversity, Mahalanobis D<sup>2</sup> statistic, Variability.

### Introduction

Maize (*Zea mays* L.) is one of the major C<sub>4</sub> plants that evolved in the Gramineae family. Maize crop is termed as “Queen of the cereals” as it has high genetic yield potential. It is cultivated across the world with a production of 1148 million metric tonnes in 2019 (FAOSTAT) and third most important cereal in India, next to wheat and rice in terms of area (9.8 million ha), production (31.6 million tonnes) and productivity (31.9 q ha<sup>-1</sup>) (Indiastat, 2020-21).

The plant breeder would benefit from accurate knowledge of the kind and degree of genetic divergence in order to select the best parents for various breeding techniques. In order to produce high yielding single cross

hybrids in maize, the inbred lines need to be accessed for the genetic diversity. Earlier studies revealed that inbreds from genetically diversified parents likely to be more productive than inbred lines from the same source (Singh, 2015). The heterosis manifestation in offspring is usually based on the genetic divergence of parents (Saxena, 1998).

Genetic diversity studies of different maize germplasm lines are primary importance in hybrid development. The genetic diversity present among the various population can be estimated by using the Mahalanobis D<sup>2</sup> analysis. It also helps in knowing the cause and nature of diversity exhibited in the natural germplasm. According to the generalized distance it will

helps in estimating the quantitation measure of association between geographic and genetic divergence (Mahalanobis, 1936).

The main goal of any maize hybrid breeding programmes is to select broad genetic base better inbreds for developing high yielding hybrids than the present cultivars, It ultimately serve as the method for achievement throughout the years (Sreckov *et al.*, 2010). Prior knowledge about genetic diversity helps the breeder to develop varieties/hybrids that boosts crop productivity (Choukan, 2011). The data of genetic diversity aids in grouping the genotypes into different heterotic categories were further used in the hybrid development programme (Dandolin *et al.*, 2008). The existing genetic variability present in the material can be evaluated to some extent by genetic diversity studies and helps in improving them (Cholastava *et al.*, 2011). The identified diverse genotypes can be utilized in hybrid breeding for better yields and other traits.

## Materials and Methods

### Plant material

Thirty maize inbred lines developed at Maize Research Centre, PJTSAU, Hyderabad were evaluated for thirteen morphological traits and the experiment was carried out at SRTC, PJTSAU, Rajendranagar, Hyderabad. The plot size was 24 m<sup>2</sup> comprising of four rows of six meter length evaluated in randomized block design during *Rabi*, 2020. The crop was raised by following the standard agronomic practices and data was recorded on ten randomly tagged plants for thirteen yield, yield components traits *viz.*, days to 50% tasseling, days to 50% silking, days to maturity, plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), number of rows/ear, number of kernels/row, 100-seed weight (g), shelling percentage (%), cob yield per plant (g), and grain yield per plant (g). Data on days to 50% tasseling, days to 50% silking, and days to maturity were recorded on plot basis.

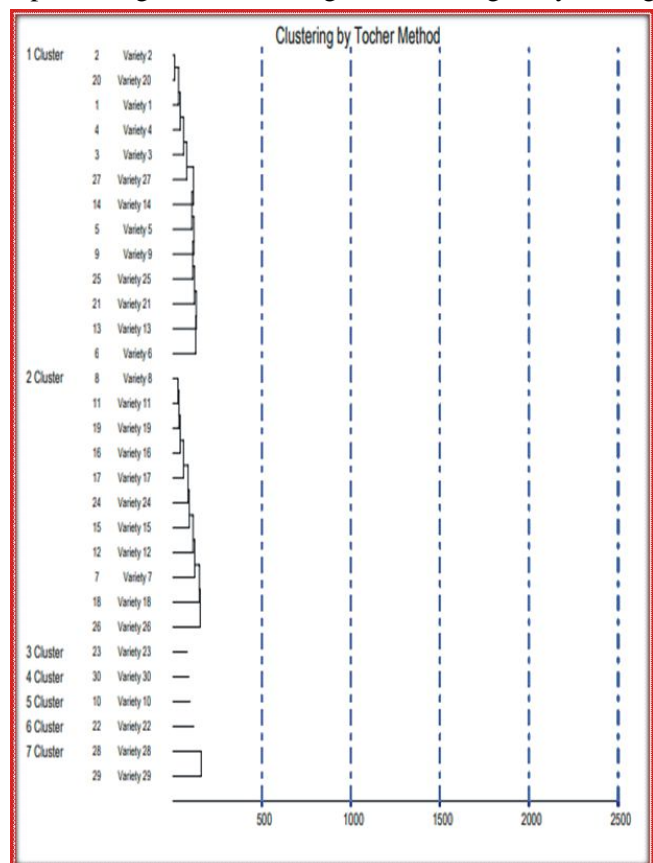
Seed quality traits *viz.*, germination 1<sup>st</sup> count, germination 2<sup>nd</sup> count, *SVI-1*, *SVI-2* and speed of germination were also recorded on freshly harvested seed of thirty maize genotypes. The seed germination at first and final count were recorded as percent normal seedlings out of 100 seeds sown on 5<sup>th</sup> and 10<sup>th</sup>, respectively. The seed vigour index 1 and 2 were estimated as per Baki and Anderson (1973). Speed of germination was estimated as the number of seedlings that germinated each day was registered daily for 7 days (Czabator, 1962).

## Statistical analysis

The data recorded on ten random plants were subjected to statistical analysis to determine the genetic diversity among the materials evaluated. The analysis was carried out using INDOSTAT software and the data observed for different traits were used for Mahalanobis D<sup>2</sup> statistics (Mahalanobis, 1928). The genotype grouping were done using Tocher's method as described by Rao (1952). The intra and inter-cluster distance, cluster mean and contribution of each trait to the diversity were estimated as suggested by Singh and Chaudhary (1977).

## Results and Discussion

According to the D<sup>2</sup> values, we have categorized the thirty maize genotypes into seven clusters by Tocher's procedure (Rao, 192). The analysis of variance (ANOVA) for yield, yield attributing traits and seed vigour traits showed highly significant variations among genotypes. Cluster analysis revealed that genotypes were grouped into seven clusters (Table 1 and Fig. 1). Among the 7 distinct clusters, Cluster I consisted of highest number of entries (13 genotypes), followed by Cluster II containing 11 genotypes, Cluster VII have two genotypes, Cluster III, IV, V and VI comprising only one genotype representing an extreme degree of heterogeneity among



**Fig. 1 :** Clustering pattern of 30 genotypes in maize on the basis of Tocher's method.

**Table 1 :** Clustering pattern of 30 maize inbred lines on the basis of D<sup>2</sup> Statistics.

Cluster no.	No. of inbreds	Inbreds
I	13	PFSR-12, PFSR-132, PFSR-9, PFSR-19, PFSR-17, GP-170, PFSR-90, PFSR-29, PFSR-49, GP-16, PFSR-135, PFSR-84, PFSR-30.
II	11	PFSR-46, PFSR-70, PFSR-130, PFSR-95, PFSR-104, PFSR-204, PFSR-92, PFSR-71, PFSR-32, PFSR-127, GP-19
III	1	PFSR-198
IV	1	MGC-137
V	1	PFSR-56
VI	1	PFSR-151
VII	2	GP-311, MGC-7

**Table 2 :** Mean intra and inter Euclidean cluster distances among the seven clusters.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	<b>323.82</b>	687.98	715.87	874.6	684.81	516.3	1574.31
Cluster II		<b>338.04</b>	546.06	621.78	577.38	890.23	2816.39
Cluster III			<b>0</b>	747.57	1038.49	948.07	1674.17
Cluster IV				<b>0</b>	1101.36	619.69	2596.46
Cluster V					<b>0</b>	1504.05	3406.1
Cluster VI						<b>0</b>	1345.69
Cluster VII							<b>424.6</b>

the entries. Similar results were drawn by Singh *et al.* (2020) and Bhadru *et al.* (2020) in maize.

The contribution of each trait to genetic divergence is represented in Table 4 and Fig. 3. The results indicated that among all the characters studied seedling vigour index -2 recorded highest in contribution towards the genetic divergence (44.13%) by ranking first, followed by the speed of germination (28.96%), seedling vigour index-1 (15.86%), ear height (7.12%), 100-grain weight (2.75%), germination 2<sup>nd</sup> count (0.91%) and germination 1<sup>st</sup> count (0.22%). Therefore, the characters *viz.*, seedling vigour index -2, speed of germination seedling vigour index-1 and ear height should be considered for the selection of diverse parents for hybrid breeding. Ramya Shree *et al.* (2016) reported the similar results in soybean.

The cluster means for yield, yield contributing traits and seed vigour traits are depicted in Table 3. Cluster VII had a high cluster mean whereas cluster V exhibited low cluster mean for the days to 50% tasseling (65.50, 57.67). For days to 50% silking (67.50, 59.67) highest cluster mean was showed in cluster VII and lowest was reported in cluster IV. Highest cluster mean for days to maturity (120.5, 111.6) was noted in cluster VII and lowest in Cluster IV. Plant height (160.7, 120.5) was found to be high in cluster VI and low in cluster VII. In case of ear height (93.60, 61.77), highest cluster mean was observed

in cluster III and lowest in cluster VI.

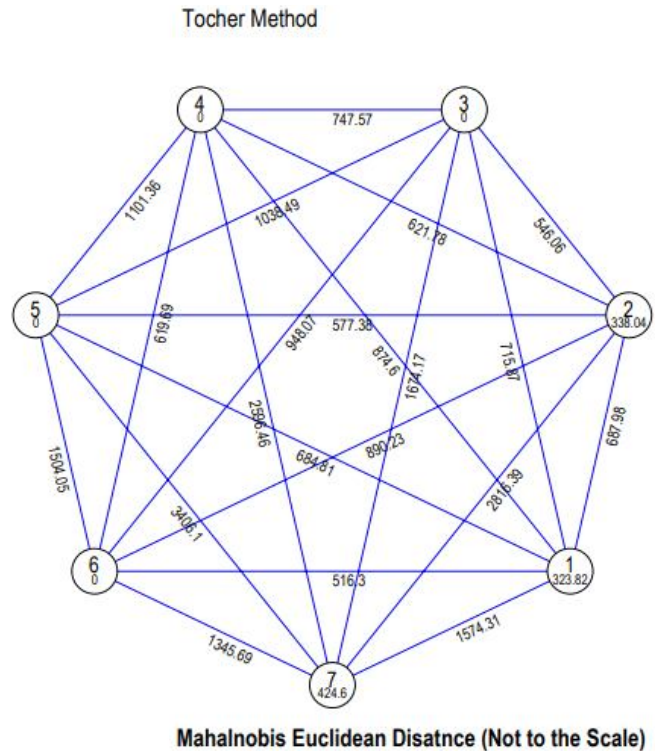
Highest cluster mean for ear length (14.63, 12.23) was noted in cluster V and lowest in cluster VII, Cluster IV recorded high cluster mean for ear diameter (4.07, 3.10), whereas lowest in cluster V. Number of rows per ear was found to have high cluster mean in Cluster IV and lowest in Cluster V, high cluster mean for number of kernels per row was recorded in cluster IV and low in cluster V, cluster IV had the highest cluster mean for number of kernels per row (32.0, 22.3) and lowest for cluster VI. High cluster mean for 100 seed weight (37.17, 23.43) was reported in cluster VI and lowest in cluster III, for shelling percentage (84.13, 75.37), highest cluster mean was observed in cluster V and lowest in cluster VII, highest cob yield per plant (122.3, 94.0) has highest cluster mean in cluster IV followed by the cluster VI, cluster II, cluster I, cluster VII, cluster V and lowest cluster III.

For seed vigour traits, germination 1<sup>st</sup> count (100, 88), germination 2<sup>nd</sup> count (100, 91), seed vigour Index -1 (3940, 2600), seed vigour Index-2 (102, 30.82) recorded highest cluster mean in cluster IV and lowest cluster mean in cluster VII, highest cluster mean for speed of germination (11.82, 5.50) in cluster IV and lowest cluster mean in cluster V, grain yield per plant (98.6, 55.0) cluster means revealed highest in cluster IV subsequently by

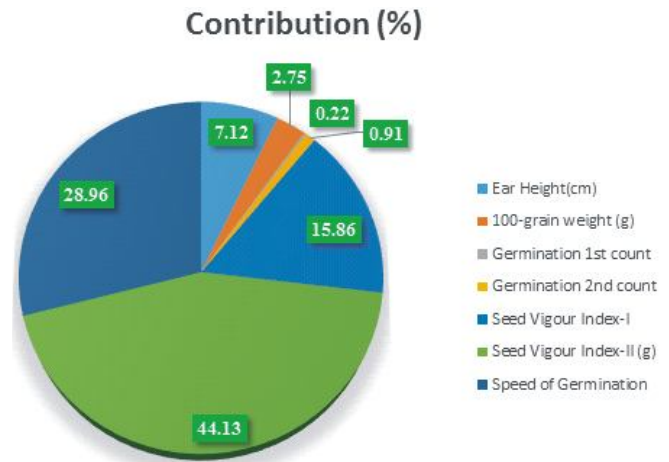
**Table 3:** Cluster means for grain yield, yield contributing and seed vigour traits in 30 maize inbred lines.

Cluster No	DT	DS	DM	PHT	EHT	HL	ED	NR	NKR	100SW	SHP	CYP	GM-1	GM-2	SVI-1	SVI-2	SPG	GYP
I	62.00	63.82	116.7	144.5	72.65	12.84	3.44	10.5	23.8	27.14	81.21	72.9	96.9	98.3	3049.8	63.58	7.79	59.23
II	61.97	63.45	116.4	156.2	83.17	13.67	3.51	10.6	23.4	28.03	81.24	76.8	95.3	98.3	2955.1	75.31	8.89	62.3
III	62.33	63.67	116.6	146.9	93.60	12.93	3.37	12.0	28.6	16.50	79.27	58.0	94.0	98.0	3287.3	64.37	9.60	46.0
IV	58.0	59.67	111.6	136.1	78.40	14.17	4.07	14.6	32.0	23.43	75.87	122.3	100	100	3940.0	102.0	11.82	98.67
V	57.67	60.33	113.3	121.0	79.43	14.63	3.10	9.3	27.3	22.33	84.13	65.3	97.6	99.0	3396.6	77.24	5.50	55.0
VI	61.0	62.67	115.3	160.7	61.77	13.50	3.60	11.3	22.3	37.17	77.50	88.3	98.0	99.6	2787.6	77.43	11.32	68.50
VII	65.50	67.50	120.5	120.5	69.98	12.23	3.72	12.6	24.5	20.70	75.37	69.67	88.0	91.0	2600.8	30.82	9.52	52.50

**DT:** Days to 50% Tasseling, **DS:** Days to 50% Silking, **DM:** Days to maturity, **PHT:** Plant height (cm), **EHT:** Ear height (cm), **HL:** Ear length (cm), **ED:** Ear diameter, **NR:** Number of rows per ear, **NKR:** Number of kernels per row, **100SW:** 100-seed weight, **SHP:** Shelling %, **CYP:** Cob yield per plant (g), **GM 1<sup>st</sup>:** Germination 1<sup>st</sup> count, **GM 2<sup>nd</sup>:** Germination 2<sup>nd</sup> count, **SVI-1:** Seed Vigour index-1, **SVI-2:** Seed Vigour index-2, **SPG:** Speed of Germination, **GYP:** Grain yield per plant.



**Fig. 2:** Intra and inter Euclidean cluster distance by using Tocher’s method.



**Fig. 3:** Relative contribution of different traits towards genetic diversity in 30 maize inbred lines.

cluster VI, cluster II and lowest cluster mean in cluster VII. Concurrent results were reported by Shankar *et al.* (2021), Kumawat *et al.* (2020) and Ganeshan *et al.* (2010). Genotypes having high cluster mean values from the clusters can be used as parents in future hybrid development programs.

The average inter and intra cluster  $D^2$  values between the seven clusters are represented in Table 2 and Fig. 2. The maximum and minimum inter cluster values are 424.60 (Cluster VII) and 0 (Cluster III, IV, V, VI) for yield, yield contributing and seed vigour traits. Hereby the cluster V and VII had the highest inter cluster



**Table 4:** Contribution percent of different traits towards genetic diversity.

S. no.	Character	No. of times ranked first	Contribution (%)
1	Days to 50% tasseling	0	0
2	Days to 50% silking	0	0
3	Days to maturity	0	0
4	Plant height (cm)	0	0
5	Ear height(cm)	31	7.12
6	Cob length	0	0
7	Cob diameter	0	0
8	No of rows/cob	0	0
9	No of kernels per row	0	0
10	100-seed weight (g)	12	2.75
11	Shelling %	0	0
12	Cob yield per plot (g)	0	0
13	Germination 1 <sup>st</sup> count	1	0.22
14	Germination 2 <sup>nd</sup> count	4	0.91
15	Seed vigour index-I	69	15.86
16	Seed vigour index-II	192	44.13
17	Speed of germination	126	28.96
18	Grain yield per plot (g)	0	0

(3406.10), proceeded by cluster II and VII (2816.39), cluster IV and VII (2596.46), cluster III and VII (1674.17) it recommends that the crossing between these clusters results in useful recombination and wider genetic base. The lowest distance was recorded between the cluster II and III (546.06). The results were coincide with the previous report of Anilkumar *et al.* (2017) and Lenka *et al.* (2020).

The results suggested that genotypes with high values for a certain character may be chosen and employed in a hybridization programme to enhance that character. To judiciously incorporate all of the sought features, hybridization between chosen genotypes from divergent clusters is required. The potential genotypes which having high cluster mean values should be involved directly in the breeding program as parents (Ali *et al.*, 2018). Evaluation of genetic diversity of the inbred lines is an utmost step in developing high yielding single cross hybrids

### Conclusion

Among the eighteen traits studied, seed vigour index-2 (SVI2) had contributed maximum for genetic diversity and the highest cluster mean was recorded in Cluster IV, VII and V for both yield and seed quality traits. Therefore, selection of genotypes that are falling in these clusters with wide genetic diversity would be useful in developing desirable high yielding hybrids.

### References

- Ali, Abdikadir Hassan (2018). Genetic Variability and Diversity Studies in Maize (*Zea mays* L.) Inbred Lines. *IOSR J. Agricult. Vet. Sci.*, **11(11)**, 69-76.
- Anilkumar, C., Lohithaswa H.C. and Pavan R. (2017). Assessment of genetic diversity in newly developed inbred lines of maize (*Zea mays* L.). *Elect. J. Plant Breed.*, **8(1)**, 193-200.
- Baki, A.A. and Anderson J.D. (1973). Vigor determination in soybean seed by multiple criteria 1. *Crop Science*, **13(6)**, 630-633.
- Bhadru, D., Swarnalatha V., Mallaiah B., Sreelatha D., Kumar M.N. and Reddy M.L. (2020). Study of Genetic Variability and Diversity in Maize (*Zea mays* L.) Inbred Lines. *Curr. J. Appl. Sci. Technol.*, 31-39.
- Cholastova, T., Soldanova M. and Pokorny R. (2011). Random amplified polymorphic DNA (RAPD) and simple sequence repeat (SSR) marker efficacy for maize hybrid identification. *Afr. J. Biotechnol.*, **10(24)**, 4794-4801.
- Choukan, R. (2011). Genotype, environment and genotype× environment interaction effects on the performance of maize (*Zea mays* L.) inbred lines. *Crop Breed. J.*, **1(2)**, 97-103.
- Czabator, F.J. (1962). Germination value: An index combining speed and completeness of pine seed germination. *Science*, **8(4)**, 386-396.
- Dandolini, T.S., Scapim C.A., do Amaral Junior A.T., Mangolin C.A., da Silva M.D.F.P., de Souza Mott A. and Lopes A.D. (2008). Genetic divergence in popcorn lines detected by microsatellite markers. *Crop Breed. Appl. Biotechnol.*, **8(4)**.
- Ganesan, K.N., Nallathambi G, Safawo T., Senthil N. and Tamilarasi P.M. (2010). Genetic divergence analysis in indigenous maize germplasm (*Zea mays* L.). *Elect. J. Plant Breed.*, **1(4)**, 1241-1243.
- Khan, A.A., Islam M.R., Ahmed K.U. and Khaldun A.B.M. (2013). Studies on genetic divergence in maize (*Zea mays*) inbreds. *Bangladesh J. Agricult. Res.*, **38(1)**, 71-76.
- Kumawat, G, Shahi J.P. and Kumar M. (2020). Assessment of genetic diversity of maize (*Zea mays* L.) hybrids under water logging condition. *Elect. J. Plant Breed.*, **11(01)**, 252-258.
- Lenka, D., Swain D., Lenka D. and Tripathy K. (2020). Assessment of genetic diversity and molecular detection of advanced inbred lines for QPM status in maize (*Zea mays* L.). *J. Crop and Weed.*, **16(3)**, 153-159.
- Mahalanobis, P.C. (1936). On the generalized distance in statistic. *Proc. Nat. Inst. Sci.*, India, **2**, 49-55.
- Marker, S. and Krupakar A. (2009). Genetic divergence in exotic maize germplasm (*Zea mays* L.). *J. Agricult. Biolog. Sci.*, **4(4)**, 44-47.
- Ramya Shree, T., Patta S., Rani K.J. and Ramesh T. (2016). Genetic variability and divergence of morphological and seed quality traits of soybean (*Glycine max* L. Merrill.)

- Genotypes. *Res. J. Agricult. Sci.*, **7(3)**, 614-616.
- Rao, C.R. (1952). *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons Inc., New York. 236-272.
- Saxena, V.K., Mathi N.S., Singh N.N. and Vasal S.K. (1998). Heterosis in maize: Grouping and patterns. In : *Proceedings 7th Asian Regional Maize Workshop*. Los Banos, Philippines (Vol. 23, No. 27, 124-133).
- Shankar, M., Shahi J.P., Singh R., Singamsetti A., Devesh P. and Singh P. (2021). Assessment of Genetic Diversity of Maize (*Zea mays* L.) Inbreds based on Morphological Traits. *Curr. J. Appl. Sci. Technol.*, 16-25.
- Singh, D., Kumar A., Kumar R., Kushwaha N., Mohanty T.A. and Kumari P. (2020). Genetic variability analysis of QPM (*Zea mays* L.) inbreds using morphological characters. *Int. J. Curr. Microbiol. Appl. Sci.*, **9(2)**, 328-338.
- Singh, P., Salgotra S.K., Singh A.K., Sharma M., Gupta A., Salgotra S.K., Singh A.K., Sharma M., Gupta A. and Sharma M. (2015). Stability and genetic divergence study of single cross hybrids in maize (*Zea mays* L.). *Afr. J. Agricult. Res.*, **10(31)**, 3080-3085.
- Singh, R.K. and Choudhary B.D. (1977). Biometrical methods in quantitative genetic analysis, *Kalyani Publishers*, New Delhi, pp. 54.
- Srekov, Z., Bocanski J., Nastasic A., Danilovic L. and Vukosavljevic M. (2010). Correlation and path coefficient analysis of morphological traits of maize (*Zea mays* L.). *Res. J. Agricult. Sci.*, **42(2)**, 292-296.