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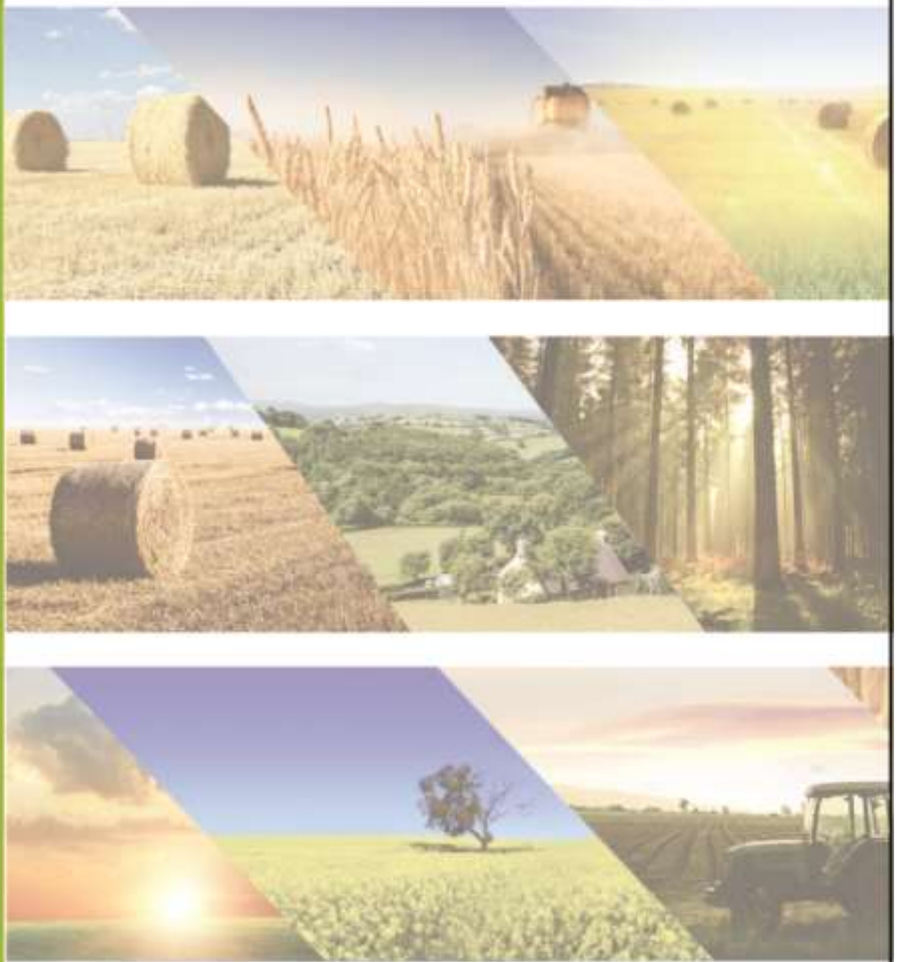

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"Agrosym 2023"
Jahorina, October 05-08, 2023

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CORRELATION, HERITABILITY AND PATH ANALYSIS OF GRAIN YIELD COMPONENTS IN SOME MAIZE GENOTYPES (*Zea Mays* L.)

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Abstract

Maize (Zea mays L.) is an important cereal crop of the world and plays a key role in worldwide agriculture with highest production and productivity. Maize is also an important grain crop grown in Serbia, used as a component of feed. Many studies have been conducted on correlations, heritability and path analysis on grain yield. The results have been widely used in maize breeding programs. The present research was carried out at the Maize Research Institute "Zemun Polje" in Serbia during the 2021 growing season effects of grain yield and quantitative traits of maize. Six inbred lines were crossed according to complete diallel method. In this way fifteen hybrids and fifteen reciprocal combinations were obtained. The hybrids and reciprocal combinations derived from these parental components were used in this paper. The objective of study was to estimate direct and indirect effects of five morphological traits on grain yield by the application of the simple coefficient correlation, heritability and path coefficient analysis. 1000-kernel weight with the value of 0.365 had the strongest direct positive effect on grain yield. Positive direct effects on grain yield were also observed for ear length (0.202), ear diameter (0.248) and number of rows per ear (0.076), while negative direct effects were observed for cob diameter (-0.057). Thousand-kernel weight had the highest indirect positive effect on grain yield via ear diameter (0.232). Cob diameter had highest negative indirect effect on grain yield via ear diameter (-0.048). The coefficient of multiple determination (R2y12345) had a value of 0.428.

Keywords: *Correlations, Heritability, Path analysis, Grain yield, Maize.*

Introduction

The selection of genotypes and the evaluation of their performance played a significant role in increasing crop yields of many crops, including maize. Grain yield is a complex quantitative trait that depends on plant genetics and its interaction with environmental conditions. Many investigations have been conducted correlations, heritability and path analysis on grain yield (Magar *et al*. 2021; Asima *et. al*, 2018, Bello *et al.*, 2012). The results have been widely used in maize breeding programs.

The coefficient of variation represents the degree of variability present in a wide range of qualities, but it excludes the heritable component. The parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV) are useful in detecting the amount of variability present in a given characteristic.

The efficiency with which genotypic variability can be exploited by selection depends upon heritability and the genetic advance (GA) of individual trait (Bilgin *et al*, 2010) Heritability provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations. Heritability coupled with high GA would be more useful in predicting the resultant effect in the selection of the best genotypes for yield and its attributing traits (Bello et al, 2010).

Coefficient of correlations are the measure of level of the relationship two or more traits or the level where these traits are mutually different. (Boćanski *et al*., 2009). Correlation estimates are useful in determining the components that influence a trait either positively or negatively. However, they do not provide exact information of the relative importance of direct and indirect effects of component traits on complex traits such as yield. For formulating selection indices for genetic improvement of yield, the cause and effect of the trait is very essential and can be done by path analysis (Dewey and Lu, 1959). In path coefficient analysis, grain yield is considered as dependent variable and the remaining traits are considered as independent variables (Singh and Chaudhary, 1985). It is necessary to have a good knowledge of those characters that have significant correlation with yield because those characters can be used as indirect selection criteria to enhance the mean performance of varieties in a new plant population (Vara Prasad and Shivani, 2017).
The objective of this investigation was to estimate of genetic variability, heritability, correlations and path coefficients for grain yield and yield component traits of maize hybrids.

Materials and Methods

Six inbred lines were crossed according to full diallel method and fifteen hybrids with 15 reciprocal combinations were created.
These hybrids, were studied in location Zemun Polje during 2021 year. The three-replicate trial was set up according to the RCB design. The selected genotypes were sown in the two-rowed plot. The length of the plot was 5 m, the inter-row distance amounted to 0.75 m. Elementary plot size was 7.5 m^2. Morphological traits were evaluated in full maturity. Mechanical sowing and harvesting were performed. All the recommended agronomic package of practices was adopted during the entire crop growth vegetative period.
The data were recorded from 5 random plants from each entry in all the two replications for ear length (cm), ear diameter (cm), cob diameter (cm), number of rows per ear, 1000-kernal weight (g) and while the grain yield (t ha^{-1}). were determined on whole plot basis with classic combine machine. The mean values were used for statistical analysis.
Data was subjected to analysis of variance using "variability" package of R studio statistical software in R Core Team R 2021, considering genotypes as fixed effects and replications and incomplete blocks within replications as random. Genotypic correlation analysis was conducted following the Pearson’s correlation coefficient method using package in R software version R-4.1.1. Genotypic, phenotypic variances, narrow sense heritability and broad sense heritability were estimated using AGD-R (Analysis of Genetic Designs with R) and Excel 2019.
Correlation and path analysis were performed following the procedure developed by Dewey and Lu using IBM SPSS AMOS 26.
Broad sense heritability (H2) was determined for various traits as per the formula suggested by Allard (1999). The estimates for heritability for a single environment were performed using the equation (1)

$$h^2 = \sigma_g^2 / \sigma_p^2 \times 100 \quad (1)$$

Where σ_p^2 is the phenotypic variance and σ_g^2 is the genotypic variance.
Heritability percentage was categorized as low when less than 30%, medium, 30-60%, and high, 60% and above as indicated by Robinson (1949).
Genetic advance (GA, Eq.2) and genetic advance as percent of the mean (GAM, Eq.3), assuming selection of the superior 5% of the genotypes, were determined by the formula illustrated by Johnson *et al.* (1955).

$$GA = \frac{K \times \sqrt{\sigma^2 p + \sigma^2 g}}{\sigma^2 p} \quad (2)$$

where GA is the expected genetic advance, K is the standardized selection differential at 5% selection intensity (K 2.063), $\sigma^2 p$ is the phenotypic variance and $\sigma^2 g$ is the genotypic variance.
The genetic advance as a percent of the mean was estimated using the following formula:

$$GAM\ \% = \frac{GA}{\bar{x}} \times 100 \qquad (3)$$

where GAM = genetic advance and *x* = population mean.

Following Falconer and Mackay (1996), the genetic advance (GAM) values were classified as low: less than 10%, moderate: 10–20% and high: greater than 20%.
A path analysis scale suggested by Lenka and Mishra (1973) was used to categorize the estimates as negligible with values ranging from 0.00 to 0.09, low with values ranging from 0.10 to 0.19, moderate with values ranging from 0.20 to 0.29, high with values ranging from 0.30 to 0.99 and more than 1.00 as very high path coefficients.

Results and Discussion

Correlation coefficients

In maize, traits like plant height, ear height, and the number of kernel rows per ear are reported to have a positive and substantial link with grain yield, according to the study (Sadek *et al*., 2006). Results displayed in Table 1., show values of simple correlation coefficients between examined traits.

Table 1. Pearson's correlation coefficients of grain yield and component traits in maize

	Ear length	Ear diameter	Cob diameter	Number of rows per ear	1000-kernel weight	Grain yield
Ear length	1	0.304**	0.149^{ns}	0.031^{ns}	0.358**	0.402**
Ear diameter	0.304**	1	0.857**	0.590**	0.636**	0.538**
Cob diameter	0.149^{ns}	0.857**	1	0.651**	0.458**	0.403**
Number of rows per ear	0.03^{ns}	0.590**	0.651**	1	0.231**	0.276**
1000-kernel weight	0.358**	0.636**	0.458**	0.231**	1	0.587**
Grain yield	0.402**	0.538**	0.403**	0.276**	0.587**	1

ns, * and **: Not significant and significant at 5% and 1% levels, respectively.

When it comes to correlation between grain yield and observed traits, the highest correlation values were found between grain yield and 1000 kernel weight (0.587**) similar with results Pavlov *et al.* (2015) and Shengu (2017), followed by ear diameter (0.538**), cob diameter (0.403**), ear length (0.402**), the lowest value of correlation coefficient was observed between grain yield and number of rows per ear (0.276**). The highest and statistically significant values of correlation coefficients among observed morphological traits were found between cob diameter and ear diameter (0.857**), followed by number of rows per ear and cob diameter (0.651**). 1000 kernel weight, also showed high positive correlation coefficients with ear diameter (0.636**).

Table 2. Estimation of Variance, PCV, GCV, H^2_{bs}, GA and GAM

	σ^2e	σ^2g	σ^2p	ECV	GCV	PCV	h_{bs}	GA	GAM (%)
Ear length	1.603	3.613	5.217	7.329	11.005	13.222	0.692	3.259	18.869
Ear diameter	0.039	0.122	0.162	4.332	7.603	8.75	0.755	0.626	13.612
Cob diameter	0.015	0.031	0.047	4.951	7.079	8.642	0.67	0.299	11.943
Number of rows per ear	1.081	1.837	2.918	7.126	9.29	11.708	0.629	2.215	15.185
1000-kernel weight	0.0007	0.0018	0.0025	7.1786	11.6392	13.7169	0.72	0.0742	20.3559
Grain yield	1.066	6.244	7.31	14.864	35.971	38.921	0.854	4.757	68.483

σ^2e - Environmental variance, σ^2g - Genotypic variance, σ^2p - Phenotypic variance, ECV - Environmental coefficient of variation, GCV - Genotypic coefficient of variation, PCV Phenotypic coefficient of variation, h_{bs}= Heritability broad sense, GA= Genetic advance, GAM= Genetic advance as percent of mean

The presence of significant variation in genotypes for most of traits was given in Table 2. GCV values for all the traits, were lower than PCV value, showing that the characters were more influenced by their surrounding environments. According to Sivasubramanian and Menon (1973), the traits evaluated in this study had low (less than 10% phenotypic and genotypic coefficients of variation), moderate (10–20% phenotypic and genotypic coefficients of variation, and high (more than 20% phenotypic and genotypic coefficients of variation. Grain yield was estimated to have high PCV and GCV values (38.921; 35.971). Similarly, low PCV and low GCV were estimated for traits like ear diameter (8.750; 7.603), cob diameter (8.642; 7.079). Ear length (13.222;11.005) and 1000 kernel weight (13.716; 11,639) recorded moderate values. Number of rows per ear had low GCV value (9.290) and moderate value for PCV (11.708).

The coefficient of variations (CV), particularly GCV, determines its reliability for use in a breeding program. In breeding works, a high proportion of GCV to PCV is preferred. Magar *et al*. (2021) reported similar findings.

Heritability and genetic advance

Heritability estimates are useful for breeding quantitative traits as it provides information on the extent to which a particular trait can be inherited to subsequent generations (Bello, 2012). According to Robinson *et al*. (1949) traits had low (less than 30%), moderate (30–60%), and high (more than 60%) estimates of heritability.

The high heritability was found in all investigated traits. Begum *et al.* (2016) reported moderately high heritability for ear diameter, ear length, number of kernels per row and grain yield. High heritability value in this study show high proportion of variation in a trait that is genetic and low influence of environment in expression of these traits, indicating improvement of the traits can be made based on phenotypic performance. High estimates of heritability for most of the variables suggested that variations were passed down to progeny, implying that a high-yielding variety may be developed by selecting desirable genotypes. High heritability provided more options for selecting plant material with the desired features. Sharma *et al.* (2018) and Magar *et al.* (2021) reported similar findings for ear length, ear diameter and *vice versa* for 1000 kernel weight.

GAM for the traits in our study ranged from 11.943% for cob diameter to 68.483% for grain yield. GAM values were classified by as low (less than 10%), moderate (10–20%), and high (greater than 20%) by Falconer and Mackay (1996). Data in Table 2 shows the GAM estimates for all traits. Grain yield (68.483%) and 1000 kernel weight (20.355) had high GAM values, while ear length (18.869), ear diameter (13.612), cob diameter (11.943) and number of rows per ear (15.185) had moderate values. Similar findings reported Kandel *et al.* (2017) for all examined traits.

Path analysis

Path coefficient analysis (Dewey and Lu 1957) furnished a method partitioning the correlation coefficient into direct and indirect effect and provides the information on actual contribution of a trait on the yield. By determining the inter relationships among grain yield components, a better understanding or both the direct and indirect effects of the specific components can be attained (Pavan *et. al.*, 2011; Pavlov *et.al.*, 2015). Such an analysis helps the breeders to identify the characters that could be used as selection criteria in maize breeding programmes (Table 3 and Figure 1).

The most positive direct effect of examined traits to grain yield was found for 1000 kernel weight (0.365), also positive direct effects were found for ear diameter (0.248), ear length (0.202) and number of rows per ear (0.076). Negative direct effects were found for remaining trait, cob diameter (-0.057). For all traits which had positive direct effect on grain yield, positive indirect effects were also observed. On the other side, for cob diameter, which had negative direct effect, their indirect effects through other traits were also negative. 1000 kernel weight had the highest indirect positive effects on grain yield by ear diameter (0.232), while cob diameter had the highest indirect negative effects on grain yield by ear diameter (-0.048).

Table 3. Direct (diagonal) and indirect (off-diagonal) effect of 5 traits on grain yield

	Ear length	Ear diameter	Cob diameter	Number of rows per ear	1000-kernel weight	Genotypic correlations with grain yield
Ear length	**0.202**	0.061	0.030	0.006	0.072	0.371
Ear diameter	0.075	**0.248**	0.212	0.145	0.157	0.837
Cob diameter	-0.001	-0.048	**-0.057**	-0.037	-0.026	-0.169
Number of rows per ear	0.002	0.044	0.049	**0.076**	0.017	0.188
1000-kernel weight	0.130	0.232	0.167	0.084	**0.365**	0.978

High values of indirect effects were observed for 1000 kernel weight via ear diameter (0.232) and ear diameter via cob diameter (0.212) in accordance with the classification established by Lenka and Mishra (1957). Moderate values were observed for 1000 grain mass over grain length (0.130), 1000 grain mass over grain diameter (0.167), grain diameter over number of rows (0.145) and grain diameter over 1000 grain mass (0.157). Low values were recorded for other indirect effects.

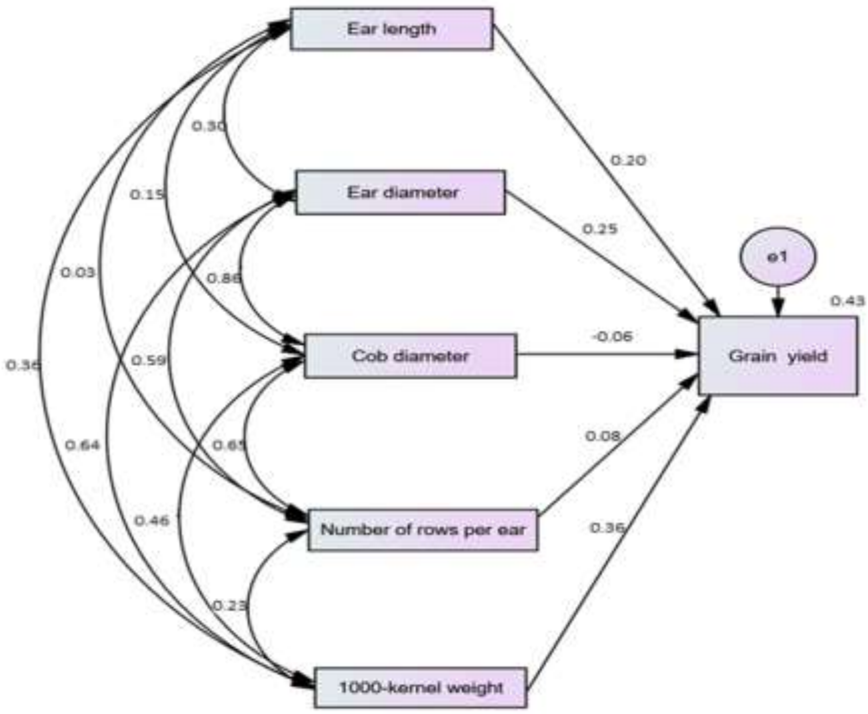

Figure 1. Path diagram for grain yield

Conclusions

High heritability was found for ear length, ear dimeter, cob diameter, number of rows per ear, 1000 kernel weight and grain yield. These traits were less influenced by environmental factors. Also, high heritability with high GAM was found in ear length, 1000 kernel weight and grain yield, these traits can therefore be used in plant breeding program. 1000 kernel weight and ear diameter had highest positive direct effect whereas cob diameter had negative value on grain yield.

These traits also exerted favorable direct and indirect effects via the other traits. Therefore, these traits could be considered as important selection criteria for grain yield improvement in maize breeding program. However, further evaluation of these genotypes at more locations and over years is important to get reliable results.

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