

Direct Selection Parameter Estimates and Path Coefficient Analysis for Grain Yield and Quantitative Traits in Maize (*Zea mays* L.)

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ABSTRACT

The study was carried out at the Maize Research Institute “Zemun Polje”, Belgrade, Serbia during 2021 growing season in three location. Six inbred lines were crossed according to complete diallel method. In this way 15 hybrids and 15 reciprocal combinations were obtained. Hybrid and reciprocal combinations derived from these parental components were used in this paper.

The present study was carried out to study the variability, broad-sense heritability (H^2_{bs}), genetic advance (GA), correlation among traits, genotypic and phenotypic path analysis among grain yield and its components. The results indicated that the genotypes were significantly different for all traits. For all traits, the phenotypic coefficient of variation was higher than the genotypic coefficient of variation. The highest heritability was found in 1000 kernel weight, followed by grain yield, ear diameter and anthesis-silking interval (ASI). In our study Genetic Advance over Mean (GAM) for the traits ranged from lowest value (9.739%) for cob diameter to the highest value (90.579%) for anthesis-silking interval.

According to results of path analysis, the trait 1000 kernel weight with the value of 0.365 has 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). The trait 1000 kernel weight had the highest indirect positive effects on grain yield via ear diameter (0.232). The cob diameter had highest negative indirect effect on grain yield via ear diameter (-0.048).

Coefficient of multiple determinations (R^2) had a value of 0.428. This indicated the important role of additive gene effect in the inheritance of these traits and could be improved through simple selection.

Keywords: direct selection parameters, heritability, genetic advance, quantitative traits, maize.

INTRODUCTION

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, dominantly used as either grain or silage, is a base for livestock feeding.

Grain yield represents one of the most important and complex traits, and its constant increase remains the main priority worldwide when developing new varieties (Araus et al., 2008). Broad genetic variability preserved in the Maize Research Institute “Zemun Polje” gene bank accessions, which originated from the Serbia and Western Balkan region,

generally considered as a part of European corn-belt, is an exceptional source of desirable traits for enriching breeders working collections for maize breeding under temperate conditions (Popovic et al., 2020). Development of hybrids depends upon the selection of superior parents, technical skill and professional competence. High production per unit area is the basic objective in maize breeding program. The development of promising genotypes to be used in the improvement of a crop is very important, as it is necessary to parental lines (Ali et al., 2020).

The grain yield of maize depends on the genetic potential of the genotype used, the characteristics of the soil, the field

management practices, and agro-climatic factors. Heritability and Genetic advance are the direct selection parameters. Information on such parameters has great importance in enhancing the selection efficiency (Lal et al., 2020). Selection based on the detailed knowledge and direction of association between yield and its attributes is very important in identifying the key characteristics, which can be exploited for crop improvement through suitable breeding programme. Many investigations have been conducted correlations, heritability and path analysis on grain yield. The results have been widely used in maize breeding programs.

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 (Singh et al., 2011).

The estimation of correlation indicates only the extent and nature of association between yield and its attributes, but does not show the direct and indirect effects of different yield attributes on yield per se. Grain yield is dependent on several characters which are mutually associated; these will in turn impair the true association existing between a component and grain yield. A change in any one component is likely to disturb the whole network of cause and effect. Thus, each component has two paths of action, the direct influence on grain yield, indirect effect through components which are not revealed from the correlation studies (Jakhar et al., 2017).

Path coefficient analysis is a standardized partial regression coefficient that allows partitioning of correlation coefficient into direct and indirect effects of various traits towards dependent variable, and also helps in assessing the cause-effect relationship as well as effective selection. Path analysis plays an important role in determining the degree of relationship between yield and its components (Bello et al., 2010). A path coefficient is a standardized partial regression coefficient that measures the direct influence

of one variable upon another (Dewey and Lu, 1959). It also provides a means partitioning both direct and indirect effects and effectively measuring the relative importance causal factors (Ojo et al., 2006).

The objective of study was to estimate direct and indirect effects of six morphological traits on grain yield by the application of the variability, coefficient correlation, heritability, genetic advance and path coefficient analysis.

MATERIAL AND METHODS

Experimental site

The study was conducted on three location during the main cropping season of 2021 year at Maize Research Institute "Zemun Polje", Belgrade, Serbia. Experimental fields were located, two at Zemun Polje and one in village named Kukujevci, both on chernozem soil type. Zemun Polje is located near Belgrade (44°52'1" North, 20°19'16" East), at mean elevation of 82 meters above sea level. Kukujevci, District Srem, Vojvodina province is located (45°03'1" North, 19°20'16" East), at mean elevation 96 above sea level.

Experimental materials design and cultural practices

Six inbred lines were crossed according to full diallel method and fifteen hybrids with 15 reciprocal combinations were created.

These hybrids were studied in Maize Research Institute experimental plots in 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 and sowing density was 69.316 plants per ha⁻¹. Elementary plot size was 7.5 m⁻². Mechanical sowing and harvesting were performed. All the recommended and conventional agronomic package of cultural practices was adopted during the entire crop growth vegetative period of maize.

Data collection

The data were recorded from 5 random plants from each entry in all the two

replications for anthesis-silking interval (ASI), ear length (EL), ear diameter (ED), cob diameter (CD), number of rows per ear (NRPE), 1000-kernal weight (KW), while the grain yield per ha⁻¹ (GYPH) were determined on whole plot basis with combine machine for experimental plots Wintersteiger.

The following formula was used to compute grain yield (kg ha⁻¹) at 14% moisture content using fresh ear weight: the mean values were used for statistical analysis.

$$\text{Grain yield t ha}^{-1} = \frac{F.W. \text{ kg ha}^{-1} \times (100 - HMP) \times 10000}{(100 - DMP) \times NPA \times 1000}$$

where: F.W. - the fresh weight of ear per plot (kg) at harvest; HMP - moisture percentage of grain at harvest; DMP - desired moisture percentage, *i.e.* 14%; NPA - the area of net harvest plot, m².

Statistical analysis

Phenotypic, genotypic and environmental variances were computed from the respective mean squares following the procedures suggested by Allard (1960). The genotypic and phenotypic coefficients (GCV; PCV) of variation were estimated according to the procedure outlined by Johnson et al. (1955) GCV and PCV values were categorized as low when less than 10%, moderate, 10-20% and high, greater than 20% as indicated by Deshmukh et al. (1986). Broad-sense heritability (H^2_{bs}) was estimated according to the procedure suggested by Singh and Chaudhary (1985). Heritability percentage was categorized as low when less than 40%, medium, 40-59%, moderately high, 60-79% and very high, 80% and above as indicated by Singh (2001). Genetic advance (GA) and genetic advance as percent of the mean (GAM), assuming selection according to Shukla et al. (2006). 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%. Phenotypic and genotypic correlation coefficients were estimated using the standard procedure suggested by Miller et al. (1958) using the corresponding variance and covariance components. The genetic correlation coefficients of all the traits were partitioned into direct and indirect effects by path coefficient analysis, using the R Studio software following the procedure Dewey and Lu (1959). 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.

The data were analyzed using a randomized complete block design (RCBD) with two-ways ANOVA in AGD-R software - Analysis of Genetic Designs with R, version 5.0 (Rodriguez et al., 2018). All experimental data reported as averages analyzed the other parameters in this investigation using package of R statistical software in R studio Team. Version 4.2.3 (2023) (<https://www.r-project.org/>). Considering genotypes as fixed effects and replications and incomplete blocks within replications as random.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA)

The analysis of variance showed there was a very highly significant difference among the genotypes evaluated for all traits (Table 1). This indicates the genotypes are highly variable. Thus, the possibility genetic improvement through selection is highly promising. High variability of breeding materials will increase the probability of producing desirable recombinants in successive generations.

Table 1. The analysis of variance for grain yield and and yield contributing characters in maize (*Zea mays* L.)

	Environment (df=2)	Replication (df=3)	Genotype (df=35)	Residuals (df=105)
Mean squares				
Anthesis-silking interval	0.347	0.192	3.423**	0.248
Ear length	10.399	75.099	22.262**	1.38
Ear diameter	0.055	0.44	0.851**	0.036
Cob diameter	0.175	0.066	0.199**	0.015
Number of rows per ear	1.199	0.305	11.015**	0.829
1000-kernel weight	0.005	0.002	0.013**	0.0002
Grain yield	48.716	5.612	37.706**	1.043

ns, * and **: not significant, significant at the 5% and 1% levels of probability, respectively.

Genetic variability

For all the traits, the GCV values were lower than PCV value, showing that the characters were more influenced by their surrounding environments (Table 2). Following Falconer and Mackay (1996), 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 (43.229; 40.730) and anthesis-silking interval (58.693; 50.801) were estimated to have high PCV and GCV values. Similarly, low PCV and low GCV were estimated for traits like ear diameter (8.418; 7.455) and cob diameter (8.726; 6.422). The number of rows per ear had moderate PCV and low GCV (11.911; 9.117). The trait 1000-kernel weight had moderate PCV and GCV values (13.300; 13.020). 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).

Heritability and genetic advance

The data in Table 2 shows the heritability values for all traits. Heritability plays a vital role in deciding the suitability and strategy for selection of a particular character. According to Robinson et al. (1949) traits had low (less than 30%), moderate (30-60%), and high (more than 60%) estimates of heritability. The highest heritability (0.958) was found in 1000-kernel weight, followed

by grain yield (0.887), ear diameter (0.784) and anthesis-silking interval (0.749). The rest of the traits studied were moderately heritable.

Similarly, GAM for the traits in our study ranged from 9.739% for cob diameter to 90.579% for ASI. According to Falconer and Mackay (1996), the observed GAM values were classified as low (less than 10%), moderate (10-20%), and high (greater than 20%). Table 2 shows the GAM estimates for all traits. ASI, grain yield, 1000 grain weight had greater estimates of GAM percent.

When additive gene effects controlled a characteristic, it usually resulted in both higher heritability and genetic advance, whereas when non-additive gene actions controlled a trait, it might result in high heritability but poor genetic advance. 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. Our findings on the heritability of traits namely grain yield, 1000-kernel weight and (ASI) were consistent with those of Shengu (2017). According to Najeeb et al. (2009), high heritability and high genetic progress are not always linked. As a result, high heritability does not imply a large genetic gain. A heritability estimate in conjunction with genetic advance is proposed to anticipate the effectiveness of picking superior genotypes.

Table 2. Estimation of Variance, PCV, GCV, Heritability, GA and GAM

	σ^2_e	σ^2_g	σ^2_p	ECV	GCV	PCV	H^2_{bs}	GA	GAM (%)
Anthesis-silking interval	0.276	0.824	1.100	29.398	50.801	58.693	0.749	1.619	90.579
Ear length	1.755	3.018	4.774	7.721	10.124	12.732	0.632	2.846	16.584
Ear diameter	0.032	0.116	0.148	3.908	7.455	8.418	0.784	0.623	13.601
Cob diameter	0.021	0.025	0.046	5.909	6.422	8.726	0.541	0.241	9.739
Number of rows per ear	1.271	1.798	3.069	7.665	9.117	11.911	0.585	2.114	14.376
1000-kernel weight	0.0001	0.002	0.002	2.103	13.020	13.300	0.958	0.096	26.253
Grain yield	0.826	6.536	7.363	14.485	40.730	43.229	0.887	4.962	79.054

σ^2_e - Environmental variance, σ^2_g - Genotypic variance, σ^2_p - Phenotypic variance, ECV - Environmental coefficient of variation, GCV - Genotypic coefficient of variation, PCV - Phenotypic coefficient of variation, H^2_{bs} - Heritability broad sense, GA- Genetic advance, GAM - Genetic advance as percent of mean.

Table 3. Genotypic (above) and phenotypic (below) correlations among yield and yield contributing characters in maize (*Zea mays* L.)

	ASI	EL	ED	CD	NRPE	KW	GY
Anthesis-silking interval	1	-0.112 ^{ns}	-0.120 ^{ns}	-0.049 ^{ns}	-0.124 ^{ns}	-0.231 ^{ns}	-0.423*
Ear length	-0.095 ^{ns}	1	0.414*	0.062 ^{ns}	-0.027 ^{ns}	0.505**	0.631**
Ear diameter	-0.096 ^{ns}	0.268*	1	0.962**	0.517**	0.767**	0.596**
Cob diameter	-0.076 ^{ns}	0.035 ^{ns}	0.799**	1	0.778**	0.502**	0.401*
Number of rows per ear	-0.097 ^{ns}	0.083 ^{ns}	0.522**	0.633**	1	0.210 ^{ns}	0.329*
1000-kernel weight	-0.197 ^{ns}	0.403**	0.667**	0.384**	0.160 ^{ns}	1	0.691**
Grain yield	-0.346**	0.491**	0.497**	0.288*	0.267*	0.646**	1

ns, * and **: not significant, significant at the 5% and 1% levels of probability, respectively.

The values in Table 3 shows genetic and phenotypic correlation coefficients between pairs of traits. It is noted that both types of correlations were similar in strength and direction for most cases. The genotypic correlations in general were higher than the phenotypic correlation, that mean interrelationships were strongly inherent and low phenotypic expression were due to environmental factors.

Correlation coefficients

In genotypic and phenotypic levels grain yield showed highly significant positive correlation with 1000-kernel weight (0.691; 0.646), ear length (0.631; 0.491) and ear diameter (0.596; 0.497). Number of rows per ear (0.329; 0.267) and cob diameter (0.401; 0.288) had significant positive correlation with grain yield (Table 3). Similar result was reported by Pavan et al. (2011).

The trait anthesis-silking interval showed negative significant association with grain yield. Negative correlation of ASI revealed that genotypes with short ASI desirable for higher grain yield because of quick translocation of photosynthates in the short interval of days to anthesis to days to silking (Saidaiyah et al., 2008).

In terms of the correlation between other independent variables, a highly significant positive correlation at both phenotypic and genotypic levels was discovered between ear diameter with cob diameter (0.962; 0.799), number of rows per ear with cob diameter (0.778; 0.633) and 1000-kernal weight with ear diameter (0.767; 0.667) (Table 3). The results were supported by the earlier findings of Nataraj et al. (2014).

Sometimes, correlation coefficients give misleading results because the correlation between two variables may be due to third

factor. It is therefore necessary to analyze the cause and effect relationship between dependent and independent variables to entangle the nature of relationship between the variables. Path coefficient analysis (Dewey and Lu, 1959) 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 (Pavan et al., 2011).

Path analysis

Path coefficient analysis is done in order to study the direct and indirect effects of individual component characters on the dependant variable - grain yield. Study of

path coefficients enables breeder to concentrate on the variable which shows high direct effect on grain yield per plant. Ultimately we can reduce time in looking for more number of component traits by restricting selection to one or few important traits (Dewey and Lu, 1959). 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 (Pavlov et al., 2015).

The path coefficient analysis (Table 4) revealed that most of the traits had positive direct effect on grain yield.

Table 4. Genotypic (G) and phenotypic (P) path coefficient for yield and yield contributing characters in maize (*Zea mays* L.)

		ASI	EL	ED	CD	NRPE	KW	GY
ASI	P	-0.181	-0.020	0.020	-0.002	-0.019	-0.142	-0.346**
	G	-0.255	-0.045	-0.007	0.004	-0.033	-0.086	-0.423*
EL	P	0.017	0.218	-0.055	0.001	0.017	0.293	0.491**
	G	0.028	0.403	0.023	-0.005	-0.007	0.188	0.631**
ED	P	0.017	0.058	-0.208	0.021	0.106	0.502	0.497**
	G	0.032	0.166	0.057	-0.087	0.140	0.286	0.596**
CD	P	0.013	0.007	-0.164	0.026	0.129	0.275	0.288*
	G	0.012	0.025	0.055	-0.090	0.210	0.187	0.401*
NRPE	P	0.017	0.018	-0.108	0.017	0.203	0.119	0.267*
	G	0.031	-0.011	0.029	-0.070	0.270	0.078	0.329*
KW	P	0.035	0.087	-0.143	0.010	0.033	0.608	0.646**
	G	0.059	0.203	0.044	-0.045	0.056	0.373	0.691**

* Significant at 5% level;

** Significant at 1% level;

Diagonal bold values indicate direct effects.

Residual effect at phenotypic level = 0.409;

Residual effect at genotypic level = 0.291;

Positive and higher genotypic direct effects on grain yield was observed with ear length (0.403) followed by 1000-kernel weight (0.373) and number of rows per ear (0.270). These characters can be considered as the main components for selection in a breeding program designed for higher grain yield improvement. Grain yield was used as the dependent variable in a path coefficient analysis at the phenotypic level, and it was discovered that the 1000-kernel weight (0.608), followed by ear length (0.218) and number of rows per ear (0.203) had a positive and direct phenotypic influence on grain yield as well as a positive association with grain

yield. This suggests that, provided other traits are maintained constant, an increase in one of these traits will concurrently result in an increase in grain yield, confirming that these traits are the main factors influencing yield improvement at the phenotypic level.

The weight of 1000-kernel exhibited high positive direct effect coupled with significant positive correlation at both phenotypic (0.608) and genotypic (0.373) levels on grain yield (Table 4). Similar results of positive direct effect on grain yield per plant at both phenotypic and genotypic levels were reported by Raghu et al. (2011), and Kumar et al. (2014). Because the direct influence of

1000-kernal weight on grain yield at both the genotypic and phenotypic levels accounted for the majority of the total correlation between them, direct selection on 1000-kernal weight will be beneficial in improving grain yield.

Number of rows per ear also had positive direct effect and significant positive association with grain yield at both phenotypic and genotypic levels. Similar results of positive direct effect of number of rows per ear were reported by Raghu et al. (2011), Prasanna Kumar and Ratna Babu (2015), at both phenotypic and genotypic levels.

The trait ear length had high positive direct effect coupled with significant positive correlation at both phenotypic (0.218) and genotypic (0.403) levels on grain yield. Similar results with significant positive correlation at phenotypic level reported by Prasanna Kumar and Ratna Babu (2015).

Ear diameter recorded positive direct effect coupled with significant positive correlation at genotypic (0.057) level and negative direct effect coupled with significant positive correlation at phenotypic (-0.208) level. The positive indirect effects of this trait *via* ear length, 1000-kernel weight and number of rows per ear also contributed to the total correlation on grain yield. This indicate that, direct selection on ear diameter along with the other three indirect causal will be effective in selection. These findings were in agreement with Rafiq et al. (2010), Nataraj et al. (2014) and Filipovic et al. (2014).

The trait, cob diameter exhibited positive direct effect (0.026) coupled with significant positive correlation at phenotypic level and negative direct effect (-0.090) coupled with significant positive correlation at genotypic level. Similar result of positive direct effects on grain yield on phenotypic level was reported by Jakhar et al. (2017).

Anthesis-silking interval (ASI) influence with negative effects at both phenotypic (-0.181) and genotypic (-0.255) levels on grain yield. This trait also had negative and significant genotypic correlations with grain yield. It indicates that the value of ASI could

be used as an indirect selection criterion for improving yield. High grain yield was associated with small ASI (Saidaiah et al., 2008).

CONCLUSIONS

The success of breeding programs depends on genetic variability. It may be concluded that traits with high to moderate genetic variance, heritability, and genetic advances, such as the 1000-kernel weight, ear length, ear diameter and number of rows per ear indicated a scope for improvement of grain yield through selection. Phenotypic coefficient of variation is larger than genotypic coefficient of variation, indicating that there was an environmental influence. The high positive correlation of grain yield was found with the 1000-kernel weight, ear length and ear diameter. The path analysis shows that traits number of rows per ear, ear length and 1000-kernel weight had a direct positive effect on grain yield both at the phenotypic and genotypic levels. Therefore, these characters should be considered as important selection criteria for the improvement of grain yield.

In the present study, the genotypic and phenotypic residual effects recorded 0.291 and 0.409 respectively indicating that the characters used in our experiment are contributing more than 59 per cent of variability pertaining the dependent variable - grain yield.

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