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GENETIC VARIABILITY AND PATH COEFFICIENT ANALYSIS FOR THREE-WAY CROSS IN MAIZE

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SUMMARY

A field experiment at the Maize Research Station, General Authority of Agricultural Research in Abu-Ghriab, Iraq, began on six inbred lines of maize (1- UMGW 16, 2- UMGW 4, 3- DAQ, 4- HNG 9, 5- FAR 30, and 6- ABS – 32) as samples to generate 15 F1 single crossings through half-diallel cross. Crossing the parents and single crosses sought to produce 60 three-way cross hybrids. Grown seeds of three-way crosses became specimens to study the most effective traits that could affect the yield and become selective indicators to improve maize grain yield. The experiment proceeded as a randomized complete block design (RCBD) with three replicates. The analysis of variance results revealed statistically significant differences among all studied traits. The values of genetic variance were higher than the environmental variance for all studied traits except for plant height. The highest broad-sense heritability (0.956) appeared in grain yield per plant, followed by the days from planting to 50% silking (0.803). A significant positive genetic and phenotypic correlation was apparent between grain yield, 100-grain weight, and the number of grains per row, while a negative genetic correlation between grain yield and the number of days from planting to 50% silking occurred. The path analysis revealed that the number of grains per row has the highest positive direct effect (0.537) and the total of all effects (0.828). The number of grains per row gave the utmost indirect positive influence of 0.259 by the 100-grain weight.

Keywords: Maize (*Zea mays* L.), genetic variability, path coefficient analysis, genotypic and phenotypic variances, broad-sense heritability, yield-related traits

Key findings: Quantitative inheritance methods contribute to choosing the researcher's direction toward selection or crossing between genotypes. Correlation and pathway analysis also helped in understanding the appropriate breeding method and which traits directly impact increasing the yield..

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INTRODUCTION

Maize crop (*Zea mays* L.) is one of the most valuable grain crops farmed in broad areas worldwide. This crop ranks third behind wheat and rice based on economic importance and productivity. It is a cereal grain, with its seeds and plants beneficial as food, animal feed, and industrial items, such as, vegetable oils (Sharif and Al-Rawi, 2019). The biggest challenge for the plant breeder is improving the quantitative traits because they have several pairs of genes (polygenes) controlling them, which have low expression and are easily affected by environmental factors. The quantitative trait expression can result from the genetic \times environmental interaction, where the environment can positively or negatively affect those traits (Allard, 1999).

The selection definition can mean choosing plants characterized by the desired traits from genetically heterogeneous sources. Al-Rawi *et al.* (2013) mentioned that the selection process has a strong effect if it is only for one trait, and it will be more effective if there are wide variations in the original population. Grain yield is a result of many components having high correlations with them. Therefore, it is a complex economic trait, which, in its heritability, has many genetic factors in control; it can also incur strong influences from environmental factors. Allard (1999) reported that plant breeders depend on indirect selection for the yield components to increase it. Indirect selection is considerably one of the components that may have significant correlations with a yield, eventually impacting it substantially and improving it. Heritability is the most vital genetic parameter of the trait under selection. However, it can affect genetic accumulation after the selection process. Also, the heritability of a correlated trait with yield does not guarantee the required genetic improvements unless there is a highly positive correlation with the yield trait.

Manivannan *et al.* (2008) mentioned that the selection for the yield component has more effect than the selection for the yield itself. Therefore, selecting one or more traits

as alternatives to yield became crucial by looking for the most correlated traits with yield through different statistical methods, viz., coefficient of phenotypic and genotypic correlations. Since the correlation relation may not determine how much each trait can contribute a direct and indirect effect, researchers should use alternative statistical approaches, such as path coefficient analysis, because the correlation relationship cannot indicate how much each feature might contribute a direct and indirect effect, as indicated by Wright (1921) and developed by Li (1956).

Path coefficient analysis has become the most relevant method that plant breeders can use to enable them to select prominent genotypes. It evaluates the direct and indirect effects of yield components that are independent and correlate with dependent traits. Its calculation can succeed by choosing diverse genotypes; however, genotypes require assessment first, then estimating the variance and covariance of those characters and their combinations. This method has many researchers' applications (Al-Rawi *et al.*, 2018; Ahmed *et al.*, 2020; Taiwo *et al.*, 2020; Islam *et al.*, 2020; Kumawat *et al.*, 2020; Hamdi and Al-Rawi, 2021). They obtained different results, finding that some yield components have direct and others have indirect yield effects.

The obtainable information from direct and indirect effects through partitioning correlations between yield and its components is valuable for getting better traits that affect yield. Those traits that can incur environmental factors' effects could benefit as selective indicators of ineffective selection methods. This study aimed to estimate many genetic parameters, including phenotypic, genotypic, and ecological variances, genotypic and phenotypic coefficients of correlations, and heritability, to identify selection criteria, evaluate genotypic and phenotypic coefficients of correlation, and measure the direct and indirect effect of different features on grain yield, and eventually improve the grain yield of maize through selection.

MATERIALS AND METHODS

A field experiment commenced in the Maize Research Station/General Authority of Agricultural Research in Abu-Ghriab, Iraq, on six inbred lines of maize (1- UMGW 16, 2- UMGW 4, 3- DAQ, 4- HNG 9, 5- FAR 30, and 6- ABS - 32) as subjects for generating 15 F1 single crosses using half-diallel crosses. Combining the parents and single crosses has produced 60 three-way cross hybrids. The seed of the three-way cross was grown to study the most effective traits that could affect the yield and could become selective indicators to improve maize grain yield. The experiment applied an RCBD with three replicates. All agricultural operations, such as, fertilizer applications, irrigation, soil preparation, and weed control, observed scientific guidelines on the following characteristics studied: Number of days to 50% silking DS (day), Plant height PH (cm), Leaf area LA (cm²), Number of rows per ear (NRE), Number of grains per row (NGR), 100-grain weight (100 GW), and Grain yield per plant GY (g). Finding the direct and indirect effect of different traits on yield through partitioning the genotypic correlation into its direct and indirect components employed the method developed by Li (1956) and used by Singh and Chaudhary (1977). The study found environmental, phenotypic, and genotypic variances, heritability, and phenotypic and genotypic correlations by using the path coefficient analysis according to Agarwal and Ahmad (1982):

$$\delta^2 G = (\delta^2 \text{ Genotypes} - \delta^2 E) / r$$

$$\delta^2 E = Mse$$

$$\delta^2 P = \delta^2 G + \delta^2 E$$

$$P.C.V = \sqrt{\delta^2 P} / \text{Mean of Genotypes}$$

$$G.C.V = \sqrt{\delta^2 G} / \text{Mean of Genotypes}$$

$\sigma^2 G$ = Genotypic Variance

$\sigma^2 E$ = Environmental Variance

$\sigma^2 P$ = Phenotypic Variance

CV% = Coefficient of Variance

GCV% = Genotypic Coefficient of Variance

PCV% = Phenotypic Coefficient of Variance.

H_{b,s} = Broad-sense

Heritability used the formula below:

$$H_{b,s}^2 = \frac{\delta^2 G}{\delta^2 P} \times 100$$

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences for all traits (Table 1). This highly substantial variance is evidence of a difference between genotypes used in this study and their response to their sown environment; therefore, these genotypes can best perform for selection. The variance components differed. Table 2 shows genotypic variance values higher than the environmental variance for studied traits except for plant height. Grain yield gave the highest genetic variance of 572.5, followed by plant height at 17.85 and leaf area at 16.60, whereas the number of rows per ear gave the lowest value of genetic variance (0.516). The high variance values indicate that the genes played a significant role in this variance, and selection can be very effective (Boonlertnirun *et al.*, 2012; Khalid *et al.*, 2020; Islam *et al.*, 2020; Kumawat *et al.*, 2020; Reddy *et al.*, 2022).

The relative environment-to-genotypic variance increase has reflected its effect on broad-sense heritability. The highest broad-sense heritability values manifested in various plant variables studied (Table 2). The highest heritability estimates appeared in grain yield per plant (0.944), the number of days to silking (0.803), the number of grains per row (0.727), 100-grain weight (0.694), and the number of rows per ear (0.653). Moreover, the results illustrated medium broad-sense heritability estimates of 0.578 for leaf area and 0.374 for plant height. The high heritability values allow plant breeders to improve the trait through direct selection. It proves that the phenotypes in this study will be available in the genotypes of the next generation. The same results emerged that broad-sense heritability

Table 1. Mean squares for analysis of variance of different traits of 60 three-way cross hybrids of maize.

S.O.V	D.f.	DS (day)	PH (cm)	LA (cm ²)	NRE	NGR	100 GW (g)	GY (g)
Replications	2	2.55	42.57	23.52	0.304	17.37	0.439	9.17
Genotypes	59	37.27	83.38**	61.91**	1.82**	27.11**	18.3**4	1751.06**
Error	118	2.82	29.82	12.10	0.274	3.01	2.35	33.71

*and ** significance at p= 0.05 and 0.01 respectively.

Number of days to 50% silking= DS (day), Plant height= PH (cm), Leaf area= LA (cm²), Number of rows per ear= NRE, Number of grains per row= NGR, 100-grain weight= 100 GW, and Grain yield per plant= GY (g).

Table 2. Values of genotypic, environmental, and phenotypic variances and broad-sense heritability.

Genetic parameters	DS (day)	PH (cm)	LA (cm ²)	NRE	NGR	100 GW (g)	GY (g)
$\delta^2 G$	11.48	17.85	16.60	0.516	8.03	5.33	572.5
$\delta^2 E$	2.82	29.82	12.11	0.274	3.01	2.35	33.71
$\delta^2 P$	14.31	47.68	28.70	0.789	11.04	7.68	606.16
$h_{b,s}$	0.803	0.374	0.578	0.653	0.727	0.694	0.944

Number of days to 50% silking= DS (day), Plant height= PH (cm), Leaf area= LA (cm²), Number of rows per ear= NRE, Number of grains per row= NGR, 100-grain weight= 100 GW, and Grain yield per plant= GY (g).

Table 1. Genotypic and phenotypic coefficient of variance.

Genetic parameters	DS (day)	PH (cm)	LA (cm ²)	NRE	NGR	100 GW (g)	GY (g)
CV%	2.79	3.07	7.09	3.32	4.78	6.09	4.12
GCV%	5.64	2.37	8.31	4.55	7.81	9.15	16.95
PCV%	6.29	3.88	10.93	5.63	9.16	10.99	17.45

Number of days to 50% silking= DS (day), Plant height= PH (cm), Leaf area= LA (cm²), Number of rows per ear= NRE, Number of grains per row= NGR, 100-grain weight= 100 GW, and Grain yield per plant= GY (g).

was high in some traits and low in others (Dermail *et al.*, 2018; Sharif and Al-Rawi, 2019; Muliadi *et al.*, 2021; Kaler *et al.*, 2022).

Genotypic and phenotypic coefficient of variance

The comparison between populations based on variance and standard deviation may not be valid, as high means for a trait, its variance values are also often high; therefore, comparing traits according to covariance coefficients is preferable. The genotypic and phenotypic parameter values were excessive in grain yield, followed by 100-grain weight and leaf area (Table 3). The highest genotypic coefficient of variance was for grain yield and 100-grain weight (16.95 and 9.15,

respectively) and for the phenotypic coefficient of variance (17.45 and 10.99). The elevated differences between those traits have led to efficient selections compared with the other features (Sharif and Al-Rawi, 2019; Kalapakdee *et al.*, 2020; Kumawat *et al.*, 2020; Reddy *et al.*, 2022).

Genotypic and phenotypic correlation

Each variable's genotypic and phenotypic correlation values can benefit breeding programs with information on the genetic environment for those two traits. The genotypic correlation values between grain yield and 100-grain weight were positive and significant with the number of grains per row and the number of rows per ear (Table 4).

Table 2. The values above the diagonal represent the Genotypic correlation, and the values under the diagonal represent the Phenotypic correlation.

Traits	DS (day)	PH (cm)	LA (cm ²)	NRE	NGR	100 GW (g)	GY (g)
DS (day)	1	-0.431	-0.021	-0.373	-0.722**	-0.522*	-0.675*
PH (cm)	-0.578*	1	0.254	0.037	0.244	0.499	0.386
LA (cm ²)	0.242	-0.367	1	-0.032	0.033	0.071	0.080
NRE	0.043	0.261	-0.543*	1	0.399	0.533*	0.771**
NGR	0.604*	-0.071	0.106	-0.242	1	0.483	0.828**
100 GW (g)	0.678*	0.371	-0.018	-0.104	0.031	1	0.833**
GY (g)	0.673*	0.374	0.309	0.056	0.031	-0.202	1

Number of days to 50% silking= DS (day), Plant height= PH (cm), Leaf area= LA (cm²), Number of rows per ear= NRE, Number of grains per row= NGR, 100-grain weight= 100 GW, and Grain yield per plant= GY (g).

Table 5. Path coefficient values for traits under study.

Traits	Direct effect	Indirect effect through					Total effect
		PH (cm)	LA (cm ²)	NRE	NGR	100 GW (g)	
DS (day)	0.0878	- 0.039	- 0.0006	- 0.147	- 0.387	- 0.189	- 0.675
PH (cm)	0.0898	- 0.038	0.007	0.0144	0.131	0.181	0.386
LA (cm ²)	0.029	- 0.002	0.023	- 0.012	0.0177	0.026	0.080
NRE	0.394	- 0.033	0.003	- 0.0009	0.213	0.193	0.771
NGR	0.537	- 0.063	0.0219	0.0009	0.157	0.175	0.828
100GW (g)	0.362	- 0.045	0.0448	0.002	0.210	0.259	0.833

Number of days to 50% silking= DS (day), Plant height= PH (cm), Leaf area= LA (cm²), Number of rows per ear= NRE, Number of grains per row= NGR, 100-grain weight= 100 GW, and Grain yield per plant= GY (g).

Research suggested that improving these traits would invariably enhance grain yield (Bello *et al.*, 2010). However, a negative and significant ($P < 0.05$) association with the number of days to 50% silking occurred.

The positive correlation values indicate a synergistic effect of polygenes in each correlated trait. Selecting either of them will affect the other in the same direction. The 100-grain weight and the number of grains per row emerged as the most relevant yield components. It can refer to the effect of polygenes that affected antagonistically on those traits. Therefore, the plant breeder should take this into consideration because the improvement in one trait will lead to impairment in the other one, which requires a study of path analysis to be able to use it in grain yield improvement; it will eventually make a plant breeder focus on one of these traits as a tool for selecting prominent genotypes with the high ability for production (Reddy *et al.*, 2022).

Path coefficient analysis

Partitioning the genotypic correlation using a path coefficient analysis gives more information about the nature, size, and importance of the relationship between grain yield and its components. Afterward, the divided total effects of direct and indirect effective traits determine the traits that most affect grain yield and, eventually, the result as the selection indicator. Path coefficient analyses also obtained further information on trait interrelationships and their impacts on grain yield, as shown in Table 5. The number of grains per row (0.537) had the broadest direct effect on grain yield, followed by the number of rows per ear (0.394) and 100-grain weight (0.362). Islam *et al.* (2020) reported that the number of grains per row directly affected grain yield. The leaf area and days to 50% silking showed a low positive absolute effect on grain yield (0.29 and 0.087, respectively).

The 100-grain weight had a moderate indirect positive impact on grain yield by the number of grains per row (0.259) and the number of rows per ear (0.210), while the number of rows per ear had moderate indirect positive effects on grain yield by the number of grains per row (0.213) and 100-grain weight (0.193). It also indicates that plant height moderately indirectly affected grain yield positively by the number of grains per row (0.131) and 100-grain weight (0.181). However, it is visible that other variables could have effects on grain yield. In this study, the number of grains per row, rows per ear, and 100-grain weight appeared to be the prominent traits that could benefit selecting for high yield because of their highly significant genotypic and phenotypic correlations with grain yield. These traits also had the maximum direct and indirect effects through most other attributes.

However, the studies carried out by Abdulkhaleq and Tawfiq (2014), Hassan *et al.* (2018), Islam *et al.* (2020), Kumawat *et al.* (2020), and Reddy *et al.* (2022) demonstrated that interrelationship and route coefficient study in maize exhibited that direct selection for the number of grains per row, the number of rows per ear, and 100-grain weight are helpful for yield improvement since they revealed a positive and significant correlation with grain yield. As a result, it is debatable whether these agronomic factors could serve as chief selection criteria in enhancing open-pollinated maize varieties and hybrids for high grain production (Reddy *et al.*, 2013).

CONCLUSIONS

Through the previous discussion, the study found a relationship between genetic and phenotypic correlations between yield, the number of rows, and the number of grains per row. The highest direct effect on yield was evident with the 100-grain weight and the grains per row. Therefore, the selection of plants based on these traits helps plant breeders choose plants with high production.

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