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Relationship between Seed Properties and Outcome Components for Selection Criteria of Corn (*Zea Mays* L.) Products at Various Dosages of Popostium Fertilizer

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This research was conducted to determine the relationship between seed developmental characteristics and yield components in a population of maize (*Zea mays* L.) grown at different potassium fertilizer rates. The information could be utilized as alternative selection criteria for maize genotypes with high-yielding potential. This research was conducted at the Experimental field of the Horticulture Seed Agency, Pekanbaru. Seven maize genotypes with four potassium fertilizer rates were grown in a 350 cm x 200 cm experimental plot with three replications. The genotypes used were Bisi 228. Pertiwi 3. Bisi 2. Decoral, Bisi 18. Betras 4. and Srikandi. Potassium fertilizer rates included 30 kg, 50 kg, 70 kg, and 90 kg per ha, respectively. Traits observed were plant height, tesseling flowering date, silking date, seed dry accumulation rate, effective seed filling period, cob length, cob weight, number of seed rows, number of seeds per cob, seed weight per cob, the weight of 100 seeds and seed yield per m^2. Analysis of variance was performed to the data using SAS and further tested by honesty significant difference at 5% level. Variance component, heritability, genetic correlation coefficient, and selection response were calculated for all characters and effective seed filling duration. The results indicated that the genetic variance component was significant for all characters except for the dry matter accumulation rate. All characters' heritability values were quite high except for effective seed-filling duration and the number of seeds per cob. Phenotypic correlation coefficients were positively significant between seed yield per m^2 and plant height, seed development rate, cob length, ear weight, number of seeds per ear, seed weight per ear, and weight of 100 seeds. The genetic correlations was significant between seed yield per m^2 and plant height, seed development rate, number of seeds per ear, and seed weight per ear. All characters' direct selection response value is higher than the indirect selection response value.

Keywords: *Genetic variance, heritability, maize, calium fertilizer, selection response.*

1. INTRODUCTION

In terms of carbohydrates and fats, corn (Zea mays L.) is the second most important food item in Indonesia. Corn kernels are the primary raw material in the animal feed business and meet human dietary demands. More than 55% of domestic maize demands are anticipated to be used for animal feed, 30% for human food consumption, and the remainder for food industry needs (Fitria, 2018). Corn plants have a significant prospect for development based on their usage potential and economic worth (Wahyudin, 2016). National corn productivity remains low due to poor land management, ineffective cultivation and fertilization practices, ineffective pest and disease control, and a lack of hybrid seed utilization. The selection of hybrid corn plays a critical role in determining the amount of maize produced. Each variety has unique qualities regarding yield potential, pest and disease resistance, drought resilience, and harvest time. (Maharani, 2018).

Selection activity is a critical step in developing a new variety, as it searches for genotypes with high yield potential using specific selection criteria. To ensure an appropriate population, direct selection is done on corn plant yields, typically done in later generations. The size of the corn kernels is one of the yield components that impact corn productivity. Seed size is determined by multiplying the speed of filling the dry matter into the seeds by the effective seed filling time, commonly given as the dry weight of the seeds. High seed yields are frequently associated with early maturity and are inversely associated with seed fat content (Rasyad, 1994). As a result, it took a long time to obtain high-producing and early maturing types and high-fat content due to the slow selection progress.

When combined with suitable fertilization, variety selection can maximize maize output. Like other plants, corn requires adequate nutrients for growth, including macronutrients and micronutrients. The use of proper and balanced fertilizers is one part of agriculture that still needs to be developed because the availability of these nutrients in the soil varies depending on the kind of soil and different land locations.

Potassium (K) is one of the macronutrients that must be consumed at suitable levels. Element K regulates the balance of ions in the cell, which holds numerous metabolic pathways such as photosynthesis, glucose, protein, and fat synthesis. Furthermore, element K acts as an activator for several enzymes involved in respiration, aids in translocation in plant tissues, and boosts plant resilience to pests and diseases. (Firmansyah and colleagues, 2017). The goal of this study was to determine the components of diversity, heritability, and genetic correlation of maize seed developmental traits and yield components of various maize varieties at different potassium fertilizer doses and to determine which characters could be used as criteria for direct or indirect selection for selecting maize varieties with high yield potential.

2. MATERIAL AND METHODS

The study was conducted in the Central Horticulture Seed Center's experimental garden in Pekanbaru City. The study lasted from November 2021 through March 2022. Analytical balances (Shimadzu type AUY 220), a hygrometer, an oven (Memmert Model HM-113L), and a dexicator were utilized in the laboratory. Hoes, tractors, gembor, hand sprayer, plastic bag zippers, plastic bags, staple guns, manila paper envelopes, rulers, sticker labels, manila cardboard, and tweezers are among the tools used in the field. Hybrid corn seeds, chicken manure, potassium fertilizer (KCL), urea fertilizer, and TSP fertilizer are among the components used. Pesticides Curater, Decis 25 EC, and Dithane M-45.

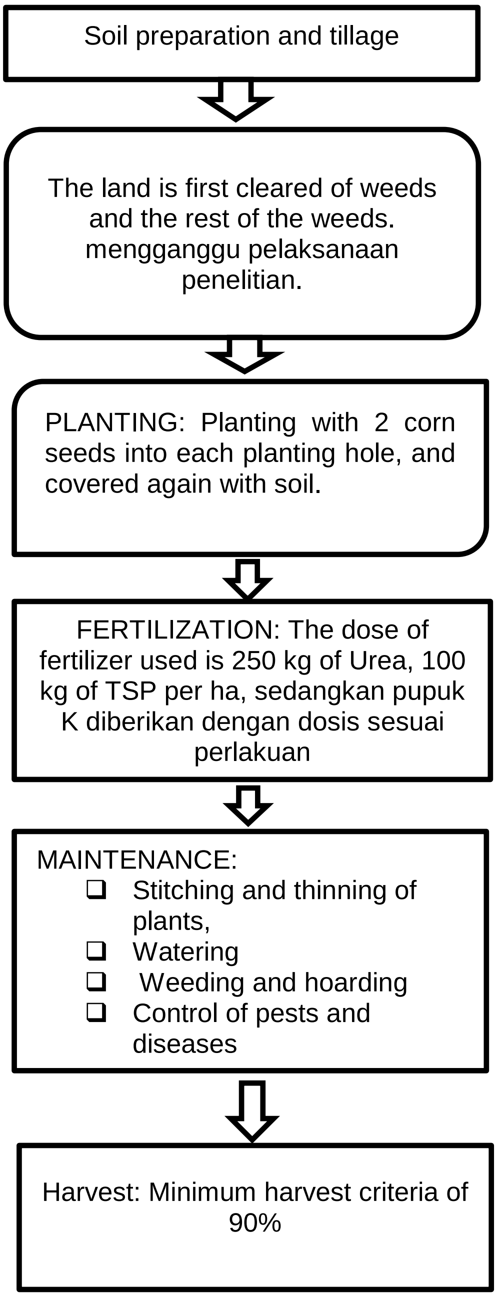
The study used a factorial experiment with two factors: seven types of maize and four doses of potassium fertilizer. The experimental plan was laid out using a randomized block design with a plot size of 350 cm × 200 cm and each treatment was repeated three times.

The first factor was 7 corn genotypes which were hybrid types, including: Bisi 228. Bisi 2. Bisi 18. Srikandi, Pertiwi 3. and Decoral varieties.

The second factor is 4 levels of K2O fertilizer doses, e.g: 30 kg K2O per ha, 50 kg K2O per ha, 70 kg K2O per ha and 90 kg K2O per ha.

28 treatment combinations were developed based on the levels of the two components employed. Each treatment combination was performed three times, yielding 84 experimental units. In each experimental plot, up to six plants were randomly selected as sample plants.

Research Implementation



Soil preparation and tillage

The land is first cleared of weeds and the rest of the weeds. mengganggu pelaksanaan penelitian.

PLANTING: Planting with 2 corn seeds into each planting hole, and covered again with soil.

FERTILIZATION: The dose of fertilizer used is 250 kg of Urea, 100 kg of TSP per ha, sedangkan pupuk K diberikan dengan dosis sesuai perlakuan

MAINTENANCE:
- ☐ Stitching and thinning of plants,
- ☐ Watering
- ☐ Weeding and hoarding
- ☐ Control of pests and diseases

Harvest: Minimum harvest criteria of 90%

RESEARCH PARAMETER

Plant height (cm), male flower emergence (HST), female flower emergence (HST), seed development rate (mg/seed/day), effective seed filling time (days), cob length (cm), weight cobs (grams), number of seed rows per cob (row), number of seeds per cob (seeds), seed weight per ear (grams), weight of 100 seeds (grams), and seed yield per m2 (grams) were observed.

Data Analysis

SAS software was used for variance analysis and estimate of diversity components (SAS User Manual, 2004). A technique developed by Hallauer et al. (2010) was used to determine a variable's diversity and heredity components. As indicated in Table 1. the middle square of the source of variety in the analysis of variance table is first translated into the middle square of expectations.

Table 1. Analysis of variance and mean square of expectations for various characters of seed development and yield components of maize populations on maize plants.

Source of Diversity	DB	KT	KTH
Test	r-1	KT 5	$\sigma^2e + pv\sigma^2r$
Fertilizer K(j)	j-1	KT 4	$\sigma^2e + r\sigma^2pv + rv\sigma^2p$
Variety (k)	k-1	KT 3	$\sigma^2e + r\sigma^2pv + rp\sigma^2v$
Interaction PxV (jk)	(j-1)(k-1)	KT 2	$\sigma^2e + r\sigma^2pv$
Error	jk(r-1)	KT 1	σ^2e
Total	(rjk-1)		

Then the expected middle square is calculated with the following procedure:

σ^2e = KT1
σ^2pv = (KT2-KT1)/r
σ^2v = (KT3-KT2)/rp
σ^2p = (KT4-KT2)/rv

Note:
σ^2e = the mean square of the expected error
σ^2pv = the middle square of the expected interaction of K fertilizer and variety
σ^2v = the mean square of the varietal expectation
σ^2p = the middle square of the expectation of K fertilizer

The expected mean squared value for each source of diversity is then converted into a component of diversity as follows:

$\sigma^2g = \sigma^2v$
$\sigma^2l = \sigma^2e + \sigma^2p + \sigma^2pv$
$\sigma^2f = \sigma^2g + \sigma^2l$

Note:
σ^2g = Genotype range
σ^2l = environments range
σ^2f = phenotypes range

The heritability value is calculated using the following formula:

$$h^2 = \frac{\sigma^2 g}{\sigma^2 f}$$

Note:
h^2 = heritability
σ^2g = Genotype range
σ^2f = phenotypes range

For determining genetic covariance between two variables, first created a dummy variable, the sum of the two variable values for which the genetic correlation will be selected. Since the dummy variable "Z" is X+Y, the square of $(X+Y)^2$ will equal X2 + 2XY + Y2. Thus, the XY value can be searched by the formula:

$$\boldsymbol{Cov_{g(x,y)}} = \frac{\boldsymbol{(XY) - X^2 - Y^2}}{\boldsymbol{2}}$$

Where:
Covg(x,y) = Genetic covariance between x and y characters
X^2 = Genetic variety of character x
Y^2 = Genetic variety of character y

After obtaining the Cov (g) xy value, then the genetic correlation coefficient is then calculated using the following formula:

$$r_{g(x,y)} = \frac{cov_g(x,y)}{\sqrt{var_g\, x}\sqrt{var_g\, y}}$$

Where:
$r_{g(x,y)}$ = Genetic correlation coefficient between x and y variables

Cov_g (x,y) = Genetic covariance between x and y variables
Var_g (x) = Genetic variance of character x
Var_g (y) = Genetic variance of character y

The direct selection response is calculated for all characters used as selection criteria with the formula:

$$\Delta S = i.h.\sigma g$$

Where:

Δ_S = Selection response
i = Selection differential for 10% selection intensity
h = The square root of heritability ($\sqrt{h^2}$)
σ_g = The square root of the genotype variance ($\sqrt{\sigma^2 g}$)

Indirect selection responses are calculated using the following formula (Falconer, 1981):

$$\Delta s_{y(x)} = i.h_x.h_y.\sigma_{gy}.r_{gx.y}$$

Where:

$\Delta s_{y(x)}$ = The change in the middle value of character Y if a selection is made of character x for one selection cycle
i = Selection differential for the variables that are the selection criteria
h_x = The square root of the heritability of the variable that is the criterion
h_y = The square root of the heritability of the changing variables
σ_{gy} = square root σ^2g ufor character y
$r_{gx.y}$ = Genotype correlation between variable x and variable y.

3. RESULT AND DISCUSSION

Diversity and Heritability

Table 2 shows the findings of genetic diversity estimation, the standard deviation for genetic diversity, and phenotypic diversity of various seed development features and yield components.

Table 2. Components of genetic diversity (σ²g), standard error of genetic diversity (SE σ²g), and phenotypic diversity (σ²f) of various characters in maize populations with various doses of potassium fertilizer.

Character	σ²g	SE σ²g	σ²f
Plant Height (cm)	1716.00 *	511.27	1995.37
Age of Male Flower Emergence (HST)	5.65*	1.76	9.48
Age of Female Flower Emergence (HST)	5.19*	1.64	9.23
Seed Development Rate (mg/seed/day)	4.71	1.46	7.85
Effective Seed Filling Time (days)	19.09*	6.90	70.63
Cob Length (cm)	1.97*	0.60	3.05
Cob Weight (g)	2204.60*	657.85	2703.00
Number of Rows of Seeds Per Cob (rows)	2.92*	0.87	3.37
Number of Seeds Per Cob (seeds)	5073.20*	1650.98	11471.96
Seed Weight Per Cob (g)	2216.20*	668.52	2804.50
Weight of 100 Seeds (g)	77.34*	22.86	83.68
Seed Yield Per M2 (g)	102105.30*	30488.21	263551.8

Note: * = The components of diversity are expressed broadly ($\sigma^2 g \geq 2(SE\ \sigma^2 g)$)
= diversity components are expressed narrowly ($\sigma^2_g < 2(SE\ \sigma^2_g)$

Plant height, age of male flower emergence, age of female flower emergence, effective seed filling time, cob length, cob weight, number of seed rows per ear, number of seeds per ear, seed weight per ear, weight of 100 seeds, and seed yield per m2 are shown in Table 2. The wide and narrow diversity criteria were developed by Hallauer et al. (2010), and Barmawi et al. (2013), and genetic diversity is considered wide if the diversity value is twice the standard deviation and narrow diversity if the variance in genetics is less than twice the standard deviation. A character's wide genetic variety shows that genetic control over that character is greater than environmental control. Wide genetic variety indicates that the likelihood of successful character selection is increasing because the more different the look of individuals in a population, the easier it is to isolate selected individual plants to obtain a better genotype. Because of the restricted genetic range, individuals tend to be homogeneous, making selection for trait development less effective. This is consistent with Effendy (2018) who states that the wider the genetic diversity of a character in the population, the more varied the traits in that character reflect genetic control in the population..

Heritability illustrates the size of the genetic contribution to a character. Heritability values for the various characters observed are presented in Table 3.

Table 3. Estimated values of heritability (h2) and standard errors for various characters in several maize varieties applied with various doses of potassium fertilizer

Character	h^2	$SE(h^2)$	Criteria
Plant Height (cm)	0.86	0.26	High
Age of Male Flower Emergence (HST)	0.60	0.19	High
Age of Female Flower Emergence (HST)	0.56	0.18	High
Seed Development Rate (mg/seed/day)	0.60	0.19	High
Effective Seed Filling Time (days)	0.27	0.20	Low
Cob Length (cm)	0.65	0.20	High
Cob Weight (g)	0.82	0.24	High
Number of Rows of Seeds Per Cob (rows)	0.87	0.26	High
Number of Seeds Per Cob (seeds)	0.42	0.24	Low
Seed Weight Per Cob (g)	0.79	0.24	High
Weight of 100 Seeds (g)	0.92	0.27	High
Seed Yield Per M2 (g)	0.39	0.12	High

Note: - Height or size of zero if $h^2 \geq 2(SE_h)$,
- Low or equal to zero if $h^2 < 2(SE_h)$

Table 3 reveals that almost all of the observed features have a heritability that is significant or more than zero, indicating that they are highly heritable or easily inherited. The only traits with poor heritability are effective seed filling time and quantity of seeds per cob, implying that these traits are difficult to pass on to children from this population.

Heritability is a criterion for determining if changes in a character's appearance are due to hereditary or environmental factors. Characters with a high heritability value demonstrate that genetic variables play a larger role in regulating the character of a plant, allowing these characteristics to be easily handed on to the next generation (Safani, 2011). A high heritability predictive value suggests that genetic factors are more important than environmental influences, whereas a low heritability predictive value shows that environmental factors are more prominent (Carsono *et al.,* 2004).

Genetic Correlation Coefficient and Phenotype Between Characters

Table 4. Phenotypic correlation coefficient between various seed development characters and yield components in maize populations.

Character	UBB	LPB	WPE	PTK	BRTK	JBBPT	JBPT	BBT	BSB	HBPM
TITAN	0.16	0.51**	0.16	0.62 **	0.78**	0.15	0.48**	0.72**	0.85**	0.75**
UBJ	0.93**	-0.06	0.12	-0.26	0.09	-0.55	0.37**	-0.62*	0.19	0.20
UBB		0.11	0.11	0.28*	0.00	0.52*	0.39**	-0.02	0.15	0.14
LPB			-0.38**	0.46**	0.59**	-0.12	0.40**	0.76**	0.63**	0.68**
WPE				0.07	0.14	0.17	-0.14	-0.09	0.07	-0.08
PTK					0.72**	-0.04	0.22	0.61**	0.52**	0.52**
BRTK						0.21	0.42**	0.78**	0.82**	0.75**
JBBPT							0.47**	0.05	0.11	0.21
JBPT								0.49**	0.50**	0.56**
BBT									0.77**	0.80**
BSB										0.82**

Note: : *, ** = the correlation coefficient differs from 0 at the level of 5% and 1%; TITAN = plant height; UBJ = age at which male flowers appear; UBB = age at which female flowers appear; LPB = seed development rate; WPE = effective seed filling time; PTK = cob length; BRTK = weight of cob ; JBB = number of seed rows per cob; JBBPT = number of seeds per cob; BBT = seed weight per cob; BSB = weight of 100 seeds; HBPM = seed yield per m^2.

Table 4 indicates a favorable relationship between plant height and seed development rate, cob length, ear weight, number of seeds per ear, seed weight per ear, weight of 100 seeds, and seed yield per m2. Plants with taller stems have faster seed development rates, longer cobs, heavier cobs, more seeds, heavier seed weight per cob, heavier 100 seed weight, and greater seed yields per m2. If the correlation value approaches +1. it suggests that an increase will follow a rise in one trait in another, and if it approaches -1. it means that an increase in one trait will be followed by a decrease in another (Nugroho et al., 2008). The correlation coefficient indicates the size and direction of the association between two characters. The correlation coefficient value indicates that choosing one character also entails choosing other characters who have a positive correlation with that character (Marie & Mohammed, 2010). The positive and significant difference in correlation between the characters at the 1% level indicates that the correlated characters have the same direction and the correlation is quite strong. Although phenotypic correlation can describe the relationship between features in a population, it is not very useful in plant breeding due to environmental factors. Genetic correlation coefficients between various seed development characters and yield components can be seen in Table 5.

Table 5. Genetic correlation coefficient between various characters and yield components on several maize varieties applied with various doses of potassium fertilizer

Character	BKBP	JBPT	BBT	BSB	HBPM
TITAN (cm)	0.97	0.55	0.62	0.55	0.96
UBJ (HST)	0.20	0.84	0.75	-0.16	0.35
UBB (HST)	0.25	0.78	-0.14	0.19	0.26
LPB (mg/seed/day)		0.25	0.72	0.81	0.84
WPE(mg)		0.57	0.31	0.18	0.21
PTK (cm)		0.96	0.37	0.18	0.72
BRTK (g)		0.76	0.81	-0.14	0.08
JBBPT (Row)		0.24	0.27	0.28	0.30
JBPT(seeds)			0.64	0.16	0.86
BBPT (g)				0.54	0.91
BSB (g)					0.61

Note: Titan = plant height ; UBJ = age of appearance of male flowers; UBB = age at which female flowers appear; LPB = seed development rate; WPE = effective seed filling time; PTK = Cob length without corns; BTK = weight of cob ; JBBPT = number of seed rows per cob; JBPT = number of seeds per cob; BBPT = seed weight per cob; BSB = weight of 100 seeds; HBPM = seed yield per m^2.

The genetic correlation coefficient has the same direction as the phenotypic correlation coefficient, as seen in Table 5. The genetic correlation coefficient is greater than the phenotypic correlation coefficient for certain traits. According to Oktarina (2017), the genotype correlation coefficient has a higher value than the phenotypic correlation coefficient; the higher the value of the genetic correlation coefficient, the closer the relationship between the two characters. Plant height, seed development rate, cob length, number of seeds per ear, seed weight per ear, and weight of one hundred seeds all had high genetic correlation coefficient values with HBPM. The number of seed rows per cob has a strong genetic association with seed weight per cob. The genetic correlation coefficient between the weight of 100 seeds and the rate of seed development is high. The results of the research by Timesela et al. (2020) reported that phenotype correlations tended to be in the same direction as genotypic correlations for all quantitative traits, namely plant height, number of branches, harvest age, length of harvest days, number of pods, number of seed pods, number of seeds, number of seeds and percentage of seeds in green beans.

Selection Response

The selection response is the magnitude of the average change of a character if a character is selected. The direct and indirect responses of various characters used as selection criteria with a selection intensity of 10% are presented in Table 6

Table 6. The value of the direct selection response and the indirect response of various characters used as selection criteria in the maize population

Character X	Direct Response	Indirect Response (Character Y)				
		BKBP	JBPT	BBT	BSB	HBPM
TITAN (cm)	72.79	118.85	63.57	47.37	7.85	497.83
UBJ (HST)	4.13	30.61	808.00	46.71	-9.03	151.12
UBB (HST)	3.96	24.77	72.018	-51.90	-9.12	109.04
LPB(mg/seed/day)	3.78		43.447	45.95	-9.66	363.84
WPE(mg)	7.60		23.976	26.12	-3.04	206.41
PTK (cm)	2.44		96.152	64.73	10.88	323.52
BRTK (g)	81.70		85.552	60.26	-7.50	40.40
JBBPT (Row)	2.97		102.06	20.70	12.60	156.10
JBPT(seeds)	123.93			35.06	4.71	369.80
BBT (g)	81.91				7.39	452.35
BSB (g)	15.30					327.93
HBPM (g)	555.99					

Note: Titan = plant height ; UBJ = age of appearance of male flowers; UBB = age at which female flowers appear; LPB = seed development rate; WPE = effective seed filling time; PTK = Cob length without corns; BTK = weight of cob ; JBBPT = number of seed rows per cob; JBPT = number of seeds per cob; BBT = seed weight per cob; BSB = weight of 100 seeds; HBPM = seed yield per m^2.

Table 6 illustrates that the direct selection response is generally more valuable than the indirect answer. This is evident in the number of seeds per cob character, where direct selection changes the median value of 123.93 seeds. In contrast, alternative character selection criteria result in a change in the median value of less than 123.93 seeds, namely 102.06 seeds. Similarly, the direct selection response values for seed weight per cob, weight of 100 seeds, and seed yield per m2 were 81.91 g, 15.30 g, and 555.99 g, respectively. At the same time, the indirect selection response has a lower value than the direct selection response. Because the character of the seed yield per m2 has extensive genetic variety and high heredity, the changes that occur when selecting the seed yield per m2 are relatively considerable. This is consistent with what Vidia et al. (2002) indicated: breeding efforts for character improvement can be carried out by selecting traits with a high heritability predictive value and high genetic diversity.

Indirect selection responses were conducted between all observable features and yield components: the number of seeds per cob, seed weight per ear, seed weight per 100 seeds, and seed yield per m2. To acquire the highest seed yield per m2 based on indirect selection response observations, selection criteria for plant height, seed weight per cob and number of seeds per cob, seed development rate, the weight of 100 seeds, and cob length can be used.

4. CONCLUSION

Aside from the pace of seed development, the data revealed that all the observed traits had a high diversity component. The observed features exhibited a high general heredity value, except for the effective seed-filling time and the quantity of seeds per cob, which had a low hereditary value. Plant height, seed development rate, cob length, ear weight, number of seeds per ear, seed weight per ear, and weight of 100 seeds were all positively connected with seed yield per $m^{2,}$ according to the phenotypic correlation coefficient. Plant height, seed development rate, number of seeds per ear, and seed weight per ear exhibited a high genetic connection coefficient on seed production per $m^{2.}$, according to the genetic correlation coefficient. This suggests that this trait can be utilized as a selection factor to achieve a high seed output per m2.. The value of indirect selection response indicates that plant height, cob length, seed weight per ear and 100 seed weight can be selection criteria to obtain maize genotypes with high seed yields per m^2.

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