



# Heritability and Genetic Advance Estimates among some Selected Morphological Traits and Fall Armyworm Resistance in Double Cross Hybrid Maize (*Zea mays* L.)

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## Abstract

The study was carried out to assess the genetic variability, heritability and the amount of genetic gain present in twenty four double cross maize hybrids. The phenotypic coefficient of variation of the double crosses ranged from 10.77 to 24.36 while the genotypic coefficient of variation span from 1.85 to 15.75. The phenotypic coefficients of variation estimates were slightly higher than their genotypic coefficient of variation counterparts. The highest heritability was recorded for ear height (0.83) followed by DFDR3 (0.66) and DFDR2 (0.53). The genetic advance as percent of mean was highest for DFDR3 (27.3) ear height (24.08) and DFDR2 (23.66). The moderate to high magnitude of heritability in addition to the genetic advance as percent of mean of the traits under consideration proved the characters were under the control of additive genetic effects. The desirable lines included (CML343\*CML346)\*(CML124\*MP713), (MP713\*MP705)\*(CML123\*MP713), (CML331\*MP701)\*(MP702\*MP705), (CML330\*MP702)\*(CML123\*MP706), (CML122\*MP713)\*(CML330\*MP701), (OBT\*MP708)\*(MP713\*MP705\*CML264), (MP704\*CML122)\*(CML123\*MP713), (CML123\*MP708)\*(CML122\*MP713) and (CML330\*MP701)\*(MP713\*MP705). The mean grain yield was 3.21 t/ha ranging from 2.57 t/ha in (CML331\*MP701)\*(MP702\*MP705) to 4.12 t/ha in (MP708\*CML331)\*(MP708\*MP704) which was higher than Obatanpa, the check (3.32 t/ha). In addition, (MP702\*MP708\*MP702\*MP705 = 3.68 t/ha), (CML330\*MP701\*MP713\*MP705 = 3.73 t/ha) recorded grain yield which was slightly higher than Obatanpa the check.

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**Keywords:** Double cross; Heritability; Genetic advance; GCV; PCV; Fall armyworm.

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## Introduction

Genetic variation is the source of raw material for selection. The extent of variation is determined by the Genotypic Coefficient of Variance (GCV) and Phenotypic Coefficient of Variance (PCV) [1,2]. given a clear view of the relative amount of variation in each character. From the view point of [1] the phenotypic variances and its PCV estimates are generally higher than the genotypic variances and its GCVs. However, for the purposes of breeding, higher GCV estimates compared to PCV is usually required [3].

According to [1], the disparity between genotypic and phenotypic coefficient of variation gives rise to environmental influence. Smaller differences between the PCV and GCV shows environment has marginal effects on selected traits but where the PCV is higher compared to the GCV then the environmental impact on selected traits will be higher. [4] categorized PCV and GCV into greater than 20 % as high, 10-20 % as medium and less than 10% as low. Environmental factors may affect the heritability of a metric character hence information on predicted genetic gain will be needed during selection [1,2,5] Genetic gain according to [6] is the difference between the mean phenotypic value of the progenies of selected plants and the mean of the original parental population. Genetic advance (GA) however, involves improving genotypic value of traits for a new population in reference to the original population over one cycle of selection at a specified selection pressure [7]. Additive genes may be operating where a trait obtains high heritability with high GA estimates and may be under less environmental effect [8]. Genetic gain as percent of mean (GAM) may be classified as low (0–10%), moderate (10–20%) and high (20% and above) [9] where low GAM may mean that the trait is being influenced by non-additive genes.

[6] recommended heterosis breeding under such circumstance. The magnitude of genetic variability determinants such as phenotypic and genotypic variances, Phenotypic and Genotypic Coefficient of Variation (PCV and GCV), broad sense heritability and genetic gain provide the avenue for a possible genetic improvement of a crop. Breeding methods are formulated

for further improvement on the basis of these parameters [2]. GAM for characters on the other hand could be high indicating the effect of additive gene action on the expression of the said characters demonstrating the possibility of effective selection for improvement of traits in subsequent generations [1].

High heritability combined with high expected genetic advance as percent of mean obtained for traits demonstrate the presence of additive gene effects for potential crop improvement through selection of these traits [5]. Non-additive genes may be influencing traits as a result of high heritability and low genetic advance which may not favour improvement through early generation selection. Hence improvement through hybridization and hybrid vigour will be the alternative [1]. Moderate heritability in association with high genetic advance provide little chance for further improvement of traits while low heritability together with low genetic advance may indicate non-additive genetic effects controlling such traits [1]. There is also the possibility of obtaining negative values for genetic advance due to negative values for genotypic variance and heritability [2].

The determination of characters influencing selection should be based on both high heritability estimates and substantial amount of genetic advance since heritability is influenced by the environment [10,11]. The current study was carried out to assess the genetic variability, heritability and to estimate the amount of genetic gain expected to occur during selection for crop improvement.

## Material and methods

### Plant materials

Twenty-four double cross hybrids developed from different F1 plants from two-way crosses were evaluated through natural infestation on the field. These two-way cross hybrids were developed using the diallel mating design, which were further evaluated for their resistance to fall armyworm using artificial and natural infestations. The recombination of the hybrids to pyramid the desirable genes were conducted over two cropping seasons in Ghana to obtain the double cross hybrids (**Table 1**).

**Table 1:** Double cross hybrids developed from F1's with parental lines from USDA- Agriculture services and CYMMIT origin.

SN	ENTRY	GENOTYPE	SN	ENTRY	GENOTYPE
1	FAW M 8	OBATANPA	13	FAW M 23	(707*708)*(713*702)
2	FAW M 16	(343*346)*(124*713)	14	FAW M 6	(705*708)*(713*705)
3	FAW M 21	(713*705)*(123*713)	15	FAW M 18	(713*708)*(705*708)
4	FAW M 19	(713*706)*(708*704)	16	FAW M 2	(708*701)*(702*705)
5	FAW M 1	(124*713)*(713*330)	17	FAW M 22	(702*708)*(702*705)
6	FAW M 3	(122*124)*(702*713)	18	FAW M 15	(330*705)*(707*708*713)
7	FAW M 13	(331*701)*(702*705)	19	FAW M 9	(708*331)*(708*704)
8	FAW M 26	(330*702)*(123*706)	20	FAW M 12	(332*713)*(713*MPs)
9	FAW M 10	(343*713)*(122*124)	21	FAW M 5	(704*122)*(123*713)
10	FAW M 24	(122*713)*(330*701)	22	FAW M 17	(704*122)*(713*MPs)
11	FAW M 20	(343*346)*(330*705*707)	23	FAW M 7	(704*708)*(713*707)
12	FAW M 4	(OBT*708)*(713*264*705)	24	FAW M 11	(123*708)*(122*713)
			25	FAW M 27	(330*701)*(713*705)

\*FAW M = Fall armyworm maize.

### Location of experimental site

This research was carried out at the Animal Science maize breeding pipeline experimental station, Kwame Nkrumah University of Science and Technology, Kumasi Ghana. This site was located at latitude 6°40'38.8"N and longitude 1°32'42.28"W at an elevation of 277m.a.s.l. Mean annual rainfall at the station is 1500 mm and an average monthly temperature of 20 - 25°C. Land preparation involved ploughing and harrowing, followed by pre-emergence weed control with Round-Up (Glyphosate, 360 g/L) applied at 5.0 L/ha and Gramoxone (Paraquat 276g/L) applied at 3.5 L/ha. Field screening was carried out using Randomized Complete Block Design (RCBD) with 3 replications under natural infestation. An experimental plot consisted of 5 m long single row with 0.75 m between rows planted to 14 hills per row. Blocks were separated by 2 m alleys with intra row planting distance of 0.35 m. All agronomic practices were carried out as and when required.

### Data collection and analysis

The data on the levels of FAW injury were recorded 30, 37 and 44 days after planting based on the rating scale described by [12] and [13] guided by a modified scale of 1 (highly resistant) to 9 (highly susceptible) as described by [14]. Plant architectural as well as yield data were measured following the maize descriptor list developed by IBPGR and CIMMYT (1991).

Means, standard deviation, minimum and maximum values, as well as Coefficient of Variation (CV) for the FAW foliar feeding damage were estimated. Data was subjected to analysis of variance using GenStat software version 12 to determine the significance of main effect associated with parameters measured. The mean square values from the ANOVA tables were used to estimate the genotypic ( $\sigma^2g$ ), phenotypic ( $\sigma^2p$ ), variances components according to [15] as

$$\sigma^2g = (MSg - Mse)/r$$

$$\sigma^2p = \sigma^2g + \frac{\sigma^2\varepsilon}{nr}$$

where  $\sigma^2g$  = genotypic variance,  $\sigma^2p$  = phenotypic variance,  $\sigma^2\varepsilon$  = pooled error, and nr = number of replications.

Genotypic coefficients of variation and phenotypic coefficients of variation were estimated based on the method suggested by [16] as follows:

Genotypic coefficient of variation (GCV):

$$= \frac{\sqrt{\sigma^2g}}{\mu} \times 100$$

Phenotypic coefficient of variation (PCV):

$$= \frac{\sqrt{\sigma^2p}}{\mu} \times 100$$

Where  $\mu$  is the grand mean of the trait,  $\sqrt{\sigma^2g}$ , genotypic standard deviation, and  $\sqrt{\sigma^2p}$  phenotypic standard deviation.

Broad sense heritability ( $H^2$ ), as percentage, was derived for each character using variance components as explained by [17].

$$H^2 = \frac{\sigma^2g}{\sigma^2p} = \frac{\sigma^2g}{\sigma^2g + \frac{\sigma^2\varepsilon}{nr}}$$

The heritability estimate was interpreted as described by [18] as follows:

0-30% = low, 30-60% = medium and >60% = high

### Expected genetic advance from selection

The genetic advance at selection intensity (k) at 5% (2.06) was estimated by using the following formula [9]:

$$EGA = k \cdot \sigma p \cdot H^2 b$$

where EGA denotes the expected genetic advance under selection,  $\sigma p$  is the phenotypic standard deviation,  $H^2 b$  is heritability in broad sense as well as k, the selection intensity. The genetic advance as percent of population mean was also derived by using the procedure of [9].

$$GAM = \frac{(GA)}{Mean} \times 100$$

### Results and discussion

#### Genetic variability

The analysis of variance revealed significant differences for DFDR2 (3.31\*), DFDR3 (2.16\*\*\*) and ear height (257.92\*\*\*), but no significant difference for DFDR1, plant height and grain yield as displayed by their mean squares (**Table 2**). This is an indication that the genotypes were divergent on the basis of their resistance to fall armyworm larvae attack during the second and third ratings as well as their ear height positions. [19] reported significant difference among genotypes in their study of heritability and correlation among some morphological traits and their relationship with fall armyworm damage in corn. Similarly, [20] also found significant differences among some hybrid checks in their study of diallel crossing among maize populations for resistance to fall armyworm. [21] revealed significant differences among genotypes for all the characteristics evaluated for fall armyworm resistance in popcorn genotypes which indicated the existence of significant genetic variability.

#### Mean performance

##### Fall armyworm damage ratings

The average performance of the fall armyworm damage rating showed that DFDR1 ranged from the lowest of 1.93 in FAW M 26 ((330\*702)\*(123\*706)) to the highest of 5.87 in Obatanpa, the check. DFDR2 also had a mean performance ranging from 2.00 in FAW M 21 ((713\*705)\*(123\*713)) to 6.33 (Obatanpa), with DFDR3 recording a mean rating of 2.67 FAW M 24 ((122\*713)\*(330\*701)) to 6.33 in Obatanpa (**Table 2**). On the basis of the fall armyworm rating scale from 1 to 9 where 1 represent highly resistant with completely clean plant and 9 highly susceptible with plants having the whorl completely destroyed (dead heart) [14], the generally good performers could be selected for either improvement programmes or as improved cultivars for farmers. They were FAW M 16, FAW M 21, FAW M 13, FAW M 26, FAW M 24, FAW M 4, FAW M 5, FAW M 11, FAW M 27. Similarly, FAW M 3, FAW M 10, FAW M 20, FAW M 23, FAW M 6, FAW M 18, FAW M 2, FAW M 22. FAW M 9 and FAW M 20 (**Table 2**) could also be exploited for their potential to tolerate the fall armyworm larvae foliar feeding.

#### Plant architectural characteristics

Although plant height did not show significant difference from the analysis of variance, coefficients of variation of at least 14.90% was enough to explain the variability of this trait among the genotypes. The metrical character plant height ranged from 120.10 cm in FAW M 13 to 187.20 cm in FAW M 24 on the basis of their mean performances with an overall mean plant height of 146.30 cm (**Table 2**). The maize plant typically exhibits a height of about 250 cm with heights up to 152.5 cm consid-

ered as short. On this basis, all the entries in this current study could best be described as short to medium plants [22]. Recorded plant height of 161.0 to 288.0 cm with a mean of 217 cm among some maize genotypes from Ethiopia. [23] found plant height among Italian landraces ranging from 110.0 to 215.0 cm with a mean of 166.0 cm. The plant heights of 131 European maize populations 82.4 to 206.7 cm having an average of 164.2 cm [24] did not vary from the genotypes in this current study. In a similar manner [25] registered mean plant height of 171.5 cm ranging from 114.2 to 219.8 among Bangladesh genotypes while [26] also found among Turkey genotypes a mean of 214.61±5 cm and a range of 176.0 to 232.0 cm plant heights. Mean plant heights reported for other maize genotypes include 213.2 cm [27] and 270.1±25.8 [28].

In maize breeding, short plants resist lodging and drought and can be planted at higher densities. Therefore, there will be fewer occurrences of stem lodging problems among the shorter plants [29]. Tall plants usually yield better as they have enough time to accumulate a lot of biomasses. Planting short plants at higher densities will compensate for the low yield [30]. These improved hybrids would be beneficial in breeding for short plants which resist lodging.

Ear height ranged from 53.78 cm in FAW M 21 to 85.45 in FAW M 9 with a mean 65.49 cm on genotype mean basis. As expected, the medium to tall plants exhibited a corresponding higher ear height while the shorter plants had a proportionate short ear height. Ear height is an important factor when breeding for root and stock lodging resistance. The ear heights were similar to that of Ethiopian accessions which exhibited values ranging from 74.0 to 227.5 cm and mean of 125.9±26.3 [22], Italian landraces with a range of 32.0 to 120.0 and mean of 77.01±22.42 [23], European inbred lines with a range of 20.9±129.3 and mean of 72.9 cm, [24], but taller than Bangladesh landraces which had EHT range and mean of 46.8 to 67.1 cm and 57.2±1.1 cm, respectively [25].

### Grain yield

The mean grain yield was 3.21 ranging from 2.57 t/ha in FAW M 13 to 4.12 t/ha in FAW M 9 which was higher than Obatanpa, the check (3.32 t/ha) (Table 2). These entries recorded grain yield similar to Obatanpa including FAW M 10, FAW M 15, FAW M 16, FAW M 18, FAW M 2, FAW M 21, FAW M 23, FAW M 26, FAW M 3, FAW M 5, FAW M 6 and FAW M 7 (Table 2). In addition to FAW M 9, three other entries performed slightly higher than Obatanpa the check, including FAW M 12, FAW M 22, and FAW M 27 (Table 2). However, FAW M 1, FAW M 11, FAW M 17, FAW M 19, FAW M 20, and FAW M 24 produced grain yield lower than the check under the prevailing circumstances.

### Percentage of plants with typical FAW damage/injury symptoms

The analysis of variance showed highly significant differences ( $p < 0.001$ ) among the number of plants that were attacked by the fall armyworm larvae on plot-to-plot basis. The entries were categorized into four (Table 2) based on the percentage of plants having the FAW infestation per plot. Five entries including FAW M 21, FAW M 26, FAW M 18, FAW M 12 and FAW M 27 had an infestation level of between 70-89 %. Within the range of 50-69 %, five entries including FAW M 8, FAW M 15, FAW M 9, FAW M 7 and FAW M 11 were observed (Table 2).

Obatanpa, the check, was among this class of genotypes which recorded 66.00 % infestation rate. As many as twelve entries were found within the 30-49 % bracket (Table 2). Only three entries were observed to have less than 30% of the plants within the plot been infested by the FAW larvae. They were FAW M 2, FAW M 5 and FAW M 17. In spite of the higher fall armyworm presence depicted by the greater number of plants under attack on plot basis, the following entries were able to perform desirably well with lower average foliar damage across the ratings including FAW M 21, FAW M 26, FAW M 18, FAW M 12 and FAW M 27 (Table 2).

[31] recommended action threshold for smallholder farmers if 20 % of plants at early whorl stage (VE to V6) are infested with FAW. They again suggested action threshold if 40 % of plant at late whorl stage (V7 to VT) exhibit FAW injury symptoms. During the tasselling and silking stage (R1 to R3), a 20 % action threshold is required. Applying insecticides during and after the VT stage can be harmful to the farmer and his or her household [31].

This is necessitated by the fact that smallholder farmers in most cases lack Personal Protective Equipment (PPE), proper spray equipment, and the requisite knowledge on the safe and efficient use of pesticides. As a result, insecticide application at an earlier maize growth stage (pre-VT) may be helpful in eradicating the possibility where smallholder farmers would be spraying overhead during the VT or reproductive stages.

Again, the avoidance of the insecticide application can reduce poisoning to natural enemies thereby supporting biological control. Notwithstanding the above, where there is 20 % of tasselled plants infested with FAW or exhibit ear/cob damage, an insecticide application may be permitted. It is worthy to note that thresholds are expressed as percentages of plants with typical FAW damage/injury symptoms.

**Table 2:** Mean, standard error, mean squares and coefficient of variation of agro-morphological and FAW traits evaluated in 25 double cross hybrids in Kumasi in 2021 major rainy season.

SN	ENTRY	GENOTYPE	% DAMAGE	DFDR 1	DFDR 2	DFDR 3	PLHT	EHT	GY
1	FAW M 8	OBATANPA	66.00	5.87	6.93	6.33	175	85.3	3.32
2	FAW M 16	343*346*124*713	45.80	3.17	4.3	3.93	133.7	60.75	3.45
3	FAW M 21	713*705*123*713	78.90	3.33	2	3.20	129.3	53.78	3.24
4	FAW M 19	713*706*708*704	46.70	2.73	3.83	4.23	148.5	60.13	2.79
5	FAW M 1	(124*713)*(713*330)	46.70	3.62	4.33	5.28	141.6	65.48	2.8
6	FAW M 3	122*124*702*713	43.5	3.94	5.18	5.21	149.7	63.18	3.25
7	FAW M 13	331*701*702*705	41.30	2.54	4.38	4.23	120.1	55.3	2.57
8	FAW M 26	330*702*123*702*706	81.10	1.93	3.5	4.98	132.1	56.05	3.09

9	FAW M 10	343*713*122*124	46.10	5.06	4.69	4.73	163.2	79.1	3.42
10	FAW M 24	122*713*330*701	47.80	2.92	4.25	2.67	187.2	61.92	2.67
11	FAW M 20	343*346*330*705*707	36.70	4.62	5.57	4.53	135.7	63.07	2.95
12	FAW M 4	OBT*708*713*264*705	47.80	2.9	3.9	4.8	158.5	74.45	3.3
13	FAW M 23	707*708*713*702	30.00	2.83	5.18	5.15	141.9	63.7	3.15
14	FAW M 6	705*708*713*705	48.20	3.4	5.67	3.53	133.1	62.4	3.06
15	FAW M 18	713*708*705*708	71.10	3.8	5.63	3.32	141.6	61.63	3.38
16	FAW M 2	708*701*702*705	18.00	3.39	5	3.48	140.8	60.08	3.03
17	FAW M 22	702*708*702*705	49.90	3.45	6.4	3.68	142.3	61.31	3.68
18	FAW M 15	330*705*707*708*713	59.69	4.13	6.3	3.99	142	68.72	3.5
19	FAW M 9	708*331*708*704	68.40	4.5	5.53	5.07	164.1	85.45	4.12
20	FAW M 12	332*713*713*MPs	73.30	4.48	6	3.88	147.1	60.15	3.6
21	FAW M 5	704*122*123*713	27.0	3.03	4.57	3.78	152.9	70.03	3.1
22	FAW M 17	704*122*713*MPs	27.33	3.45	4.43	4.18	149.2	67.7	2.94
23	FAW M 7	704*708*713*707	63.33	2.67	5.9	4	165.4	83.23	3.2
24	FAW M 11	123*708*122*713	56.40	3.67	3.67	2.91	126.5	55.03	2.84
25	FAW M 27	330*701*713*705	81.10	3.7	5.3	4	134.8	59.29	3.73
		Grand Mean	51.60	3.6	4.87	4.22	146.3	65.49	3.21
		Std. Error	0.69	1.02	1.016	0.69	17.81	5.48	
		LSD	2.00	2.04	2.04	1.41	35.92	11.04	
		Mean Square	4.92***	2.31ns	3.31*	2.16***	745.4ns	257.92***	0.39ns
		C.V (%)	17.20	34.6	25.5	20.3	14.9	10.2	19.2

DFDR = Double cross fall foliar damage rating.

**Percent GCV and PCV estimation**

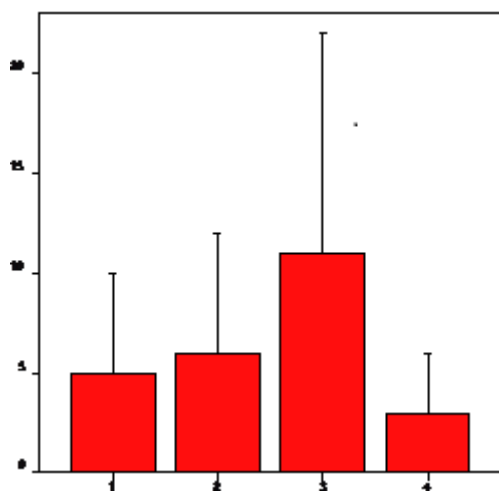


Figure 1: Percent distribution of fall armyworm larvae injury.

Genetic variability in breeding materials is a basic requirement for a successful plant breeding program. Understanding the scope of variability present in crop species is vital as it provides the criteria for selection. The degree of variability for a particular trait is a prerequisite for the breeding of maize and other field crops. The estimates of genotypic variation ( $\sigma^2g$ ), phenotypic variation ( $\sigma^2p$ ), Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), broad sense heritability ( $h^2b$ ), Expected Genetic Advance (EGA), and Genetic Advance as Percentage of Mean (GAM) for different characters have been presented in **Table 3**.

The GCV estimates in this current study ranged from 1.85-16.30 %. The highest GCV of 16.30 % was observed for the fall armyworm trait DFDR3 and the lowest GCV of 1.85 % for grain yield. A GCV of 6.48 % was recorded for plant height while ear height obtained 12.86 %. The GCV for the fall armyworm ratings included DFDR1 (13.97 %), DFDR2 (15.75 %) and DFDR3 (16.30 %) (**Table 3**). High GCV estimates reflect the availability of exploitable genetic variability for the traits, which can promote selection.

**Table 3:** Estimation of genetic parameters for fall armyworm and other selected agro-morphological characters of 24 double cross maize lines.

	$\sigma^2G$	$\sigma^2e$	$\sigma^2P$	$\sqrt{\sigma^2G}$	$\sqrt{\sigma^2P}$	GCV (%)	PCV (%)	$H^2b$	EGA	GAM
DFDR1	0.25	0.52	0.77	0.50	0.88	13.97	24.36	0.33	0.59	16.51
DFER2	0.59	0.51	1.10	0.77	1.05	15.75	21.56	0.53	1.15	23.66
DFDR3	0.47	0.25	0.72	0.69	0.85	16.30	20.09	0.66	1.15	27.30
PLHT	89.83	158.64	248.47	9.47	15.76	6.48	10.77	0.36	11.73	8.02
EHT	70.98	15.99	85.97	8.43	9.27	12.86	14.15	0.83	15.77	24.08
GY	0.004	0.126	0.13	0.06	0.36	1.85	11.24	0.03	0.02	6.3E-05

\*DFDR = Double cross fall foliar damage rating.

On the other hand, the highest phenotypic coefficient of variation (PCV) of 24.36 % was recorded for DFDR1 which was closely followed by DFDR2 (21.56 %) and DFDR3 (20.09). The plant architectural characters, PLHT and EHT, produced a PCV of 10.77 % and 14.15 %, respectively. Grain yield recorded a PCV of 11.24 % which was higher than that of PLHT. High PCV indicates the existence of a greater scope of selection for the trait being considered, depending on the amount of variability present [32]. Again, it was observed that the phenotypic Coefficient of Variation (PCV) estimates was generally slightly higher than the Genotypic Coefficient of Variation (GCV) values for all traits.

The low disparities between PCV and GCV were a reflection of low influence of the environment in the expression of the traits. This implied that, there was a greater genetic control governing the inheritance of the traits as oppose to their sensitivity to the environment. This was in agreement with [33]. Also, the findings from previous studies were similar to this current investigation [34-36] postulating that environmental influence is not noticeable in the expression of phenotypic characters. From the view point of [37], traits that are less affected by environment in selecting a phenotype independent of genotype is expected to be reliable for the improvement of the traits involved.

In addition to the above, [38] found Phenotypic Coefficient of Variation (PCV) was higher than Genotypic Coefficient of Variation (GCV). The results of the current study also corroborated with the findings of who recorded higher phenotypic coefficients of variations than the genotype coefficient of variations for all studied traits. [39] reported similar findings. A great deal of authors reported similar result as the above [26, 40-43] in sweet corn and field maize.

The magnitude of genotypic variances was higher than their corresponding environmental variances for DFDR2, DFDR3 and ear height but the opposite was recorded for DFDR1, plant height and grain yield (**Table 3**). This indicates that the genotypic component of variation was the major contributor to total variation in DFDR2, DFDR3 and ear height while environmental influence was highest for DFDR1, plant height and grain yield.

#### Heritability estimation

The heritability estimates were from moderate (0.33) to high (0.83) for the traits under study with the exception of grain yield. The heritabilities of the fall armyworm traits DFDR1, DFDR2 and DFDR3, meant the greater percentage of the variation in FAW resistance among the double cross progenies was due to genetic effect. [19] estimated heritability among F3 of maize families for FAW resistance using the variance component method (0.61), the parent-offspring regression (0.22) as well as the standard-unit method (0.44). They attributed the moderate to high heritability estimates to genetic causes influencing a large percentage of variation in FAW resistance among F3 families.

The plant architectural characteristics in a similar manner produced moderate to high heritability estimates of 0.36 and 0.83 for plant height and ear height, respectively. The genetic control for ear height expression was massive while plant height was also genetically influenced to some extent. Grain yield recorded a very low heritability estimate (0.03) compared to the other trait in the study. In the study of maize germplasm from Lowland, midaltitude and highland regions of Africa, [44] reported heritabilities of grain yield and its components ranging between 18-36%. [45] obtained relatively high heritability

estimates of 0.58 to 0.91 for plant architectural traits, ear characteristics, and yield and yield components. [1] and [46] also found very high heritability above 90 % for plant height, ear height and grain yield. The very low heritability of grain yield as indicated implied the trait was mostly influenced by the environment [47]. Stated that grain yield and quality traits were mainly under the influence of the environment, whereas the genotype was of no significance. The low heritability implied that successive selection could possibly be difficult for such traits owing to the masking effect of the environment on the phenotypic traits. In spite of the low heritability value of grain yield, there is the possibility to improve upon it through many cycles of recurrent selection. Also, the erratic rainfall pattern during the study period might have greatly impacted negatively on the grain yield recorded.

#### Estimation of genetic advance as percent of mean

The genetic advance expressed as a percentage of the mean (GAM) in the current study indicated that the highest GAM was observed for DFDR 3 (27.3) which was followed by EHT (24.08), DFDR 2 (23.66), DFDR 1 (16.51) and PLHT (8.02). Grain yield was observed to have recorded a much lower GAM of 6.28. In this current study, DFDR 3 and ear height (EHT) exhibited higher heritability estimates coupled with high genetic advance as a percent of mean (Table 3).

Apart from these, three other parameters including DFDR 1, DFDR 3 and plant height (PLHT) also showed moderate heritabilities combined with high genetic advance as percent of mean values. These findings are in agreement with that of other researchers who suggested additive gene action in the expression of traits of such nature, hence favouring selection [48-50]. Grain yield in sharp contrast to the above, had low heritability (0.03) coupled with low genetic advance as percent of mean (0.00006). This occurrence reflects the influence of non-additive gene action combined with larger environmental effect on the trait in question [51].

According to [52], trait showing high heritability may not necessarily translate into high genetic advance. [9] however, were of the opinion that high heritability should be proportionate to high genetic advance to arrive at more reliable conclusion. [1] recorded higher genetic advance for plant height, number of kernels/ear and yield/plant. In the current study the moderate to high heritability coupled with the high genetic advance as percent of mean revealed the preponderance of additive gene action for the expression of these traits which was fixable in subsequent generations.

#### Conclusion

Generally, good performers for fall armyworm resistances could be selected for either improvement programs or as improved cultivars for farmers. The short to medium plant height recorded for this study will result in fewer occurrences of stem lodging problems. Identifying maize lines for fall armyworm resistance will result in the avoidance of insecticide application thereby reduce poisoning to natural enemies as well as supporting biological control and host plant resistance. The moderate to high magnitude of heritability in addition to the genetic advance as percent of mean of the traits under consideration proved the characters were under the control of additive genetic effects.

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