

## Estimates of Combining Abilities and Components of Variances of Tropical Maize Genotypes under Northern Leaf Blight Disease Infection

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### Abstract

Northern Leaf Blight (NLB) disease is among the most devastating disease of maize worldwide contributing about 50% yield losses annually. 45 single cross hybrids generated through half diallel from ten tropical maize (*Zea mays* L.) inbreds including their ten parents and one hybrid check were evaluated at five environments using  $9 \times 7$  alpha lattice designs with three replications across five environments to determine their combining abilities and genetic variance components. The significant mean squares detected for environment, genotype, and Genotype  $\times$  Environment (G  $\times$  E) for measured traits revealed uniqueness of the test environments, and adequate genetic variability among the inbred lines to allow good progress from selection for improvements in most of the measured traits. Significant effects of GCA and SCA expressed for all traits across environments indicated the participation of both additive and non-additive gene effects in the inheritance of the traits. The greater proportion of General Combining Ability (GCA) effects over Specific Combining Ability (SCA) effects across environments suggested that additive gene played a dominant role in the inheritance of the studied traits in the single cross hybrids evaluated. This indicated that additive gene action was more important than the non-additive gene effects in modulating the inheritance of the measured traits associated with NLB disease resistance. Higher GCA variance expressed by grain yield, NLB score and ear weight shows the preponderance of additive gene actions in controlling the inheritance of these traits, thus, indicates the importance of additive gene effects than non-additive gene effects in the expression of these traits. Higher significant relationship revealed between the characters for genotypic correlation over phenotypic correlation indicates a less influence of the environment on the characters.

**Keywords:** Maize; Combining abilities; Genetic variance; Additive gene action; Dominant gene action

### Introduction

Maize (*Zea mays* L.) is third most economically important cereal crops after wheat and rice in terms of global production [1]. Estimate of 1012 million metric tons of maize was produced all over the world in 2016 [2]. Demand for maize has been estimated to move up by about 3.2% because of increase in population and urbanization [3]. Nigeria is the largest producer of maize in Africa, followed by South Africa [1]. About 50% of human population in Sub-Saharan Africa depends on maize and it provides more than 50% of the basic calories. In Africa continent, maize is consumed as porridges, pastes, grits, and beer.

Maize has wide genetic variability with ability to perform well in diverse environment [4]. However, maize has a greatest potential to perform better in the moist savannas of West and Central Africa (WCA) because of higher incoming radiation, less disease and insect pest pressure and lower night temperatures. This accounted for higher output of maize in this zone. Nevertheless, the productivity is being hampered by both biotic and abiotic stresses. Among the biotic stresses are foliar diseases, which are the major factors responsible for reduction

of maize productivity across savannas of WCA [5]. However, Northern Leaf Blight (NLB) disease a polycyclic foliar disease induced by fungus *Exserohilum turcicum* (Pass.) Leonard and Suggs (syn. *Helminthosporium turcicum* Pass.) portend a great threat to maize productivity in Africa. Grain yield losses due to NLB disease are as high as 100% depending on genotype and time of disease attack [6]. This disease can result in food insecurity if not adequately managed. Since the use of chemical fungicides is of serious concern due to its residue, ill-health and poisoning attributed to its usage. The use of host plant resistance or tolerance is seems the most economically feasible and sustainable approach for reducing the effects of the disease among rural farmers. Selection of high yielding and stress resistance genotypes can be determine by the extent of genetic variation existing and how heritable important characters are selected in a population. The choice of efficient breeding programme need adequate information on the magnitude of genetic variances, correlation among traits, interaction of genotype and environments, as well as correlated responses to selection [7]. Therefore, this research was initiated to estimate the combining abilities and genetic variance components as well as character associations of tropical maize genotypes in NLB diseased environments.

### Materials and Methods

## Genetic materials

### Screening of inbred lines and generation of diallel

**crosses:** 75 tropical maize inbred lines adapted mostly to Nigeria were obtained from International Institute of Tropical Agriculture, (IITA) Ibadan, Nigeria, and evaluated for their reactions to NLB disease under artificial disease pressure in a greenhouse condition in 2015 at the Teaching and Research Farm of the Federal University of Technology, Akure, (T and RF, FUTA). Ten inbred lines were selected from the seventy-five (75) the screened materials, based on their reactions to NLB disease and maturity date (Table 1). The selected materials were crossed in a 10 × 10 half diallel mating pattern to generate 45 single cross F1 hybrid in 2016 at T and RF, FUTA. The 45 F1 hybrids and parents were evaluated in three tropical environments of Nigeria including; Teaching and Research Farm of the Federal University of Technology, Akure, (T and RF, FUTA) Nigeria (7°15'N, 5°15'E, 370 m altitude), Teaching and Research Farm, Obafemi Awolowo University, (T and RF, OAU) Ile-Ife, Nigeria (04°33'E, 08°28'N, 244 m altitude), and experimental field of National Cereal and Research Institute (NCRI, out station), Ibadan, Nigeria. Planting at T and RF, FUTA were done in May 2016 and April 2017, in T and RF, OAU, planting was done in June 2016 and May 2017 (Ife 2017), while planting was done in August 2016 in NCRI out station, giving a total of five environments.

S.no	Designation	Response to NLB disease infestation	Maturity group
1	TZEEI 82	Susceptible	Extra-early
2	TZEEI 9	Susceptible	Extra-early
3	TZEEI 14	Moderately resistant	Extra-early
4	TZEEI 108	Resistance	Extra-early
5	TZEI 134	Susceptible	Early
6	TZEI 27	Moderately susceptible	Early
7	TZEI 9	Moderately susceptible	Early
8	TZEI 16	Moderately resistant	Early
9	TZEI 14	Resistance	Early
10	TZEI 10	Resistance	Early

**Table 1:** Description of the 10 inbred parents used for the study.

**Field evaluation of the F1 hybrids:** 45 single cross hybrids including 10 parents and 1 hybrid check were evaluated in 2016 and 2017 cropping seasons across five environments using 9 × 7 alpha lattice design with three replications per environment. 5 m single row plots were used for both hybrids and inbred parents in each environment. 0.75 m × 0.25 m was used as inter-row and intra-row spacing respectively. Two seeds were planted per hill and later thinned to one plant per stand at 21 Days After Planting (DAP) to give a total plant stand estimate of 53,333 plants per hectare in each environments. Two border rows of local cultivars were planted on each side of the block. At One

Week After Planting (1WAP) at 2 to 3 leaf stage, 7 day old *E turcicum* conidia with spore concentration of 106 CFU/ml was used to inoculate the experimental plants in each of the test environments with the aid of hand held sprayer. Inoculation was done in the evening time. Each test plant was covered with transparent plastic bag after inoculation to ensure proper spore infectivity. The plastic bags were removed very early the following morning.

Compound fertilizer (NPK 15-15-15) was applied at the rate of 60 kg N, 60 kg P, and 60 kg K ha<sup>-1</sup> at 3 weeks after planting immediately after thinning, followed by top dressing with 60 kg N ha<sup>-1</sup> 3 weeks later. Gramazone and atrazine were sprayed for weed control at 5 L ha<sup>-1</sup> each of paraquat (1,1' dimethyl-4, 4 bipyridinium) and metolachlor (2-chloro-6'-ethyl-N-(2-methoxy-1-methylethyl)-o-acetoluidide). Herbicides were sprayed at low pressure, using a 20 L knapsack sprayer. Manual weeding was done as necessary.

### Data collection

NLB disease severity was assessed 12 days after mid-silking (NLB 2) based on visual assessment of the whole plot using a modified 1 to 9 rating scale of Soto et al. (1982) as follows; 1=0%, 2=<1%, 3=1-3%, 4=4-6%, 5=7-12%, 6=13-25%, 7=26-50%, 8=51-75% and 9=75-100% leaf area expressing symptoms of NLB disease. Recorded scores were then grouped into following disease reaction types; 1.0=symptomless, 2.0 to 4.0=resistant, 4.1 to 5.0=moderately resistant, 5.1 to 6.0=moderately susceptible, 6.1 to 9.0=susceptible.

Data were taken on plant height (cm), days to 50% silk emergence, days to 50% pollen shed, cob girth (mm), ear length (cm), field weight, ear rot, grain moisture content and grain yield. Grain yield of each plot were adjusted for average stand covariance analyses, and to grain moisture of 15% based on 80% shelling percentage.

### Statistical analysis

Data collected on grain yield and other measured traits from each and across test environments were subjected to Analysis of Variance (ANOVA) following the mixed model procedure of the Statistical Analysis System (SAS) software version 9.2 [8]. The 45 single cross hybrid, 10 inbred parents and 1 hybrid check were considered as random effects, whereas location-year, blocks and replication were considered fixed effects. The location-year combinations were considered as environments in the combined ANOVA. Variations due to hybrids sum of squares was partitioned into General Combining Ability (GCA) and Specific Combining Ability (SCA) for each of the traits following Griffing's method 2 model II (random model) procedure for diallel analysis using DIALLEL-SAS05 program developed by Zhang et al. (2005) adapted to SAS version 9.2 [9,10]. Effects of GCA and SCA for the traits were computed from the mean values adjusted for the block effects for each environment and across environments. The statistical model used for the combined diallel analysis across environments is as follows:

$$Y_{ijk} = \mu + Ee_j + g_i + g + s_{ij} + gE_{eg} + sE_{es} + e_{ijk}$$

In which  $Y_{ijk}$  is the observed measurement for the  $ij^{\text{th}}$  cross grown in the  $k^{\text{th}}$  environment,  $\mu$  is the grand mean,  $g_i$  and  $g_j$  are the GCA effects,  $s_{ij}$  is the SCA effect,  $gE_{eg}$  is the interaction

effect between GCA and the environment (E),  $sE_{es}$  is the interaction effect between SCA and the environment, and  $e_{ijk}$  is the error term associated with the  $ij^{th}$  cross evaluated in the  $k^{th}$  replication and  $E_e$  environment [7]. The following restrictions were imposed on the combining ability effects:  $\sum g_i = 0$  and  $\sum s_{ij} = 0$  for each  $j$  [9]. The GCA and SCA effects were tested for significance using t-test. The standard errors of the GCA and SCA effects were estimated as the square root of the GCA and SCA variances [9]. The relative importance of GCA and SCA in predicting progeny performance was determined using the equation:

$$2k^2_{GCA} / (2k^2_{GCA} + k^2_{SCA})$$

Modified from Baker et al. by Hung and Holland [11,12]. In this study,  $K^2_{GCA}$  is the variance of effects derived from the mean square of GCA and  $K^2_{SCA}$  is the variance of effects derived from the mean square of SCA. Since the total genetic variance among F1 hybrid is equal twice the GCA component plus the SCA component, the closer this ratio is to unity, the greater the predictability of a specific hybrid's performance based on GCA alone.

The variance components of genetic variance were estimated using SAS version 9.2. The genetic and phenotypic correlations between traits were performed sequentially for each lattice, pooled over lattice for each environment, and combined across environments using META-R v6.0.3 software package following the method of [13,14].

The additive ( $\sigma^2_A$ ), additive by environment ( $\sigma^2_{AE}$ ), dominance ( $\sigma^2_D$ ), and dominance by environment interaction ( $\sigma^2_{DE}$ ) variances were estimated as follows:  $\sigma^2_A = 4 \sigma^2_P$ ,  $\sigma^2_{AE} = 4 \sigma^2_{PE}$ ,  $\sigma^2_D = \sigma^2_{PI}$ , and  $\sigma^2_{DE} = \sigma^2_{PIE}$ .

## Results

### Analysis of variance of the traits under study

The result of the ANOVA revealed a highly significant differences ( $P < 0.001$ ) among the genotypes for the measured traits studied (Table 2). In Addition, all traits under consideration revealed significant differences across environments for Environment (E) and Genotype  $\times$  Environment Interaction (GEI), with ear rot which had no significant difference for environment, and moisture content for genotype  $\times$  environment. Partitioning of the genotypes into its components revealed highly significant differences for mean squares of GCA and SCA for traits under study (Table 2). GCA  $\times$  environment interactions expressed no significant effects for all traits under study except number of days to 50% silk emergence. Also, SCA  $\times$  E expressed no significant difference for the studied traits with exception of number of days to 50% silk emergence and moisture content. The relative importance of GCA over SCA was tested by expressing it as a ratio of GCA effects to the total genetic effects. The closer the ratio to unity, the higher the predictability based on GCA alone [11]. The GCA:SCA ratio expressed the preponderance of additive gene actions against the non-additive gene actions for the measured traits in this study.

Source of variation	DF	Plant height	Days to 50% pollen shed	Days to 50% silk emergence	NLB score	Cob girth (cm)	Ear length (cm)	Ear weight (kg)	Ear rot	Moisture content	Grain yield
Environment	4	179.98**	7.04**	6.37**	0.53*	2.23**	6.34**	1.29**	0.24 <sup>ns</sup>	72.69**	6.55**
Rep	2	1.24 <sup>ns</sup>	0.32 <sup>ns</sup>	0.23 <sup>ns</sup>	0.28 <sup>ns</sup>	0.58 <sup>ns</sup>	0.14 <sup>ns</sup>	0.27 <sup>ns</sup>	0.05	6.95 <sup>ns</sup>	0.83 <sup>ns</sup>
Block (Rep)	27	2.67 <sup>ns</sup>	0.33 <sup>ns</sup>	0.52**	0.39*	1.12**	0.97**	0.52**	0.34**	5.75 <sup>ns</sup>	2.29**
Genotype	55	2241.68**	9.25**	6.79**	35.84**	46.64**	60.62**	14.72**	5.83**	20.58**	65.08**
Gen $\times$ Env	215	12.61**	1.45**	1.24**	0.89**	1.78**	3.15**	0.32**	0.38**	4.66 <sup>ns</sup>	1.40**
GCA	9	11990.53**	10.24**	11.68**	231.19**	234.60**	288.00**	87.59**	29.99**	63.43**	388.43**
SCA	45	1009.54**	11.16**	7.34**	12.20**	25.67**	35.20**	6.63**	3.49**	15.94**	29.21**
GCA $\times$ Env	36	21.57 <sup>ns</sup>	1.44 <sup>ns</sup>	1.78**	0.81 <sup>ns</sup>	2.40 <sup>ns</sup>	5.81 <sup>ns</sup>	0.55 <sup>ns</sup>	0.47 <sup>ns</sup>	4.25 <sup>ns</sup>	2.46 <sup>ns</sup>
SCA $\times$ Env	180	10.86 <sup>ns</sup>	1.44 <sup>ns</sup>	1.12**	0.91 <sup>ns</sup>	1.24 <sup>ns</sup>	2.73 <sup>ns</sup>	0.27 <sup>ns</sup>	0.37 <sup>ns</sup>	4.77*	1.49 <sup>ns</sup>
Error	-	2.21	0.25	0.29	0.22	0.35	0.49	0.23	0.13	4.08	1
GCA: SCA	-	11.88	0.92	1.59	18.95	9.14	8.18	13.21	8.59	3.98	13.3
CV (%)	-	1.17	0.98	1.06	8.01	4.46	5.02	22.47	14.28	11.59	22.38
R2 (%)	-	0.99	0.88	0.83	0.92	0.95	0.95	0.91	0.89	0.57	0.91

**Note:** Rep=Replication, Env=environment, Gen  $\times$  Env=Genotype  $\times$  Environment, GCA=General combining ability, SCA=Specific combining ability

**Table 2:** Analysis of variance for traits under study across five environments.

Estimates of dominance variance ( $\sigma^2_D$ ) was greater than additive variance ( $\sigma^2_A$ ) in the traits under study with exception of NLB disease score, ear weight and grain yield (Table 3). Estimates of additive and dominance variances were greater than the additive by environment ( $\sigma^2_{AE}$ ) and dominance by environment ( $\sigma^2_{DE}$ )

interactions (Table 3). Also,  $\sigma^2_{DE}$  effects were greater than  $\sigma^2_{AE}$  for all the traits under consideration. Additionally, SCA variance ( $\sigma^2_{sca}$ ) was greater than GCA variance ( $\sigma^2_{gca}$ ) for studied traits with exception of NLB disease score; ear weight and grain yield (Table 3).

Traits	$\sigma^2_A$	$\sigma^2_D$	$\sigma^2_{AE}$	$\sigma^2_{DE}$	$\sigma^2_{gca}$	$\sigma^2_{sca}$	$\sigma^2_{gca}/\sigma^2_{sca}$
Plant height	243.78	266.31	1.19	104.15	60.95	66.58	0.92
Days to 50% pollen shed	0	2.59	0	2.04	0	0.65	0
Days to 50% silk emergence	0.08	1.66	0.07	1.45	0.02	0.42	0.05
NLB score	4.87	3.01	0	3.03	1.22	0.75	1.62
Cob girth	4.63	6.3	0.08	3.97	1.16	1.58	0.74
Ear length	5.55	8.66	0.34	5.95	1.39	2.17	0.64
Ear weight	1.79	1.7	0.03	0.89	0.45	0.42	1.06
Ear rot	0.59	0.83	0.01	0.67	0.15	0.21	0.7
Moisture content	1.07	2.98	0	1.55	0.27	0.75	0.36
Grain yield	7.95	7.47	0.14	3.96	1.99	1.87	1.06

**Table 3:** Estimates of the components of genetic variance and their interactions with environment, GCA and SCA of 45 F1 hybrid maize evaluated in five environments.

In breeding programs, information on the magnitudes of genetic correlation among traits is crucial since many traits can be simultaneously selected, and also give opportunity to avoid undesirable traits. NLB disease score had a highly significant negative correlation with cob girth, ear length, ear weight and grain yield, meanwhile it has positive significant relationship with ear rot and moisture content (Table 4). There was no significant relationship between NLB disease score and other traits under study. Phenotypic correlation estimates expressed same pattern of relationship was observed between NLB disease score and other traits under study as reported for genotypic correlation coefficients (Table 4). In breeding program, grain

yield happens to be the main traits of interest. Grain yield had significant negative genotypic correlation with NLB disease score, moisture content and ear rot, while a positive significant genotypic relationship was observed between grain yield and cob girth, ear length and ear weight. However, there was no significant genetic relationship between grain yield and plant height, days to 50% pollen shed and days to 50% silk emergence (Table 4). The phenotypic correlation estimates expressed the same pattern of relationship between grain yield and other traits under study as observed for genetic correlation coefficients (Table 4).

-	Plant height	Days to 50% pollen shed	Days to 50% silk emergence	NLB score	Cob girth	Ear length	Ear weight	Ear rot	Moisture content	Grain yield
Plant height	-	0.06 ± 0.09	0.04 ± 0.09	0.16 ± 0.10	0.26 ± 0.07	0.29 ± 0.10	0.27 ± 0.09	0.07 ± 0.09	0.06 ± 0.07	0.26 ± 0.10
Days to 50% pollen shed	0.06 ± 0.15	-	0.52 ± 0.05	0.06 ± 0.09	0.04 ± 0.09	0.02 ± 0.07	0.09 ± 0.09	0.02 ± 0.08	0.02 ± 0.06	0.09 ± 0.02
Days to 50% silk emergence	0.05 ± 0.15	0.63 ± 0.06	-	0.11 ± 0.09	0.14 ± 0.08	0.11 ± 0.09	0.17 ± 0.08	0.12 ± 0.08	0.11 ± 0.06	-0.17 ± 0.08
NLB score	0.18 ± 0.14	0.11 ± 0.10	0.22 ± 0.15	-	0.68 ± 0.05	0.65 ± 0.05	0.74 ± 0.04	0.63 ± 0.05	0.32 ± 0.06	0.75 ± 0.04
Cob girth	0.29 ± 0.08	0.05 ± 0.10	0.21 ± 0.15	-0.82 ± 0.05	-	0.80 ± 0.03	0.73 ± 0.04	0.65 ± 0.05	0.26 ± 0.06	0.72 ± 0.04

Ear length	0.33 ± 0.11	0.05 ± 0.16	0.20 ± 0.09	0.79 ± 0.06	0.91 ± 0.03	-	0.68 ± 0.05	0.64 ± 0.05	0.26 ± 0.06	0.68 ± 0.05
Ear weight	0.26 ± 0.13	0.11 ± 0.09	0.28 ± 0.14	0.86 ± 0.04	0.86 ± 0.04	0.81 ± 0.05	-	0.67 ± 0.04	0.32 ± 0.06	1.00 ± 0.00
Ear rot	0.07 ± 0.15	0.10 ± 0.12	0.27 ± 0.15	0.79 ± 0.06	0.84 ± 0.05	0.82 ± 0.05	0.88 ± 0.04	-	0.33 ± 0.05	0.67 ± 0.04
Moisture content	0.13 ± 0.11	0.08 ± 0.11	0.30 ± 0.14	0.59 ± 0.11	0.52 ± 0.12	0.54 ± 0.12	0.70 ± 0.09	0.73 ± 0.09	-	0.36 ± 0.05
Grain yield	0.26 ± 0.13	0.12 ± 0.07	0.28 ± 0.14	0.86 ± 0.04	0.86 ± 0.04	0.81 ± 0.05	1.00 ± 0.00	0.88 ± 0.04	0.71 ± 0.09	-

**Table 4:** Estimates of genetic (below diagonal) and phenotypic correlation (above diagonal) with their standard error for the 45 F1 hybrid maize tested in five environments in Nigeria.

## Discussion

The presence of genetic variability is of crucial significance for good progress in improving a trait in a selection program. The significant mean squares detected for Environment, Genotype, and Genotype × Environment for all measured traits except ear rot that expressed no significant effect for environment indicated that the test environments were unique and that there was adequate genetic variability among the tropical inbred lines to allow good progress from selection for improvements in most of the measured traits [15-17]. The lack of significant G × E mean squares for moisture content indicated consistency in the expression of these traits in varying test environments.

The significant interaction of GCA effects with environment on days to 50% silk emergence indicated that there were significant variations in the combining abilities of the lines under varying environments. This emphasizes the need for evaluating inbred lines in diverse environments to identify those with stable performance for the development of NLB resistance. It also suggests that selection for improvement of this trait must be done for specific environments. On the other hand, the significant SCA × E mean squares for days to 50% silk emergence and moisture content across test environments suggested variation in the expression of these traits in different test environments.

Significant GCA and SCA mean squares expressed by all measured traits across environments showed that both additive and non-additive gene effects participated in the inheritance of the traits. This shows a possibility for the improvement of these traits through selection. The results aligned to the results reported by Vivek B et al. on the quantitative inheritance of NLB disease [15]. The higher proportion of GCA for the traits under consideration than the proportion of SCA effects across test environments showed a possibility of identifying potentially discriminating testers. Additionally, the larger proportion of GCA effects of inbreds for traits under consideration than those of the SCA effects across test environments suggested that additive gene action played a dominant role in the inheritance of the measured traits in the single crosses evaluated. This implied that additive gene action was more important than the non-additive gene effects in modulating the inheritance of the measured traits associated with NLB disease resistance. So, GCA was the main component accounting for the differences among the single-cross hybrids. The results of this study also

showed that the GCA/SCA variance was higher than unity for the traits under consideration except for number of days to 50% pollen shed. Hence, the higher proportion of GCA over SCA as revealed by the GCA:SCA ratio expressed the preponderance of additive gene actions against the non-additive gene actions for the measured traits in this study. The result reported implies that it would be possible to determine the performances of progenies for NLB disease resistance for the materials used based on GCA alone.

The predominance of additive variance for grain yield, ear weight and NLB score in the set of inbreds in this study implied the effectiveness of early generation testing and selection of promising hybrids will be successful based exclusively on the prediction from GCA effects for these traits. This also implied that the alleles variation for these traits contributed more than the variation of interactions between alleles within each locus. Also, this indicates that GCA is a valuable guide to hybrid performance, so that testing based on a single representative tester should be adequate for initial hybrid selections. Inbred lines with favourable GCA effects for these traits are probable to transmit their characteristics to the progeny and could be useful in a breeding program. Such inbreds could be engaged as parents to generate a synthetic population that could be improved for stress environments. The higher proportion of dominance variance over additive variance recorded for plant height, days to 50% pollen shed, 50% silk emergence, cob girth, ear length, ear rot and moisture content indicates the preponderance of dominance gene action for these traits. This result is similar to the results reported by [18].

The higher SCA variance over GCA variance recorded for plant height, days to 50% pollen shed, days to 50% silk emergence, ear length, cob girth, ear rot and moisture content in this study indicates the preponderance of non-additive gene effects for the inheritance of these traits. This indicates the ability of dominance gene to largely influence the expression of these traits. These results aligned with the reports of other researchers concerning the predominance of dominance gene actions for days to 50% silk emergence [19], plant height, and ear length [20].

However, grain yield, NLB score and ear weight revealed higher GCA variance than SCA variance, which implies the predominance of additive gene actions in controlling inheritance of these traits. Thus, additive gene effects were more important

in the expression of these traits than non-additive gene effects. Therefore, the improvement of these traits would be achieved through selection. The predominance of additive gene effects for grain yield observed in this study aligned with the result reported by and for grain yield [21,22].

For effective selection, identification of the various yield contributing characters is desirable. Knowledge of correlation between different characters is necessary in plant breeding because it reveals mutual relationships among characters and selection for one will result to the selection and improvement of the other character [23]. The results of the present study showed that the genetic and phenotypic correlation coefficients for the traits assessed expressed similar values which suggest that both genetic and phenotypic variances slightly influence the correlation between the traits under study. Again, the result of this study also revealed that both the phenotypic and genotypic correlation coefficients were significant in most of the character association but the degree of significance was more pronounced in genotypic correlation than phenotypic correlation which may be attributed to less influence of the environment on the characters. However, the non-significant phenotypic correlation between any two characters relative to its significant genotypic counterparts suggests appreciable environmental effects. The positive and significant phenotypic correlations recorded between plant height and grain yield and some yield related components corroborate the findings of [6]. At genotypic level, significant negative correlation recorded between NLB disease score and grain yield, cob girth, ear weight, and ear length implies that the characters are probably controlled by different genes. At phenotypic level, NLB scoring had negative significant correlation with cob girth, ear weight, ear length, and grain yield. These results conform to the observation of [6]. While positive significant correlation was observed between the NLB disease score and ear rot, ear aspect and moisture content. This implies that these characters may be controlled by the same gene.

To strengthen the resistance capacity of a crop as well as improving grain yield, emphasis should be given to the correlated characters with disease ratings and grain yield based on the strength of their correlation. A character which has high degree of positive and significant correlation coefficient would be a very effective tool to improve grain yield. From this study characters that expressed positive correlation with grain yield include; plant height, cob girth, ear weight, and ear length. This implies that every significant increase in any of these characters would lead to an appreciable increase in grain yield. Hence, utmost attention should be given to these characters during selection for yield improvement [24].

## Conclusion

Genetic parameter effects like those reported in this study are specific for each population because of their dependency on both additive and dominance actions which differs among populations. Nonetheless, the results reported in this study revealed that additive gene actions were more important for the expression of NLB score, ear weight and grain yield, whereas, dominant gene effects were more important in controlling the inheritance of other traits under consideration.

## References

1. FAO (Food and Agriculture Organization) (2017) Maize.
2. FAO (Food and Agriculture Organization) (2016) Maize.
3. IITA (International Institute of Tropical Agriculture) (2009) Maize. Overview.
4. Bello OB, Ige SA, Abdulmalik SY, Afolabi MS (2013) Interrelationship and path coefficient analysis of morpho-physiological traits among maize (*Zea mays* L.) diallelic crosses in the Southern Guinea Savanna of Nigeria. *Contemp Agric* 62: 255-265.
5. Masuka B, Magorokosho C, Olsen M, Atlin GN, Banziger M, et al. (2017) Gains in maize genetic improvement in Eastern and Southern Africa ii. CIMMYT open pollinated varieties (OPVs) breeding pipeline. *Crop Sci* 57: 180-191.
6. Sibiya J (2009) Breeding investigations for resistance to phaeosphaeria leaf spot (PLS) and other important foliar diseases and a study of yield stability in African maize germplasm, PhD Thesis. Res Space.
7. Hallauer AR, Miranda JB (1981) Quantitative genetics in maize breeding. 2nd edn. Iowa State University Press, Iowa, Ames.
8. SAS Institute (2008) Statistical Analysis Software (SAS) user's guide. SAS Institute, Inc, Cary.
9. Griffings B (1956) Concept of general and specific combining ability in relations to diallel crossing system. *Aust J Biol Sci* 9: 463-393.
10. Zhang Y, Kang MS, Lamkey KR (2005) Diallel-SAS05: A comprehensive program for Griffing's and Gardner-Eberhart analyses. *Agron J* 97: 1097-1106.
11. Baker RJ (1978) Issues in diallel analysis. *Crop Sci* 18: 535-536.
12. Hung HY, Holland JB (2012) Diallel analysis of resistance to *fusarium* ear rot and fumonisin contamination in maize. *Crop Sci* 52: 2173-2181.
13. Singh RK, Chaudhary BD (1985) Biometrical methods in quantitative genetic analysis. Kalyani Publ New Dehli, India.
14. META-R v6.03 software package: (Multi Environment Trial Analysis with R for Windows) version 6.03.
15. Vivek B, Odongo O, Njuguna J, Imanywoha J, Bigirwa G, et al. (2009) Diallel analysis of grain yield and resistance to seven diseases of 12 African maize (*Zea mays* L.) inbred lines. *Euphytica* 172: 329-340.
16. Schechert AW, Geiger HH, Welz HG (1997) Generation means and combining ability analysis of resistance to *Setosphaeria turcica* in African maize. In: Proceedings of the 5th Eastern and Southern Africa Regional Maize Conference, Arusha. AGRIS pp: 211-218.
17. Vieira RA, Scapim CA, Moterle LM, Tessmann DJ, Conrado TV (2009) Diallel analysis of leaf disease resistance in inbred Brazilian popcorn cultivars. *Gen Mol Res* 8: 1427-1436.

18. Silva AR, Souza-Jr CL, Aguiardan AM, De-Souza AP (2004) Estimates of Genetic Variance and Level of Dominance in a Tropical Maize Population. I. Grain Yield and Plant Traits. *Maydica* 49: 65-71.
19. Alam AKMM, Ahmed S, Begum M, Sultan MK (2008) Heterosis and combining ability for grain yield and its contributing characters in maize. *Bangla J Agric Res* 33: 375-379.
20. Rezaei AH, Roohi V (2004) Estimate of genetic parameters in corn (*Zea mays* L.) based on diallel crossing system. New directions for a diverse planet: Proceedings of the 4th International Crop Science Congress Brisbane, Australia.
21. Vacaro E, Neto GFB, Pegoraro DG, Nuss CN, Conceicao LDH (2002) Combining ability of twelve maize populations. *Pesq Agropec Bras* 37: 67-72.
22. Ojo GOS, Adedzwa DK, Bello LL (2007) Combining ability estimates and heterosis for grain yield and yield components in maize (*Zea mays* L.). *J Sustain Develop Agri Env* 3: 49-57.
23. Husaain K, kizan A, Sadaqt HA, Amjad M (2010) Genotypic and Phenotypic correlation analysis of yield and fiber quantity determining traits in upland cotton (*Gossypium hirsutum*). *Agric Biol* 12: 348-352.
24. Sibiya J, Pangirayi T, Derera J, Neil-van RIJ (2012) Genetic analysis and genotype  $\times$  environment (G  $\times$  E) for grey leaf spot disease resistance in elite African maize (*Zea mays* L.) Germplasm. *Euphytica* 185: 349-362.