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Research Article

Genetic Diversity, Advance, Heritability and Heterosis Estimation in F1 Hybrids and Parental Lines of Maize

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Abstract

Background and Objective: Genetic variation, generally considered a key component in broadening gene pools in any given crop population, is critical to the success of yield improvement programs. Therefore, the objectives of this study were to evaluate hybrid efficiency compared to white and yellow parents and to estimate genetic variability and heterosis between hybrids and parental lines. **Materials and Method:** Two parental maize varieties and 2 hybrids were evaluated at the Teaching and Research farm, Bowen University, Iwo Nigeria. The experiment was laid out in a complete randomized block design with four blocks. Genetic parameters of established parental lines and hybrids were measured. The findings indicate that for the characters analyzed, substantial variations were found ($p < 0.05$). **Results:** The highest number of rows per cob was recorded in hybrid1 (12.38), while the lowest number was recorded in white. Compared to their parental lines, the longest cobs were recorded in hybrid1 (16.63 cm) and hybrid2 (16.50 cm). In comparison with their parents, the widest cob was observed in hybrid1 (75 cm) and followed by hybrid2 (70.63 cm). The grain yield MPH (mid-parent) ranged from 14.73-44.54%, from 14.1-43.95% for BPH (better parent). **Conclusion:** The two hybrids developed from the crossing between yellow and white and between white and yellow showed higher performance than the parents. Hybrid 1 reported the highest rate of MPH and BPH. Hybrid1 and Hybrid2 recorded the highest plant height, yields and yield components over their parents.

Key words: Hybrids, maize, heterosis, performance, genetic advance, phenotypic variance, genotypic variance, heritability

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Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Genetic variation, generally considered a key component in broadening gene pools in any given crop population, is critical to the success of yield improvement programmes^{1,2}.

Although giant strides have been made in the process of selecting superior performing plant varieties through tools of Marker Assisted Selection, traditionally, hybrids are identified and analyzed for genetic diversity through morphological traits including, but not limited to plant height, number of leaves, days to inflorescence, etc. While this approach can sometimes be time-consuming and relatively tedious, it offers an easily available way for breeders to identify improved plant traits and or better performing varieties in their quest to develop plants better adapted to the climes they are bred for. In fact, researchers Das *et al.*³; Sidwell *et al.*⁴ opine that most foods produced today are bred using conventional plant breeding methods. This is especially true in developing countries where resources and technology required to employ modern plant breeding tools are sometimes limited. Sakiyama *et al.*⁵ suggested that morphological selection may be appropriate under conditions where direct phenotypic selection is relatively inexpensive, the heritability of the trait is high and the selection of the trait does not directly require specific biological or environmental conditions for phenotypic expression.

Maize (*Zea mays*), an important crop that finds major use in food, feed, industrial products, plastics and adhesives is a member of the grass family and one of the most diverse plant species⁶. In developing countries, it is a staple food whose importance for food cannot be overemphasized; it is the most important cereal crop in sub-Saharan Africa with more than 200 million Africans dependent on the crop for food in some degree⁷. Improved crop yield is typically the ultimate goal of most crop breeding programs, but directing the entire focus of the breeding programs on this quality trait can sometimes be misleading because the phenotypic expression of yield in maize as in most other crops is a function of several plant characteristics and the influence of the environment⁸. Meena *et al.*⁹ consider the yield to be a complex character which is the function of several morphological traits. It, therefore, makes sense to ensure that adequate attention is given to the components that combine to result in the total grain yield of the plant. This will aid the breeder in maximizing scarce resources and precious time in the quest to develop an improved crop variety. To this end, a study was designed to help compare and identifies the most significant plant traits that contribute to the yield of four F1 hybrids and their progenitors using estimates of heritability, coefficient of

variation and genetic advance present in the population. These estimates could help predict the most important factors necessary in the design of a breeding program where yield and yield improvement are crucial to selection. Therefore, the objectives of this study were to evaluate the performance of hybrids as compared to the white and yellow parents and estimate the genetic variability and heterosis among hybrids and parental lines.

MATERIALS AND METHODS

Study area: The research was carried out from October, 2019 to February, 2020 at the Teaching and Research farm, Bowen University, Iwo Nigeria. The experimental area is located at latitude of 7° 38'6.97"N and a longitude of 4° 10'53.62"E.

Plant materials: The hybrids used were developed in Bowen University at the Department of Environmental Management and Crop Production. The yellow and white varieties were bought from the market and selected into pure inbred lines for the development of the two hybrids used along the two parents.

Field experimental layout: The land was cleared with manual labor and ridges were made for maize planting at the Teaching and Research farm, Bowen University, Iwo Nigeria. The two varieties and the two hybrids were planted in a complete randomized block design with 4 blocks. The experimental unit consisted of a 1.5 m long ridge with four ridges per block. The spacing adopted between rows and hills was 75×20 cm, respectively. There were 1 m intervals between blocks. The soil texture at the experimental site was loamy soil. Two healthy seedlings per hill were kept after proper thinning. In the course of the experiment, the best agronomic practices were observed.

Data collection: Two plants were selected randomly from each experimental unit for data collection. Data were collected on plant height, number of cob per plants, number of grain per cob, grain yield, leaf length and number of leaf per plant. The grain was collected and dried at 12% moisture content for calculating yield. Vernier caliper was used in measuring the length and width of cobs. Then, the electronic balance was used for seed weight.

Statistical analysis: Data collected were analyzed using variance (ANOVA) technique the mean differences were separated by LSD tests.

Estimation of variance: The phenotypic and genotypic variance, genotypic and phenotypic coefficients of variation were computed using the following formula according to Johnson *et al.*¹⁰ and Singh and Chaudhary¹¹:

$$\sigma^2_G = [(MSG)-(MSE)]/r \quad \sigma^2_P = [\sigma^2_G + (\sigma^2_E/r)]$$

where, σ^2_G is the genotypic variance, σ^2_P is the phenotypic variance, σ^2_E is the environmental variance (error mean square from the analysis of variance, MSG is the mean square of genotypes, MSE is the error mean square and r is the number of replications:

$$\text{Genotypic coefficient of variation (GCV)} = [(\sigma^2_G) / 1/2/x-] \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = [(\sigma^2_P) / 1/2/x-] \times 100$$

where, σ^2_G is the genotypic variance, σ^2_P is the phenotypic variance; is grand mean of a character.

Estimation of heritability in broad sense: Broad sense heritability (h^2) was computed using the following the formula as described by Allard¹²:

$$h^2_{bs} = [(\sigma^2_G) / (\sigma^2_P)] \times 100$$

where, h^2_{bs} is the heritability in broad sense, σ^2_G is the genotypic variance and σ^2_P is the phenotypic variance.

Estimation of genetic advance: Genetic Advance (GA) was calculated using Johnson *et al.*¹⁰ method:

$$GA = K (\sigma_p) h^2$$

where, K is the selection differential (K = 2.06 at 5% selection intensity), σ_p is the phenotypic standard deviation of the character and h^2 is the broad sense heritability.

Heterosis is expressed as an increase or a decrease of F1 hybrid value over mid-parent and better parent were computed for each trait with the aid of the following formulas according to Hayes *et al.*¹³ and Stupar *et al.*¹⁴:

$$\left(\frac{F1 - MP}{MP} \right) \times 100 \quad \left(\frac{F1 - BP}{BP} \right) \times 100$$

where, F1 is the mean performance of F1, MP is the mean mid parental value = (P1+P2)/2, P1 is the mean performance of parent one, P2 is the mean performance of parent two and BP is the mean performance of better parent.

RESULTS AND DISCUSSION

Plant height of the four genotypes is presented in Fig. 1. Hybrid 1 was 1.5 m in height followed by hybrid 2 (1.25 m) while the lowest was recorded in yellow and white variety. The developed hybrids were better in height than the parents, which indicate the hybrid vigor in terms of height as the genetic combination of the two parents. Current findings are aligned with those of Yu *et al.*¹⁵ study.

Leaf length is shown in Fig. 2, hybrid 1 recorded the longest (1.3 cm) while the shortest was observed in white variety (0.8 cm). This is an indication that hybrid 1 intercepted efficiently sunlight during photosynthesis for better photo-assimilate accumulation (biomass) production and important partitioning of dry matter into growing organs especially reproductive organs for better yield.

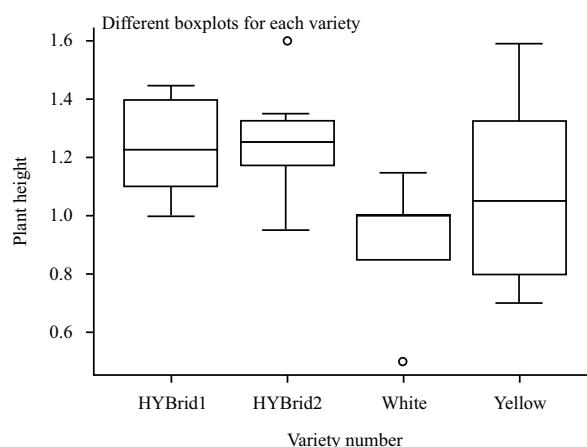


Fig. 1: Plant height per variety

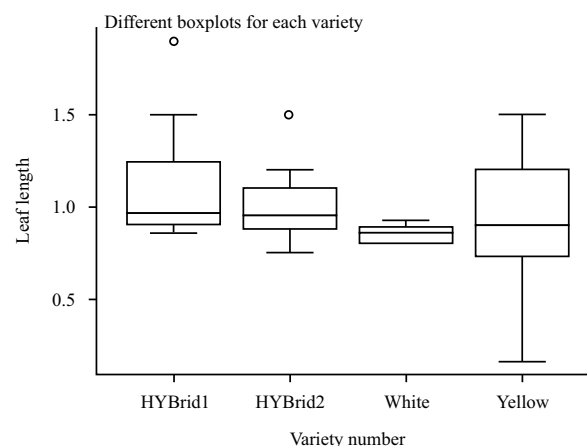


Fig. 2: Leaf length per variety

Table 1: Mean value and standard deviation for each evaluated reproductive traits in the parental lines and their hybrids

Variety	DT (NS)	DS	NC/P (NS)	NR/C (NS)	LC (NS)	WC (NS)
White	54.67±2.50	57.50±2.95 ^{ab}	2±0.55	11.65±0.41	14.33±1.51	65.25±29.9
Yellow	57.00±5.45	60.25±2.19 ^a	2±0.53	11.88±1.06	14.00±2.67	67.63±22.54
Hybrid1	55.63±3.02	59.25±3.65 ^a	2±0.55	12.38±0.35	16.63±5.55	75.33±11.50
Hybrid2	54.38±1.77	56.75±1.16 ^b	2±0.55	11.87±0.64	16.50±3.16	70.63±22.19

Different letters in the column indicate significant differences (p<0.05), NS: Not significant, DS: Days to silking, DT: Days to tasseling, NC/P: Number of cobs per plant, NR/C: Number of row per cobs, LC: Length of cob, WC: Width of cob

Table 2: Mean square of vegetative and reproductive characters of 4 genotypes

Source of variation	Df	PH	DS	LC	NR/C	WC	NS/C
Variety	3	2317.53**	20.2269*	28.34*	0.67130	0.10588*	18932.3
Block	3	768	13.0972	26.198	0.84179	0.12835	4014.7
Error	23	44.41	6.0664	11.194	0.84179	0.12835	5305.2
CV (%)		22	4.91	4.05	7.75	11.38	27.43

*Significant at 0.05, **Significant at 0.01. PH: Plant height, DS: Days to silking, NC/P: Number of cobs per plant, NR/C: Number of row per cobs, LC: Length of cob, WC: Width of cob, NS/C: Number of seeds per cobs

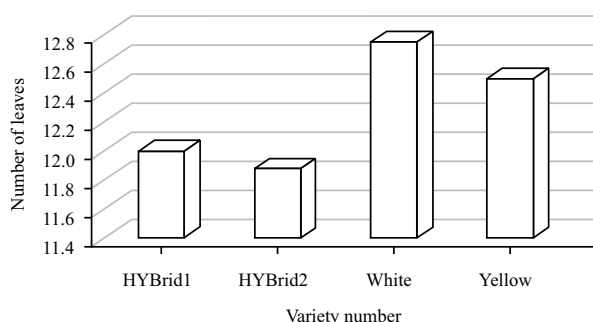


Fig. 3: Number of leaves per variety

The number of leaves per variety is presented in Fig. 3. Hybrid 1 had the highest number of leaves followed by hybrid 2 and the lowest was recorded in yellow variety. It was shown above that hybrid 1 and hybrid 2 are the tallest genotypes, thus an indication that the two hybrids had the highest number of leaves when compared to the parents.

The mean value, the standard deviation for each reproductive trait evaluated in the parental lines and their hybrids is shown in Table 1. Hybrid 2 was the first to produce tassels (54 days after planting) and silks at 57 days after sowing. The highest number of rows per cob (12.38) was recorded in hybrid1 while the lowest number was observed in white variety. The longest cobs was recorded in hybrid1 (16.63 cm) and hybrid2 (16.50 cm) when compared to their parental lines. The widest cob was observed in hybrid1 (75 cm) and followed by hybrid2 (70.63 cm) when compared to their parents. The two hybrids and the two parents recorded 2 numbers of cobs per plant. Similar findings were obtained by Yi *et al.*¹⁶, who suggested that the F1 mean was substantially greater than the ear weight per year, cob weight, ear length, ear diameter and kernel weight per year mean of each of the parental lines.

The mean square of vegetative and reproductive characters for 4 genotypes is shown in Table 2. Varieties mean squares were highly significant for plant height (2317.53**) and significant for days to silking (20.2269*), length of cob (28.34*) and Width of cob (0.10588*). No significant difference was observed with number of row per cobs (0.67130) and number of seeds per cob (18932.3). The mean squares of block were not significant: 768, 13.0972, 26.198, 0.84179, 0.12835 and 4014.7 for plant height, days to silking, length of cob, number of row per cobs, width of cob and number of seeds per cob, respectively.

Grand mean, genotype and phenotypic variation coefficient (GCV and PCV), heritability (H) and genetic advance for maize characters are shown in Table 3. Genetic variance values ranged from 0.20-1.30 and phenotypic variance values ranged from 0.34-5306.1. The highest Genetic variance values (1.30) were recorded with plant height while the highest phenotypic variance values (5306.1) were observed in number of seed per cob. The GCV and PCV values ranged from 0.32-12.95 and from 4.50-24.90 for the all the characters, respectively. The data depicted in the table demonstrated that the phenotypic coefficient of variability was higher in value than the genotypic ones for all the traits studied. The highest genetic advance was recorded in length of cob (2.91) and number of seed per cob (3). The highest heritability was observed in weight of seed (61.76) and length of cob (41.71) while the lowest were recorded in plant height (0.29) and number of seed per cob (0.02).

The number of seeds per cob and per variety is presented in Fig. 4. The highest number of seeds were recorded in Hybrid1 (376.333 seeds) followed by Hybrid 2 (301.38 seeds) and the lowest was observed in Yellow and white variety. This implies that there is better and higher yields recorded in the two hybrids when compared to the two parental lines used for

Table 3: Grand mean, genotype and phenotypic coefficient of variation (GCV and PCV), heritability (H) and genetic advance for characters of maize

Traits	Grand (Mean±SE)	σ^2_g	σ^2_p	GCV	PCV	H	GA
PH	117.85±3.37	1.30	448.71	0.97	17.97	0.29	1.26
DS	58.42±0.27	0.83	6.90	1.56	4.50	12.03	0.65
LC	15.42±0.62	0.31	11.50	3.61	21.99	41.71	2.91
NR/C	12.00±0.15	0.20	0.87	3.73	7.77	22.99	0.44
NS/C	292.58±12.19	0.90	5306.10	0.32	24.90	0.02	3
WS	3.54±0.08	0.21	0.34	12.95	16.47	61.76	0.74

PH: Plant height, DS: Days to silking, NR/C: Number of cobs per plant, NR/C: Number of row per cobs, LC: Length of cob, WC: Width of cob, NS/C: Number of seeds per cobs, $\sigma^2 G$: Genotypic variance, $\sigma^2 P$: Phenotypic variance, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, GA: Genetic advance, H: Heritability

Table 4: Heterosis (%) for yield related traits and grain yield of maize (*Zea mays* L.)

Variety	DT		DS		NR/C		LC		WC		NS/C	
	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
Hybrid1	-0.37	-2.40	0.21	-1.66	5.14	4.21	17.20	16.05	13.38	11.39	44.54	43.95
Hybrid2	-2.61	-4.60	-3.61	-2.13	0.81	0.08	16.29	15.14	6.31	6.20	14.73	14.1

DS: Days to Silking, DT: Days to Tasseling, NR/C: Number of row per cob, LC: Length of cob, WC: Width of cob and NS/C: Number of seeds per cob, MPH: mid-parent, BPH: better parent

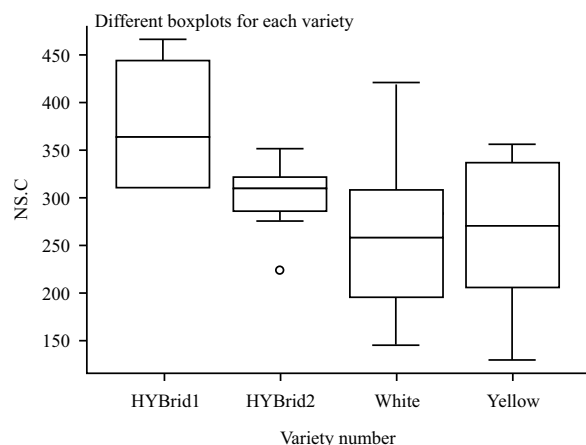


Fig. 4: Number of seed per cob per variety

their crossing. Similarly, Yi *et al.*¹⁶, da Silva and Miranda Filho¹⁷, found that in their respective tests, the hybrids performed better than the parents.

Percent (%) mid-parent (MPH), better parent (BPH) and standard heterosis (STH) were computed for grain related traits (Table 4). The MPH for grain yield ranged from 14.73-44.54%, for BPH from 14.1-43.95%. The highest of MPH and BPH were recorded in Hybrid 1. Stupar *et al.*¹⁴ in work on gene expression analyses in maize inbreds and hybrids with varying levels of heterosis reported the same results. Likewise, Abebeet *et al.*¹⁸; Keimeso *et al.*¹⁹ reported positive heterosis in hybrids in their analysis on combining ability and heterosis for yield and yield components. In their analysis, Olibaldi *et al.*²⁰ also found substantial heterosis for yield and various agronomic traits.

Negative heterosis was recorded for days for tasseling and days for silking for both MPH and BPH. This suggests that the hybrids tasseled and silked both hybrids before the parents. Similar findings have been achieved by Stupar *et al.*¹⁴ and Zeleke²¹.

CONCLUSION

The basic prerequisite for a crop improvement program is genetic diversity, heritability and anticipated genetic development with respect to maize grain yield and yield components. The two hybrids developed from the crossing between yellow and white and between white and yellow showed higher performance than the parents. The highest number of rows per cob (12.38) was recorded in hybrid1 while the lowest number was observed in white variety. Compared to their parental lineages, the longest cobs were recorded in hybrid1 (16.63 cm) and hybrid2 (16.50 cm). In comparison with their parents, the widest cob was observed in hybrid1 (75 cm) and followed by hybrid2 (70.63 cm). The grain yield MPH ranged from 14.73-44.54%, from 14.1-43.95% for BPH. In Hybrid 1, the highest levels of MPH and BPH were reported.

SIGNIFICANCE STATEMENT

This study discovered the potential of hybrids that can be used by farmers to increase their income. This study will help the researchers to uncover the critical areas of direct selection through hybridization of yield and yield components of maize.

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