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Full-Length Research Paper

Genetic variability and heritability estimate of maize endosperms using full-sib recurrent selection scheme

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ABSTRACT: In a maize breeding program, pre-requisition entails an understanding of a population's genetic variability and heritability. The present study was conducted at the Research and Teaching Farms, College of Agriculture, Lafia and Federal University of Agriculture, Makurdi, to study the genetic variability and heritability of various maize endosperms developed using full-sib recurrent selection method. A population of 100 Full-sib families each of Sweet corn, Popcorn and field corn generated was laid out in a 10 × 10 balanced lattice square design with three (3) replications. Result with regards to yield showed that Popcorn had the highest yield (1.14t/ha) in Lafia while Sweet corn and Field corn had the highest mean yield in Makurdi (1.07t/ha and 1.02t/ha) respectively as compared to Lafia. Also, the magnitudes of genetic variability in the maize families were wide. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits under consideration in both locations. The estimates of PCV and GCV were high for grain yield and anthesis-silking interval. High heritability estimate was detected for plant height, ear height, cob weight, days to 50% silking, days to first tasseling and grain yield, while estimation of genetic advance as percent of mean (GAM) at 20% selection intensity ranged from 0.60 (cob weight) to 19.82 (grain yield) in Lafia and from 5.10 (days to 50% silking) to 40.95 (cob weight) in Makurdi, indicating that these traits are under the control of additive gene action. The observed variability revealed considerable amount of diversity among the tested populations which could be manipulated for further improvement in maize breeding.

Keywords: Genetic variability, full-sib, heritability, recurrent selection

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INTRODUCTION

After wheat and rice, maize is the world's third most important food crop, providing 15% of protein and 19% of calories for developing countries (Shakoor et al., 2007). Aside from its significant agricultural and economic value as a crop for food, feed, and fuel, maize has unrivaled biological properties as a research model for genetic diversity and genome evolution Bennetzen (2009). Corn has a greater diversity of phenotypes than any other grain crop, according to Oliveira et al. (2005), and is widely grown in temperate, subtropical, and tropical regions around the world. Genetic variability and heritability are two important parameters that influence the effectiveness of a breeding program. The phenotypic variance explains the total variance among phenotypes tested in different environments of interest to the plant breeder, whereas the total genotypic variance explains the portion of the phenotypic variance attributable to genotype failure in different environments (Sujiprihati et al., 2003). Heritability measures the value of selection for a particular trait in various types of progenies (Al-Tabbal *and* Al-Fraihat, 2012; Lule *et al*., 2012). Stability of desirable genetic characters is important for development of improved varieties and useful for the commercial exploitation over a wide range of agro-climatic conditions (Esechie *et al.* 2004).

In maize breeding programs, the goal is always to improve genetics in economically important traits while maintaining a sufficient amount of variability (Hallauer, 1972). Knowledge of heritability influences the selection procedures used by plant breeders to determine which selection methods would be most useful in improving the character, predicting gain from selection, and determining the relative importance of genetic effects (Waqar et al., 2008; Kashiani et al., 2010; Laghari et al., 2010). The most important function of heritability in quantitative character genetic studies is its predictive role in indicating the dependability of phenotypic value as a guide to breeding value (Falconer and Mackay) (1996). Characters with a high heritability can be easily fixed with simple selection, resulting in rapid progress. However, it has been emphasized that heritability alone has no practical significance in the absence of genetic progress. As stated by Najeeb et al. (2009), the purpose of this study was to investigate the genetic variability and heritability of Maize endosperms using a full-sib recurrent selection scheme.

MATERIALS AND METHODS

Experimental site

The study was conducted at Research and Teaching Farms, College of Agriculture, Lafia (7º26" N, 3º54" E), and the Teaching and Research Farms, Federal University of Agriculture, Makurdi, (7^0.41"N, 8^0.28"E) Nigeria, during the 2017 cropping season.

Experimental design and layout

Single-row plots of 5m length each was used with intra and inter row spacing of 0.25m and 0.75m respectively laid out in a 10 × 10 balanced lattice square design with three (3) replications. During field evaluation a total of 100 families of full-sib were randomly selected out of 150 families with enough seeds. At 3 weeks after planting the number of plants was reduced to one plant hill^{-1} through thinning to maintain a population size of 53,333 plants ha^{-1}. Weed control was done manually three times at 2, 4 and 6 weeks after sowing. Fertilizer was applied at the recommended rates (120kg N/ha, 60kg P_2O_5/ha and 60kg K_2O/ha) using NPK 15:15:15 compound fertilizer at two weeks after sowing (WAP) while the remaining 60kg of N was dibbed at four weeks after sowing using Urea (46% N). Soil sample was randomly collected at 0- 30 cm depth across the field to determine pre-planting physical and chemical properties of the soil at the experimental sites (Table 1). Data collected includes; days to first tasseling (DFT), days to 50% silking (D50%S), days to 50% pollen shedding (D50%PS), Anthesis silking interval (ASI), plant height (PHT), ear height (EHT), cob weight (CBWT), shelling percentage (SHEL%) and grain yield (GYLD) and was subjected to Analysis of variance (ANOVA) using statistical software, SAS version 9.3.

Estimation of variance components

Genetic variability was identified by estimation of various variance components, Phenotypic (δ^2_{ph}) and genotypic (δ^2_g) variances were calculated by methods suggested by Burton and Devane (1953), thus:

$$\delta^2_{ph} = \delta^2_g + \delta^2_{e/r}$$

$$\delta^2_g = \frac{MSg - MSe}{r}$$

where,

δ^2_{ph} = Phenotypic Standard Deviation

δ^2_g = Genotypic Standard Deviation

δ^2_e = Environmental Standard Deviation (error mean square)

The genotypic (GCV) and phenotypic (PCV) coefficient of variation were estimated according to the procedure outlined by Johnson *et al.* (1955) while the genetic advance in percentage of mean was calculated by using Falconer (1989) formula thus:

$$PCV = \frac{\sqrt{\delta^2_{ph}}}{\bar{X}} \times 100$$

where $\bar{X}$ = grand mean

$$GCV = \frac{\sqrt{\delta^2_g}}{\bar{X}} \times 100$$

Heritability and genetic advance estimation

Broad-sense heritability and genetic advance expected under selection, assuming a selection intensity of 20% were calculated as suggested by Allard (1960) for each character thus:

$$H^2 = \frac{\delta_g}{\delta_p} \times 100$$

0-30% =low**,** 30-60% =moderate and >60 =high
Broad-sense heritability and genetic advance expected under selection, assuming a selection intensity of 20%

were calculated as suggested by Allard (1960) for each character thus:

$$H^2 = \frac{\delta_g}{\delta_p} \times 100$$

$H^2 = \text{Heritability in the broad sense}$

Genetic advance (GA) was estimated as devised by Johnson *et al*. (1955)

$$GA = \sqrt{\delta^2_{ph}} \times (K) \times H^2$$

where:

GA = Expected genetic advance

K = Selection differential (1.40 at 20% selection intensity)

$\sqrt{\delta^2_{ph}}$ = Phenotypic standard deviation

Genetic advance as per cent of the mean was calculated to compare the extent of predicted advances of different traits under selection.

$$GAM = \frac{GA}{\bar{X}} \times 100$$ (Falconer, 1996).

RESULTS AND DISCUSSION

Estimates of the various genetic components of maize families in Makurdi and Lafia locations are presented in (Table 2). Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) same was observed between phenotypic variance and genotypic variance for all traits under consideration in both Makurdi and Lafia locations which corroborates with the findings of Yusuf (2010) who reported higher, phenotypic coefficients of variations than the genotype coefficient of variations for all studied traits. Similar result was also reported by Ayodeji and Comfort (2019), Saleh *et al.* (2002), Alan *et al.* (2013) and Niji *et al*. (2018) in sweet corn as well as Maphumulo *et al.* (2015), Sesay *et al.* (2016) and Jilo *et al*. (2018) in field maize. Makurdi recorded high phenotypic coefficient of variation (PCV) for anthesis-silking interval (54.88%) and grain yield (47.97%).Similarly, Lafia also recorded high PCV for anthesis-silking interval (29.86%) and grain yield (25%) which implies that these traits are under the influence of genetic control and thus can be selected for further improvement. Similar results were reported by Kumar *et al*. (2014) and Nzuve *et al*. (2014) who reported the highest GCV and PCV for plant height, ear height, 1000 grain weight and kernel number per row.

In Lafia, high heritability estimate was detected for days to first tasseling (0.61), Days to 50% silking (0.57), plant height (0.78), ear height (0.77), cob weight (0.65) and grain yield (0.58). High heritability estimate was also detected for days to first tasseling (0.69), plant height (0.70), and ear height (0.67) in Makurdi. This simply means that these traits are under genetic control and the environmental factors did not greatly affect their phenotypic variation which reveals that selection for these characters could be fairly easy, indicating that such characters could easily be passed from one generation to the next then enhancing the efficiency of selection in maize improvement program. These results corroborates with the finding of Lule *et al.* (2012) and Jilo *et al.* (2018) who also recorded high heritability estimate for 1000-kernel weight, leaf length, plant height, days to 50% anthesis, days to 50% silking, leaf width, ear length and leaf area.

Traits with moderate heritability estimate could be improved through heterosis breeding or hybridization Bello *et al.* (2012). Moderate heritability values were recorded for Anthesis silking interval (0.48), shelling percentage (0.45), days to 50% pollen shedding (0.57), days to 50% silking (0.57) and grain yield (0.58) in Makurdi and for grain yield (0.58) in Lafia.This indicates a positive response to phenotypic selection. These results are in accordance with the findings of Al-Tabbal and Al-Fraihat (2012), Nzuve *et al.* (2014) and Jilo *et al.* (2018). Low broad-sense heritability estimate was detected for days to 50% silking (0.38), days to 50% pollen shedding (0.36), anthesis silking interval (0.34), cob weight (0.30), and shelling percentage (0.28), implying that successive selection could be considerably difficult for such traits due to the masking effect of the environment on the phenotypic traits. In Lafia, low, moderate and high genetic advance (GA) was observed for days to 50% silking (0.91), days to 50% pollen shedding (0.85), anthesis silking interval (0.28), cob weight (0.62), and grain yield (0.16). Moderate genetic advance was observed for days to first tasseling (2.29), shelling percentage (4.66) and high genetic advance for plant height (14.12), and ear height (6.95). In Makurdi,anthesis silking interval (0.89) and grain yield (0.38) had low genetic advance, days to 50% silking (2.88), days to 50% pollen shedding (2.34) and days to first tasseling (2.97) recorded moderate values, while high genetic advance (GA) was observed for plant height (32), ear height (25.57), and cob weight (42.14). The genetic advance as percent of mean (GAM) at 20% selection intensity ranged from 0.60% (cob weight) to 19.82% (grain yield) in Lafia and from 5.10% (days to 50% silking) to 40.95% (cob weight) in Makurdi. High genetic advance as a percent of mean was observed for grain yield (19.82%), Anthesis-

Table 1. Physio-chemical properties of soil in Lafia and Makurdi experimental site.

Location	Depth (cm)	pH H_2O	pH KCL	% O.C	% O.M	% N	P (Ppm)	Cmol/kg				(mg/100g) E. A	Cmol/kg CEC	% BS	Particle Size Dist.			
								K^+	Na^+	Mg^+	Ca^{2+}				% Sand	% Silt	% Clay	Texture
Lafia	0-15	6.68	6.14	1.05	1.81	0.21	4.28	0.21	0.14	2.32	3.45	0.66	6.12	89.2	89.8	3.4	6.8	LS
	15-30	6.72	6.23	1.27	2.18	0.28	4.42	0.28	0.13	2.36	3.63	0.83	6.38	86.9	89.8	3.4	6.8	LS
Makurdi	0-15	6.05	5.31	0.80	1.39	0.09	3.63	0.13	0.41	2.13	4.20	-	8.12	84.75	77.50	11.73	10.77	SL
	15-30	5.98	5.33	0.74	1.41	0.08	3.13	0.11	0.38	1.81	3.53	-	7.77	75.34	72.93	13.50	13.57	SL

Key: O. C= Organic Carbon, O. M= Organic Matter, E. A= Exchange Acidity, B. S= Base Saturation, LS= Loamy Sand, SL= Sandy loam

Table 2. Estimates of various genetic components of maize Families in Lafia and Makurdi.

Parameters	Lafia							Makurdi						
Traits	δ^2_g	δ^2_{ph}	*GCV%*	*PCV%*	h^2_{BS}	*GA*	*GAM%*	δ^2_g	δ^2_{ph}	*GCV%*	*PCV%*	h^2_{BS}	*GA*	*GAM%*
D50%S	1.12	2.99	1.86	3.03	0.38	0.91	1.59	7.50	13.26	4.85	6.45	0.57	2.88	5.10
DFT	3.87	5.61	4.62	5.56	0.69	2.29	5.37	4.76	7.76	5.00	6.39	0.61	2.39	5.48
D50%PS	1.04	2.92	1.86	3.12	0.36	0.85	1.55	7.84	13.69	5.18	6.85	0.57	2.97	5.50
ASI	0.12	0.36	17.32	29.86	0.34	0.28	12.03	0.85	1.78	37.85	54.88	0.48	0.89	36.61
PHT (cm)	144.85	206.31	10.09	12.04	0.70	14.12	11.83	665.99	848.87	15.49	17.49	0.78	32.00	19.21
EAR HT (cm)	36.62	54.39	7.66	9.34	0.67	6.95	8.80	433.88	564.17	23.15	26.40	0.77	25.57	28.42
CBWT (g)	5.16	215.72	2.2	14.23	0.3	0.62	0.60	1393.11	2141.83	36.27	44.97	0.65	42.14	40.95
SHEL%	39.87	143.36	10.56	20.02	0.28	4.66	7.79	124.21	279.06	15.67	23.49	0.45	10.41	14.64
GYLD (t/ha)	0.02	0.04	19.09	25	0.58	0.16	19.82	0.13	0.22	36.32	47.86	0.58	0.38	38.77

δ^2_g= Genotypic variance, δ^2_{ph}= Phenotypic variance**,** **GCV** = Genotypic coefficient of variance, **PCV** = Phenotypic coefficient of variance, h^2_{BS} = Broad sense heritability, **GA** = Genetic advance

silking interval (12.03%) and plant height (11.83%) while cob weight (0.60%) recorded low genetic advance as a percent of mean in Lafia. In Makurdi, high genetic advance as a percent of mean was observed for cob weight (40.95%), grain yield (38.77%), Anthesis-silking interval (36.61%) and ear height (28.42%) while low values was recorded for days to 50% silking (5.10%).These results indicates that the traits are under the control of additive gene action. Also these results are similar to the findings of Jilo *et al.* (2018) who also reported high GAM for grain yield, ear height and plant height. Similarly, this result is supported by the findings of Atnafu and Rao (2014), Fekadu *(*2014) and Maruthi and Rani (2015) who reported high genetic advance for plant height, kernel rows per ears, 1000 kernel weight, ear height, and grain yield per hectare.

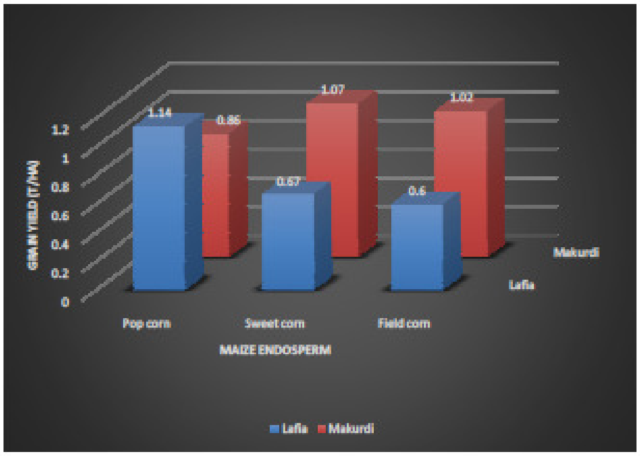

Figure 1. Mean Performance of three Maize endosperms across Lafia and Makurdi locations evaluated during 2017 growing season.

Mean performance based on yield of three Maize endosperms across Lafia and Makurdi Locations in 2017 is presented in (Figure 1). Popcorn had the highest yield (1.14t/ha) in Lafia while Sweet corn and Field corn had the highest mean yield in Makurdi (1.07t/ha and 1.02t/ha) respectively as compared to Lafia.

Conclusion

The current study showed a considerably high magnitude of genetic variability among the endosperm's population, Popcorn had the highest yield (1.14t/ha) in Lafia while Sweet corn and Field corn had the highest mean yield in Makurdi (1.07t/ha and 1.02t/ha) respectively as compare to Lafia. In Lafia, high heritability estimate was detected for days to first tasseling, Days to 50% silking, plant height, ear height, cob weight, and grain yield, high heritability estimate was also detected for days to first tasseling, plant height, ear height in Makurdi, these traits could easily be passed from one generation to the next then enhancing the efficiency of selection in maize improvement program. The estimates of PCV and GCV was high for grain yield and anthesis-silking interval, high heritability estimate was detected for plant height, ear height, cob weight, days to 50% silking, days to first tasseling and grain yield, while estimation of genetic advance as percent of mean (GAM) at 20% selection intensity was high for grain yield, Anthesis-silking interval and plant height while cob weight recorded low genetic advance as a percent of mean in Lafia, while in Makurdi, high genetic advance as a percent of mean was observed for cob weight, grain yield, Anthesis-silking interval and ear height while low values was recorded for days to 50% silking, indicating that these traits are under the control of additive gene action, the observed variability revealed considerable amount of diversity among the tested populations which could be manipulated for further improvement in maize breeding.

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