

Variability in Yield and Yield Components of Selected Pro-Vitamin A Maize (*Zea mays* L.) Varieties in a Humid Environment of Port Harcourt, Nigeria

Abstract

This study aimed at assessing the magnitude and nature of genetic variation present in seventeen pro-vitamin A (PVA) maize varieties, investigate the extent of association among agronomic characters responsible for yield and its components in the maize varieties and evaluate the performance of the maize varieties. The field experiment was carried out at the Teaching and Research Farm of the Rivers State University, Nkpolu, Port Harcourt under rain fed conditions in May, 2018 and were laid out in a randomized complete block design with three replications. Data were collected on established plants per plot, days to 50% silking, days to 50% anthesis, anthesis-silking interval, plant height, ear height, final stand count, number of ears harvested, grain moisture content, field weight and grain yield. Results showed significant differences ($P < 0.01$) among varieties for all traits evaluated. PVASYN-13 had the highest grain yield per hectare among other varieties. High heritability estimates coupled with high genetic advance were observed in established plants per plot, anthesis-silking interval, final stand count, number of ears harvested, field weight, and grain yield, an indication of the additive nature of their inheritance. Thus, the presence of variation could serve as basis for selection for yield improvement in maize.

Keywords: Grain yield, genetic advance, heritability, pro-vitamin A maize, variability

Introduction

Maize is a very important crop which serve as a food security crop in emerging countries especially those in Sub-Saharan Africa (SSA) (Kandil, 2013; Avinashe *et al.*, 2012). It is mainly consumed by humans and livestock and occasionally used in agro-allied industries (Bello *et al.*, 2010; Halilu *et al.*, 2016). Maize cultivation has spread in the world owing to its genetic diversity, adaptability and versatility (Kuleshov, 1933, Fayaz *et al.*, 2017). It is the most-produced crop worldwide and is grown on more than 197 million hectares each year and has the highest average yield per hectare compared with other cereals (FAOSTAT, 2017). Ever since the crop became popular in Nigeria, it has almost replaced traditionally grown cereals such as sorghum and millet because it grows well in all agro-ecological zones of the country (Iken and Amusa, 2004; Sowunmi and Akintola, 2009).

As a result of the peculiarity of the numerous individuals depending on maize as food, efforts have been directed to increasing its nutritional quality and yield. It has been among the target crops for bio-fortification, particularly for protein quality and vitamin A content improvement (Nuss and Tanumihardjo, 2011). Previous efforts at bio-fortification occasioned the high quality protein maize (QPM) which is crucial to meeting the protein demand in localities where it is consumed. Currently, energies are geared toward increasing the pro-vitamin A (PVA) content of maize as a food based approach to combat vitamin A deficiency (VAD) which is widespread in areas where maize is heavily consumed (FAO, 2015). Efforts made so far to bio-fortify maize with PVA carotenoids have been considered productive (Egesel *et al.*, 2003, Gupta *et al.*, 2015, Harvest Plus, 2018).

In spite of the increased area of land dedicated to maize cultivation since the mid-2000s, as well as the exploitation of heterosis (Badu-Apraku *et al.*, 2011), maize production per hectare in Africa is low (2.07 t ha^{-1}) in relation to what is obtainable (11.10 t ha^{-1}) in countries like the United States of America (FAOSTAT, 2017). The current low production level may further decline as a result of several other prevailing factors such as the geometric population growth, incidence of pests and diseases, urbanization, climate change, among others (Rosegrant, *et al.*, 2009, Cairns *et al.*, 2012, Ray *et al.*, 2013).

Numerous breeding programs have set out to significantly increase maize yield in recent years through the use of hybrid crops which usually have higher yields and often exhibit high resistance to weeds and other pests and diseases as well as early maturing (Allard, 1966). However, the full expression of these characteristics might vary based on environments. Before a crop variety is to be adopted and selected, its growth and yield potential in the target environment is expected to be evaluated. Therefore, there is need to periodically search, identify and evaluate promising maize genotypes which practically helps in selection and eventually crop improvement (Odiyi, 2018). Hence, this study was conducted with the following objectives, to:

- i. assess the magnitude and nature of genetic variation present in the selected PVA maize varieties;
- ii. investigate the extent of association among agronomic characters responsible for yield and its components in the PVA maize varieties; and
- iii. evaluate the performance of the PVA maize varieties by determining the growth and yield potentials.

Materials and Methods

The field study was conducted at the Teaching and Research Farm of the Rivers State University, Nkpolu, Port Harcourt, located in the humid tropical zone of Nigeria on latitude 4°25' and 4°28' and longitude 6°15' and 7°25'. Fifteen PVA maize varieties and two checks sourced from the International Institute of Tropical Agriculture (IITA), Ibadan, Oyo State, Nigeria were used for this study. The list of the experimental materials is presented in Table 1. The trial was laid out in a well-prepared field in a randomized complete block design with three replications. Each variety was sown 2 seeds per hill on 2-rows of 5 m long ridge at the normal spacing of 75 cm by 25 cm (intra-row and inter-row, respectively). Hand weeding was done when necessary to keep the plots weed-free. Inorganic compound fertilizer, N.P.K (15:15:15) was applied at two weeks after planting (WAP) and top-dressing with Urea at six WAP. Data were collected on parameters which include: established plants per plot - the total number of plants per plot obtained soon after thinning, days to 50% silking and days to 50% anthesis - the number of days from planting to the time when 50% of the plants in a plot have emerged silks and have tassels shedding pollens, respectively. Anthesis-silking interval - the difference between days to 50% silking and days to 50% anthesis, plant height - the average height in cm of 10 randomly selected maize plants per row from the base of the plant to where the tassel branching begins, using a meter rule, ear height - the average height in cm of 10 randomly selected maize plants per row from the base of the plant to the node bearing the upper ear, using a meter rule, final stand count - the total number of plants harvested per plot, number of ears harvested - the total number of ears harvested per plot, grain moisture content - taken in percentage by a moisture tester at harvest, field weight - it is the weight of cobs per plot measured in kilograms, grain yield - it was measured in tons per hectare and estimated as follows: $\text{Grain yield} = \text{FWT} \times (100 - \text{Grain MC}) \times 80 \times 10000 / (85 \times 5 \times 0.75 \times 100) / 1000$

Data collected on the different characters on the basis of sampled plants were averaged and the mean values obtained were used for statistical analysis. The data obtained were subjected to analysis of variance (ANOVA) using MINITAB, Version 17 statistical package. Treatment means were separated using Tukey's Honestly Significant Difference (HSD) test at 5% level of significance. Genetic parameters were estimated from the mean squares of ANOVA to determine genetic variability among the varieties and the genetic effect of the different

characters. Genotypic and phenotypic variances were determined according to the formula given by Singh and Chaudhary (1985).

Table 1: List of experimental materials used in the study

S/N	Variety
1.	PVASYN-2
2.	PVASYN-5
3.	PVASYN-7
4.	PVASYN-8
5.	PVASYN-9
6.	PVASYN-10
7.	PVASYN-13
8.	PVASYN-21
9.	PVASYN-22
10.	STR SYN 2-Y
11.	TZL COM.4 C4
12.	TZL COMP.3 C4
13.	IWD C3 SYN
14.	DT SYN 15-W
15.	AFLA SYN 3-W
16.	Local Check 1
17.	Local Check 2

Phenotypic variance (δ^2p) = $\delta^2g + \delta^2e$

Genotypic variance (δ^2g) = $\frac{MSG - MSe}{r}$

Error variance (δ^2e) = MSe

Where: MSe = Mean square of genotype, MSe = Mean Square Error, r = number of replication

Phenotypic and genotypic coefficients of variation were also computed as per the formula of Singh and Chaudhary (1985).

Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\delta^2p}}{\bar{x}}$ x 100

Genotypic Coefficient of variation (GCV) = $\frac{\sqrt{\delta^2g}}{\bar{x}}$ x 100

Where: \bar{x} = Sample mean of the character being evaluated

The PCV and GCV values were categorized as high = >20%, medium = 11-20% and low = 0-10% as suggested by Siva-Subramanian and Menon (1973).

Broad sense heritability (H^2) was estimated as: $\frac{\delta^2g}{\delta^2p} \times 100$. It was categorized as high = >50%, moderate = 21-50% and low = 0-20% according to the classification of Elrod and Stanfield (2002).

Genetic advance (GA) was worked out according to the formula of Singh and Chaudhary (1985):

$$\text{Genetic advance (GA)} = \frac{\delta^2g}{\sqrt{\delta^2p}} \times K$$

Where, K = 2.06 (selection differential at 5%)

Expected genetic gain (EGG) was calculated according to the formula given by Robinson *et al.* (1949).

$$\text{EGG} = \frac{\text{GA} \times 100}{\bar{x}}$$

Where: \bar{x} = Mean. EGG was categorized as high = >20%, medium = 11-20% and low = 0-10% based on the classification of Johnson *et al.* (1955).

Results

The mean squares obtained from the analysis of variance for the studied characters of the PVA maize varieties revealed that genotypic effect was significant ($P \leq 0.01$) for all characters evaluated (Table 2). However, the effect of replication was only significant ($P \leq 0.01$) for days to 50% anthesis and days to 50% silking. The values of coefficient of variation for the characters alternated from high to low; ranging from 2.47 (days to 50% silking) to 43.68 (anthesis-silking interval).

The mean performance of the PVA maize varieties evaluated for yield and yield components are presented in Table 3. The varieties were significantly different for all characters evaluated. PVASYN-9 had the highest plant height (117.01 cm) and ear height (48.91 cm), while IWD-C3-SYN and DTSYN-15-W had the lowest plant height (95.14 cm) and ear height (33.77 cm), respectively. In terms of grain yield, PVASYN-13 (4.90 t ha⁻¹) had the highest and was closely followed by IWD-C3-SYN (4.39). Conversely, DTSYN-15-W had the lowest grain yield with 1.28 t ha⁻¹. The highest mean value for number of ears harvested was observed in PVASYN-8 (26.00), whereas the least value was observed in DTSYN-15-W (12.67).

Estimates of components of variance, coefficients of variation, broad sense heritability, genetic advance and genetic advance in percentage of mean for the evaluated characters are presented in Table 4. The result showed that in all characters, a large portion of the phenotypic variance was accounted for by genetic components except days to 50% anthesis, days to 50% silking and grain moisture content, in which the contribution of genetic variance to phenotypic variance was less than 45%. PCV were generally higher than GCV for all characters. PCV ranged from 2.24 to 44.35% while GCV ranged from 1.32 to 34.51% for both days to 50% silking and anthesis-silking interval, respectively.

Heritability estimates were found to be high (>50%) in all characters, except days to 50% silking (34.97%), days to 50% anthesis (40.91%) and grain moisture content (35.47%), which showed moderate heritability values. Genetic advance (at 5% selection intensity) was lowest for field weight (0.68) and highest for plant height (8.80). However, for comparison to be made easily among various characters which had different units of measurements, the values of genetic advance were expressed as percentage of the variety mean for each character and displayed as genetic advance in percentage of the mean (GAM). Based on the classification of GAM by Johnson *et al.* (1955), where values above 20% is regarded as high, between 11 and 20% as moderate and below 10% as low, GAM ranged from low to high. Anthesis-silking interval (55.33), field weight (50.10), grain yield (48.88), number of ears harvested (9.87), final stand count (25.84) and established plants per plot (24.15) all had high GAM. Conversely, low GAM was recorded for days to 50% silking (1.61), days to 50% anthesis (2.08), plant height (8.15) and grain moisture content (9.29). Only ear height (13.71) recorded a moderate GAM. High heritability estimates were accompanied by high GAM for established plants per plot, anthesis-silking interval, final stand count, number of ears harvested, field weight and grain yield while ear height had high heritability estimates and moderate GAM.

Table 2: Mean squares from analysis of variance for different characters of seventeen maize varieties

SV	DF	Established Plants Per Plot	Days to 50% Silking	Days to 50% Anthesis	Anthesis-Silking Interval	Plan Height (cm)	Ear Height (cm)	Number of Plants at Harvest	Number of Ears at Harvest	Field Weight (kg)	Moisture Content (%)	Grain Yield (t ha⁻¹)
Rep	2	5.55	15.08**	18.06**	0.14	11.18	2.5	3.59	1.49	0.06	1.26	0.33
Genotypes	16	39.68**	3.92**	4.80**	1.57**	96.17**	49.41**	38.13**	38.53**	0.49**	4.45**	2.31**
Error	32	5.82	1.5	1.56	0.28	13.81	9.21	4.82	3.28	0.05	1.68	0.25
Coefficient of Variation (%)		17.53	2.47	2.74	43.68	5.86	11.03	17.71	18.21	32.23	12.57	31.91

*, ** Significant at $p \leq 0.05$ and $p \leq 0.01$ probability levels, respectively.

SV = source of variation; DF = degree of freedom; Rep = Replication

Table 3: Mean performance for different characters of 17 PVA maize varieties

Variety	Established Plants Per Plot	Days to 50% Silking	Days to 50% Anthesis	Anthesis-Silking Interval	Plant Height (cm)	Ear Height (cm)	Number of Plants at Harvest	Number of Ears at Harvest	Field Weight (kg)	Moisture Content (%)	Grain Yield (t ha ⁻¹)
PVASYN-2	24.00a-e	68.33ab	66.00a-c	2.33ab	110.40a-d	42.34a-d	21.67b-d	21.00a-d	1.27c-e	13.08ab	2.76d-g
PVASYN-5	22.00b-e	67.00ab	64.67a-c	2.33ab	102.21de	43.19a-c	21.00b-d	21.00a-d	1.17c-e	12.68ab	2.55f-h
PVASYN-7	24.67a-c	67.00ab	65.00a-c	2.00b	103.28c-e	38.89b-d	22.00a-d	21.00a-d	1.20c-e	12.42ab	2.62e-h
PVASYN-8	28.00ab	66.33ab	64.00bc	2.33ab	108.75a-d	42.86a-d	27.33ab	26.00a	1.40b-d	14.08ab	3.02c-f
PVASYN-9	21.67b-e	69.33ab	67.33a-c	2.00b	117.01a	48.91a	21.33b-d	21.33a-d	1.66a-c	12.32ab	3.65bc
PVASYN-10	24.33a-d	66.00b	63.67c	2.33ab	115.72ab	47.17ab	24.00a-c	23.33a-d	1.42b-d	12.23ab	3.12c-f
PVASYN-13	22.67b-e	68.00ab	66.67a-c	1.33bc	114.47a-c	44.95a-c	22.33a-d	20.33b-e	2.27a	13.67ab	4.90a
PVASYN-21	19.67c-e	68.00ab	66.67a-c	1.33bc	107.12a-d	42.80a-d	18.33cd	17.67d-f	0.85de	12.82ab	1.86hi
PVASYN-22	21.00b-e	68.00ab	65.33a-c	2.67ab	107.32a-d	38.76b-d	20.67b-d	19.00c-e	1.36b-d	11.40ab	3.02c-f
STRSYN-2-Y	22.33b-e	68.33ab	66.33a-c	2.00b	110.03a-d	46.59ab	21.00b-d	19.00c-e	1.32b-d	11.32ab	2.93c-f
TZL.COMP.3.C4	23.33a-e	70.00a	66.33a-c	3.67a	105.17b-e	40.72a-d	23.00a-c	22.00a-d	1.55b-d	11.85ab	3.44c-e
TZL.COMP.4.C4	24.33a-d	68.33ab	68.00a	0.33c	111.33a-d	44.61a-c	22.00a-d	20.33b-e	1.44b-d	11.82ab	3.19c-f
IWD-C3-SYN	27.00a-c	66.33ab	65.00a-c	1.33bc	95.14e	35.75cd	26.00ab	25.67ab	2.01ab	12.75ab	4.39ab
DTSYN-15-W	16.67e	67.00ab	65.33a-c	1.67bc	101.87de	33.77d	15.67d	12.67f	0.59e	13.63ab	1.28i
AFLATOXIN-SYN-3-W	26.33a-c	69.33ab	67.67ab	1.67bc	106.18a-e	39.35b-d	26.00ab	24.00a-c	1.64a-c	14.90a	3.50cd
LocalCheck1	30.67a	67.33ab	65.67a-c	1.67bc	106.57a-d	43.58a-c	28.67a	25.67ab	1.12c-e	10.23b	2.53f-h
LocalCheck2	17.00de	68.67ab	67.33a-c	1.33bc	113.95a-c	45.69ab	16.00d	15.33ef	0.95c-e	14.53a	2.03g-i

Means with different alphabets in a column differed significantly at 5% level of probability according to Tukey's Honestly Significant Difference (HSD) test.

Table 4: Genetic parameters of different characters of 17 PVA maize varieties

Characters	Mean	Environmental variance (Ve)	Genotypic variance (Vg)	Phenotypic variance (Vp)	Phenotypic Coefficient of Variation (%)	Genotypic Coefficient of Variation (%)	Heritability in Broad-Sense (%)	Genetic Advance	Genetic Advance in percentage of mean (%)
Established plants per plot	23.28	5.82	11.29	17.11	17.77	14.43	65.98	5.62	24.15
Days to 50% Silking	67.84	1.50	0.81	2.31	2.24	1.32	34.97	1.09	1.61
Days to 50% Anthesis	65.94	1.56	1.08	2.64	2.46	1.58	40.91	1.37	2.08
Anthesis-Silking Interval	1.90	0.28	0.43	0.71	44.35	34.51	60.56	1.05	55.33
Plan Height (cm)	108.03	13.81	27.45	41.26	5.95	4.85	66.53	8.80	8.15
Ear Height (cm)	42.35	9.21	13.40	22.61	11.23	8.64	59.27	5.81	13.71
Final Stand Count	22.18	4.82	11.10	15.92	17.99	15.02	69.73	5.73	25.84
Number of Ears Harvested	20.90	3.28	11.75	15.03	18.55	16.40	78.18	6.24	29.87
Grain Moisture Content (%)	12.69	1.68	0.92	2.60	12.71	7.57	35.47	1.18	9.29
Field Weight (kg)	1.36	0.05	0.15	0.20	32.61	28.16	74.58	0.68	50.10
Grain Yield (t ha ⁻¹)	2.99	0.25	0.69	0.94	32.37	27.71	73.31	1.46	48.88

Discussion

Genetic improvement in characters that are of economic importance along with maintaining sufficient amount of variability is often the desired objective in maize breeding programmes (Hallauer, 1972). The presence of variability in any crop's base population has been adjudged key to such a crop's improvement (Welsh, 1981). In this study, genotypic effect was highly significant ($p \leq 0.01$) for all characters under study, showcasing significant differences among the maize varieties evaluated which revealed the presence of a wide range of genetic variation among the varieties thus, indicating the possibility of selection. The variation observed might be owing to the differences in the genetic makeup of the studied varieties. Many researchers including Grzesiak (2001), Ihsan *et al.* (2005), Reddy *et al.* (2012), Anjorin and Ogunniyan (2014), Ogunniyan and Olakojo (2015), Khan *et al.* (2017) and Odiyi (2018) had earlier observed and reported the presence of considerable genotypic variability among numerous maize genotypes for different characters.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are useful for comparing the relative amount of phenotypic and genotypic variations among different characters and they are useful in selection (Bello *et al.*, 2012). The phenotypic coefficient of variation was higher than genotypic coefficients of variation for all corresponding characters in this study, indicating the contribution of the environment in the expression of these characters. Higher phenotypic coefficient of variation has been reported in maize (Rahma *et al.*, 2017 and Odiyi, 2018) and other crops like soybean (Mohammedi and Pourdad, 2009), fluted pumpkin (Fayeun *et al.*, 2016), rice (Olawamide *et al.*, 2018, Tiwari *et al.*, 2019, Saha *et al.*, 2019), barley (Jalata *et al.*, 2011) and African eggplant (Denton and Nwagburuka, 2011).

Heritability estimates helps to partition variability (into either heritable or non-heritable). The higher the heritability estimate for a character, the more likely it is for the characters to be easily passed on to the next generation. The heritability values ranged from medium to high for all characters under study indicating that the environment has little influence on them, but are rather largely under genetic control. Authors such as Ojo *et al.* (2006), Rafiq *et al.* (2010), Olakojo and Olaoye (2011), Kumar *et al.* (2014), Nzuve *et al.* (2014), Ogunniyan and Olakojo (2015) and Odiyi (2018) have all earlier reported high heritability estimates for different yield controlling characters in maize. High heritability estimates for characters practically often denote the ease and efficiency of selection in any breeding program as it suggests that the characters are likely to be easily passed on to the next generation. Although, it is more reliable to consider heritability values along with those of genetic advance (Reddy

et al., 2012), as high heritability coupled with genetic advance reveals the presence of lesser environmental influence and prevalence of additive gene action in their expression (Sabale *et al.*, 2018). Similarly, high values of genetic advance in percentage of the mean (GAM) are indicative of additive gene effect whereas low values are indicative of non-additive gene effect (Singh and Marayanan, 1993). The characters with high heritability estimates accompanied with high GAM such as established plants per plot, anthesis-silking interval, final stand count, number of ears harvested, field weight and grain yield as observed in this study are indicative that they are under the control of additive gene action, suggesting that effective progress in improvement through selection could be achieved. Similar results of high heritability estimates accompanied by high GAM for similar characters were reported by Shengu (2017) and Odiyi (2018).

Conclusion

This study revealed the existence of considerable amount of genetic variability among the studied PVA maize varieties. The high broad sense heritability estimates obtained for characters such as established plants per plot, anthesis-silking interval, plant height, ear height, final stand count, number of ears harvested, field weight and grain yield show that these characters are genetically controlled and the environment had less influence on them. The high heritability estimates accompanied by high GAM for established plants per plot, anthesis-silking interval, final stand count, number of ears harvested, field weight and grain yield suggests that selection for these characters may be more promising because the variation observed is attributable to high degree of additive effect.

References

- Allard, R. W. (1966). *Principle of Plant Breeding*. John Wiley and Sons Inc., New York, USA.
- Anjorin, F. B. and Ogunniyan, D. J. (2014). Comparison of growth and yield components of five quality protein maize varieties. *International Journal of Agriculture and Forestry*. 4(1): 1-5. <https://doi.org/10.5923/j.ijaf.20140401.01>
- Avinashe, H. A., Jaiwar, S. S., Khanorkar, S. M., Ukey, A. P. and Girase, V. K. (2012). Heterosis studies for grain yield and biochemical characters in Quality Protein Maize (*Zea mays* L.). *Journal of Soils and Crops*, 22: 337-344.
- Badu-Apraku, B., Oyekunle, M., Akinwale, R. O. and FontemLum, A. (2011). Combining ability of early-maturing white maize inbreds under stress and nonstress environments. *Agronomy Journal*. 103: 544-557.
- Bello, O. B., Abdulmalik, S. Y., Afolabi, M. S. and Ige, S. A. (2010). Correlation and path

- coefficient analysis of yield and agronomic characters among open pollinated maize varieties and their F₁ hybrids in diallel cross. *African Journal of Biotechnology*. 9(18): 2633-2639.
- Bello, O. B., Ige, S. A., Azeez, M. O., Afolabi, M. S., Abdulmalik, S. Y. and Mahmood, J. (2012). Heritability and genetic advance for grain yield and its component characters in maize (*Zea mays* L.). *International Journal of Plant Research*, 2(5): 138-145.
- Cairns, J. E., Sonder, K., Zaidi, P. H., Verhulst, N., Mahuku, G., Babu, R., Nair, S. K., Das, B., Govaerts, B., Vinayan, M. T., Rashid, Z., Noor, J. J., Devi, P., San Vicente, F. S., and Prasanna, B. M. (2012). Maize Production in a Changing Climate: Impacts, Adaptation, and Mitigation Strategies. *Advances in Agronomy*. 114: 1-57. <https://dx.doi.org/10.1016/B978-0-12-394275-3.00006-7>
- Denton O. A. and Nwangburuka, C. C. (2011). Heritability, Genetic Advance and Character Association in Sux Yield Related Characters of *Solanum anguivi*. *Asian Journal of Agricultural Research*, 5: 201-207. <http://doi.org/10.3923/ajar.2011.201.207>.
- Egesel, C. O., Wong, J. C., Lambert, R. J. and Rocheford, T. R. (2003). Gene dosage effects on carotenoid concentration in maize grain. *Maydica*. 48: 183-190.
- Elrod, S. and Stanfield, W. (2002). Genetics 4th Ed. Tata McGraw Hill Co., New Delhi.
- FAO, (2015). The State of Food Insecurity in the World – Meeting the 2015 International Hunger Targets: Taking Stock of Uneven Progress. Food and Agriculture Organization of the United Nations, Rome.
- FAOSTAT (2017). “Food and Agricultural Organization of the United Nation”. FAOSTAT Database. Assessed December 20, 2017. <http://www.fao.org/faostat/en/#data/QC>
- Fayaz, A. S., Zahoor, A. D., Sofi, P. A. and Ajaz, A. L. (2017). Recent Advances in Breeding for Abiotic Stress (Drought) Tolerance in Maize. *International Journal of Current Microbiology and Applied Sciences*. 6(4): 2226-2243.
- Fayeun, L. S., Lateef A., Olusegun A., Jide U., and Edith U. (2016). Estimates of Genetic Variability for Seedling Traits in Fluted Pumpkin (*Telfairia occidentalis* Hook. F); *Journal of plant breeding and biotech.*,4(2) pp 262-270.
- Grzesiak, S. (2001). Genotypic variation between maize (*Zea mays* L.) single cross hybrids in response to drought stress. *Acta Physiologiae Plantarum*, 23(4): 443-456.
- Gupta, H. S., Hossain, F. and Muthusamy, V. (2015). Development of biofortified maize through molecular breeding. IBS News report pp. 1-5.

- Halilu, A. D., Ado, S. G., Aba, D. A. and Usman, I. S. (2016). Genetics of carotenoids for provitamin A biofortification in tropical-adapted maize. *Crop Journal*. 4: 313–322.
- Hallauer, A. R. (1972). Third phase in the yield evaluation of synthetic varieties of maize. *Crop Science*, 12: 16-18.
- HarvestPlus (2018). HarvestPlus: Biofortified Crop Map. Available at: <http://www.harvestplus.org/content/biofortified-crop-map> Accessed 24th July, 2018.
- Ihsan, H., Khalil, I. H. and Rahman, H. (2005). Genotypic variability for morphological and reproductive traits among exotic maize hybrids. *In Proceedings. 2005, 211pp.IITA (2001). International Institute of Tropical Agriculture. Annual Report on Maize Production. www.iitaresearch.org.*
- Iken, J. E. and Amusa, N. A. (2004). Maize research and production in Nigeria. *African Journal of Biotechnology*. 3(6): 302-307.
- Jalata, Z., A. Ayana and H. Zeleke, 2011. Variability, heritability and genetic advance for some yield and yield related traits in Ethiopian barley (*Hordeum vulgare* L.) landraces and crosses. *International Journal of Plant Breeding and Genetics*, 5: 44-52.
- Johnson, H. E., Robinson, H. F. and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* 47: 314-318.
- Kandil, E. E. (2013). Responses of some maize (*Zea mays* L.) hybrids to different levels of Nitrogenous Fertilization. *Journal of Applied Sciences Research*, 9(3): 1902-1908 ISSN 18190544X.
- Khan, B., Nawab, N. N., Qamar, M., Abbas, M., Haroon, M., Intikhab, A., Ahmed, H., Ahmed, I., Khan, K. and Afreen, M. (2017). Genetic variability in different maize (*Zea mays* L.) genotypes for comparative yield performance under local conditions of Rawalakot, Azad Jammu and Kashmir. *International Journal of Biosciences*, 11(3): 102-107.
- Kuleshov, N. N. (1933). World's diversity of phenotypes of maize. *Journal of Agronomy*. 25: 688-700.
- Kumar, G. P., Reddy, V. R., Kumar, S. S. and Rao, P. V. (2014). Genetic variability, heritability

- and genetic advance studies in newly developed maize genotypes (*Zea mays* L.). *International Journal of Pure and Applied Bioscience*. 2(1): 272-275.
- Mohammadi, R. and Pourdad, S. S. (2009). Estimation, interrelationships and repeatability of
Moreno, J. A., Díaz-Gómez, J., Nogareda, C., Angulo, E., Sandmann, G., Portero-Otin, M., Serrano, J. C. E., Twyman, R. M., Capell, T., Zhu, C. and Christou, P. (2016). The distribution of carotenoids in hens fed on biofortified maize is influenced by feed composition, absorption, resource allocation and storage. *Scientific Reports*. 6: 35346. <https://doi.org/10.1038/srep35346>
- Nuss, E. T. and Tanumihardjo, S. A. (2011). Quality Protein Maize for Africa: Closing the protein inadequacy gap in vulnerable populations. *Advances in Nutrition*. 2: 217–224.
- Nzuve, F., Githiri, S., Mukunya, D. M. and Gethi, J. (2014). Genetic variability and correlation studies of grain yield and related agronomic trait in maize. *Journal of Agricultural Science*. 6(9): 166-176.
- Odiyi, A. C. (2018). Variation and heritability of pro-vitamin A maize synthetics in a rainforest ecology. *Applied Tropical Agriculture*, 23(2): 184-195.
- Ogunniyan, D. J. and Olakojo, S. A. (2015). Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.). *Nigerian Journal of Genetics*. 28(2): 24-28. <https://doi.org/10.1016/j.nigjg.2015.06.005>
- Ojo, D. K., Omikunle, O. A., Oduwaye, O. A., Ajala, M. O. and Ogunbayo, S. A. (2006). Heritability, character correlation and path coefficient analysis among six inbred-lines of maize (*Zea mays* L.). *World Journal of Agricultural Sciences*. 2(3): 352-358.
- Olakojo, S. A. and Olaoye, G. (2011). Correlation and heritability estimates of maize. *African Journal of Plant Science*. 5(6): 365-369.
- Olawamide, D. O., Mogaji, B. O., Nnamaka, S. A. and Fayeun, L. S. (2018). Genetic variability of seedling traits among seventeen upland rice (*Oryza sativa* L.) genotypes. *Proceedings of the 4th Annual Conference of Association of Seed Scientists of Nigeria*, 24 – 28th June, 2018, Akure, Nigeria. Pp. 85-93.
- Rafiq, C. M., Rafique, M. and Hussain, A. (2010). Studies on heritability, correlation and path analysis in maize (*Zea mays* L.). *Journal of Agricultural Research*. 48: 1-35.

- Rahman, M., Hoque, A., Hossain, M. A. and Al Bari, M. A. (2017). Variability and Traits Association Analyses in Maize (*Zea mays* L.) Genotypes. *The Agriculturists*, 15(2): 101-114.
- Ray, D. K., Mueller, N. D., West, P. C. and Foley, J. A. (2013). Yield trends are insufficient to double global crop production by 2050. *PLoS ONE*. 8(6): e66428. <https://doi.org/10.1371/journal.pone.0066428>
- Reddy, V. R., Seshagiri Rao, A. and Sudarshan, M. R. (2012). Heritability and character association among grain yield and its components in maize (*Zea mays* L.). *Journal of Research ANGRAU*. 40(2): 45-49.
- Robinson, H., Comstock, R. and Harvey, P. (1949). Estimate of heritability and degree of dominance in corn. *Agronomy Journal*. 41: 353-359.
- Rosegrant, M. R., Ringler, C., Sulser, T. B., Ewing, M., Palazzo, A., Zhu, T. (2009). Agriculture and food security under global change: Prospects for 2025/2050. International Food Policy Research Institute. Washington, D.C., USA.
- Sabale, G. R., Bhave, S. G., Desai, S. S., Dalvi, M. B. and Pawar, P. R. (2018). Variability, Heritability and Genetic Advance Studies in F2 Generation of Cowpea (*Vigna unguiculata* sub sp. *Unguiculata*). *International Journal of Current Microbiology and Applied Sciences*, 7(9): 33414-3320. <https://doi.org/10.20546/ijcmas.2018.709.411>.
- Saha, S. R., Hassan, L. Haque, M. A., Islam, M. M. and Rasel, M. (2019). Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces. *Journal of Bangladesh Agricultural University*, 17(1): 26-32. <http://doi.org/10.3329/jbau.v17i1.40659>
- Shengu, M. K. (2017). Studying yield and yield components of Early Maturing Maize (*Zea mays* L.) Inbred Lines in Central Rift valley of Ethiopia. *International Journal of Plant Breeding and Crop Science*, 4(2): 268-275.
- Sowunmi, F. A. and Akintola, J. O. (2009). Effects of Climatic Variability on Maize Production in Nigeria. *Research Journal of Environmental and Earth Sciences*. 2(1): 19-30.
- Singh, P. and Marayanan, S. S. (1993). Biometrical Techniques in plant breeding. Kalyani, Publishers New Delhi, pp 14-84.
- Singh, R. K. and Chaudhary, B. D. (1985). Biometrical Methods in Quantitative Analysis, Kaljuni Publishers, New Delhi, pp 318.
- Siva-Subramanian, S. and Menon, M. (1973). Heterosis and Inbreeding Depression in Rice.

Madras Agricultural Journal. 60: 1139-1141.

Tiwari, D. N., Tripathi, S. R., Tripathi, M. P., Khatri, N. and Bastola, B. R. (2019). Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. *Advances in Agriculture*, 9pp.

Welsh, J. (1981). Fundamentals of plant breeding and genetics. John Wiley & Sons, New York.

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