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GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE STUDIES FOR PRO-VITAMIN A (PVA) TRAIT IN SORGHUM (*SORGHUM BICOLOR* [L.] MOENCH) GENOTYPES

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ABSTRACT

The study was conducted at the research field of the Ahmadu Bello University, Zaria, Nigeria to determine genetic variability, broad and narrow sense heritability and genetic advance of Pro-Vitamin A (PVA) trait among Sorghum genotypes. Six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) were derived from two crosses (SAMSORG 17 × SAMSORG 44) and (SAMSORG 17 × SAMSORG 14) which were sown in a randomized complete block design with three replications. Mean sum of squares due to genotypes from the analysis of variance revealed sufficient genetic variation ($P < 0.01$) for Pro-Vitamin A (PVA) trait. High broad sense heritability for PVA was estimated in the crosses, these estimates indicate that genetic factors play a major role in determining the PVA concentration and possibility of a positive response to selection. High narrow sense heritability and high genetic advance as percentage of mean observed for PVA indicates the importance of additive genetic variation hence selection may be effective in early generations for this trait.

INTRODUCTION

Sorghum (*Sorghum bicolor* [L.] Moench) is a cereal of the family *Poaceae*. It is called *milo*, *jowar*, *kafir*, *chulam*, *dawa*, *oka baba* in some Nigerian languages, and Guinea corn in English language. Sorghum originated in equatorial Africa i.e. East Africa likely from Ethiopia (Ecoport, 2010) and is distributed throughout the tropical, semi-tropical, and arid regions of the world. It is quantitatively the fifth major cereal crop of the world following wheat, rice, maize and barley in terms of production and utilization (Taylor and Dewar, 2001). In terms of tonnage, sorghum is Africa's second most important cereal. It is also the second cheapest source of energy and micronutrients (after pearl millet.) Vast majority of the populations in Africa and central India depend on sorghum for their dietary energy and micronutrient requirements (Parthasarathy et al., 2006).

Sorghum has unique tolerance to drought and adaptation to dry tropical and subtropical ecosystems throughout the world. Africa produces about 20 million tons of sorghum per annum (Taylor and Dewar, 2001). Sorghum production in Nigeria is increasing rapidly with a record of 8.5 million tons in 2008, 9.32 million tons in 2009, 11.5 million tons in 2011 and 63.7 million tons in 2014, making the country the largest producer in the world (Obilana, 2011). The magnitude of genetic variability present in a given population is of great importance for the success of any plant breeding program. Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotypes. Hence knowledge about genetic advance coupled with heritability is very essential. This research was carried out to determine genetic variability, broad and narrow sense heritability

as well as estimates of genetic advance Pro-Vitamin A (PVA) trait among Sorghum genotypes for effective selection desirable genetic material useful for production and use as breeding line.

MATERIALS AND METHODS

The research was conducted between 2014 and 2015 at the research farm of the Institute for Agricultural Research (IAR), Samaru in Ahmadu Bello University, Zaria, Kaduna State, Nigeria. Samaru is located on latitude 11° 11' N, longitude 7° 38' E, and 686 m above sea level in the Northern Guinea savannah ecological zone of Nigeria.

The average annual rainfall of the area is about 1,058 mm which is distributed within 160 days (May – September). The temperature distribution is fairly uniform with a mean daily temperature of 27°C. The soil is mostly sandy loam (Hamma *et al.*, 2012). The plant materials used in this study comprised of three (3) IAR sorghum genotypes: SAMSORG 17, SAMSORG 44, and SAMSORG 14. SAMSORG 17 (bearing yellow endosperm) was chosen for its improved level of PVA while, the other two varieties SAMSORG 44 and SAMSORG 14 (both bearing white endosperm), were chosen because they constitute part of the most commonly grown cultivars by the farmers within the sorghum ecological zones of Nigeria.

Population development and evaluation

The F₁ hybrids

In the 2013 main season (June to September), the parents seeds were sown in order to make crosses between the yellow endosperm variety (as male) and the two white endosperm varieties (as female) using North Carolina Design II (factorial mating design). Staggered planting of the genotypes was adopted in order to synchronize the flowering period and subsequent pollination. Arrangement of the field layout comprise of 15 row plots each measuring 5 m long, with a spacing of 0.75 m between rows and 0.30 m between plants within a row. All agronomic practices such as land preparation, ridging, fertilizer application, weeding carried out accordingly. The female parents (SAMSORG 44 and SAMSORG 14) were

hand emasculated using cellophane bags to abort their pollen since they are not male sterile and further pollinated with the male parent SAMSORG 17 to produce F₁ seeds.

The F₂ populations

In the 2014 dry season (January to June), the F₁ hybrids developed from the crosses in 2013 together with the parental lines were sown under irrigation in the research farm of IAR Samaru. Standard agronomic practices including good and clean seed bed preparation, weeding to keep the crop free of weed competition and recommended fertilizer application were carried out to maintain a healthy crop. At heading, F₁ plants were selected randomly in each cross and their panicles covered with paper bags to ensure complete selfing. Seeds from the selfed plants in each cross were harvested at maturity threshed and kept in clearly labeled paper envelopes as F₂ seeds.

The backcross population

From the same plot used to produce the F₂ seeds, 10 plants for each replication were randomly selected and the heads were covered with paper envelopes. Ten plants from each of the replications were also selected within the parental lines and were emasculated in preparation for the backcross exercise. The F₁ of each cross were backcrossed to the parental to generate BC₁P₁ and BC₁P₂ via hand pollination. At maturity, seeds developed from the plants were harvested and kept in labeled paper envelopes as backcrossed seeds.

Evaluation of the populations

The parental lines, six each of F₁, F₂, and the backcross populations were evaluated in the 2014 main season at the IAR Research farm. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Plot size for non-segregating populations (P₁, P₂ and F₁) was 2 rows of 4 m long and 0.75 m apart and the segregating populations (F₂, BC₁P₁ and BC₁P₂) were 5 rows of 4 m length and 0.75 m apart, the inter – row spacing was 0.30 m with two plants per hill in every plot.

Data collection

The following agronomic data were collected and recorded: Days to 50% Flowering, Plant Height, Panicle length, Panicle Weight, Grain Weight per panicle, One Thousand Grain Weight and Grain yield per panicle. Compositional analysis for Vitamin A was carried out at the National Research Institute for Chemical Technology (NARICT) using the procedures given by Rutkowski and Grezegorczy (2007).

Statistical Analysis

Analysis of Variance was conducted using the General Linear Model (GLM) procedure of the Statistical Analysis System (SAS) version 9.0 Software (2002). Least Significant Difference Test Fisher, (1935) was used to separate the means where significant differences exist. Broad and narrow sense heritability estimates were obtained using the variance component methods. The F_2 variances were used to compute the broad sense heritability according to Roham *et al.* (2011). The heritability percentage was categorized as low, moderate and high (Robinson *et al.*, 1949, Feyissa *et al.* 2014). 0-30% = low, 30-60 % = moderate, 60-100%=high. Genetic Advance (GA) was calculated in accordance with the method described by Allard (1960), Wolie *et al.* (2013) as: $GA = h_n^2 \sqrt{\sigma_p^2} \times K$ at 10 % selection intensity, Where, K is the standardized selection differential, at 10 % selection intensity, $K=1.755$ and GA (as % of the mean) = $\left[\frac{GA}{\bar{X}} \right] \times 100$ | Where, k = selection differential (at 10% selection intensity), σ_p = phenotypic standard deviation, $h_n^2 =$

RESULTS

The variances among the six generations were presented in Table 1 for both crosses (SAMSORG 17 × SAMSORG 44 and SAMSORG 17 × SAMSORG 14). The results indicated highly significant ($P < 0.01$) differences for PVA and for all measured traits including days to 50% flowering, plant height, panicle length, panicle weight, grain weight, 1000-seed weight, Pro-vitamin A and total grain yield.

Phenotypic variances σ_p^2 were large for all the traits compared to genotypic variances σ_G^2 in the crosses (Tables 2). Positive values were obtained for genotypic variance. Genotypic variance was then partitioned into additive and dominance variances. It was observed that additive variances were higher than the dominance variances in the crosses studied. The broad sense heritability estimates were high for PVA and all the measured traits in the two crosses (Tables 2). Low narrow sense heritability was recorded for 1000-grain weight (15%) and panicle length (17%) in the cross of SAMSORG 17 × SAMSORG 14. PVA however, recorded high genetic advance as percent of mean in the two crosses (SAMSORG 17 × SAMSORG 44 and SAMSORG 17 × SAMSORG 14), respectively according to Falconer and Mackay's (1996) classification.

Narrow sense heritability and \bar{X} = grand mean. Falconer and Mackay (1996) classified genetic advance as percent of mean as low (0-10%), medium (10 - 20%) and high (20% and above).

Table 1 Mean squares for pro-vitamin A concentration and other agronomic traits involving SAMSORG 17, SAMSORG 44 and SAMSORG 14

Source of Variation	Degrees of Freedom	Days to 50% Flowering	Plant Height (cm)	Panicle Length (cm)	Panicle Weigh (g)	Grain Weight (g)	1000-Grain Weight (g)	Pro-vitamin A (µg/g)	Grain Yield (kg/ha)
CROSS 1 (SAMSORG 17 × SAMSORG 44)									
Generation	5	14512.9**	40348.7**	95.6**	136818.7**	134930.1**	2325.4**	964.3**	2665286.0**
Replication	2	1.9	520.8	0.0	123.2	102.7	45.0	0.2	2034.0
Error	10	80.3	381.3	4.1	825.2	825.7	57.1	6.8	16309.9
CROSS 2 (SAMSORG 17 × SAMSORG 14)									
Generation	5	9048.5**	116250.3**	81.9**	101452.0**	102779.3**	1032.0**	1984.0**	2030209.0**
Replication	2	1.1	29.3	2.8	324.5	180.1	27.2	0.1	3557.5
Error	10	44.7	688.7	4.2	1184.2	1368.8	43.9	5.3	27037.3

Table 2 Variance Components, Heritability and Genetic Advance for pro- vitamin A and other traits of six generations of sorghum involving SAMSORG 17, SAMSORG 44, SAMSORG 14 and CSR01 evaluated at Samaru in 2014

Trait	σ_p^2	σ_E^2	σ_G^2	σ_A^2	σ_D^2	Broad Sense Heritability	Narrow Sense Heritability	GA (10%)	GAM%
SAMSORG 17 × SAMSORG 44									
Days to 50% flowering	100.27	21.42	78.85	43.30	35.55	0.78	0.43	75.67	80.37
Plant Height (cm)	103.34	60.67	42.67	23.10	19.57	0.41	0.22	39.90	24.09
Panicle Length (cm)	4.71	0.25	4.46	2.17	2.29	0.94	0.46	3.80	10.20
panicle weight (g)	147.40	62.40	85.00	47.30	37.70	0.57	0.32	82.78	33.52
1000-Grain Weight (g)	97.74	24.44	73.30	27.82	45.48	0.75	0.28	48.03	221.13
Pro-Vitamin A (µg/g)	7.04	0.12	6.92	3.68	3.24	0.98	0.52	26.42	75.58
Grain Yield (kg/ha)	214.00	82.00	132.00	122.40	9.60	0.61	0.57	214.07	21.02
SAMSORG 17 × SAMSORG 14									
Days to 50% flowering	127.88	31.20	96.67	64.12	50.55	0.75	0.36	80.79	83.43
Plant Height (cm)	176.50	51.70	124.80	88.12	36.68	0.70	0.49	151.78	67.83
Panicle Length (cm)	29.11	3.49	25.62	5.12	20.50	0.88	0.17	8.68	23.15
panicle weight (g)	197.50	51.02	146.48	55.74	85.74	0.74	0.28	97.05	40.58
1000-Grain Weight (g)	41.39	12.68	28.70	6.30	22.40	0.69	0.15	10.90	51.35
Pro-Vitamin A (µg/g)	11.30	3.21	8.09	5.75	2.34	0.71	0.51	20.11	156.08
Grain Yield (kg/ha)	221.90	51.90	170.00	146.50	23.50	0.76	0.60	233.66	23.72

DISCUSSIONS

The separation of total genetic variance into its components revealed the presence of variability due to additive (a) and dominance (d) gene effects for PVA and the agronomic traits studied. Estimate measures of high broad sense heritability for PVA in the crosses indicated that genetic factors play a major role in determining the PVA concentration. These observations are in congruence with report of Chander *et al.*, (2008) who reported 85% broad sense heritability for PVA estimated in maize Recombinant Inbred Lines. High heritability of PVA could be due to the involvement of a few major genes in the carotenoid biosynthetic pathway (Pfeiffer *et al.*, 2007). Moderate to high heritability estimates for carotenoids have also been reported in the past for maize (Wurtzel *et al.*, 2004). Therefore, expressions for PVA and most of the agronomic traits were genetic which can be exploited in breeding programs. This finding is in agreement with the findings of Basu (1981) and Abu-Gasim and Kambal (1985) and Bello *et al.* (2001) who reported that the expressions for several quantitative characters in sorghum genotypes were genetic. Zaveri *et al.* (1989) also reported similar results in pearl millet. Bello *et al.* (2001) observed that high environmental variance estimates for some characters similar to what was obtained in this study for plant height in SAMSORG 17 × SAMSORG 44 could be attributable to large sample size.

The greater the genetic variability the higher would be the heritability hence the better the chances of success of improvement to be achieved through selection. In this study days to 50% flowering, plant height, panicle length, panicle weight, grain weight, 1000-grain weight, grain yield and pro-vitamin A showed high broad sense heritability indicating the possibility of a positive response to selection. This is because there is a likelihood of transferring the heritable factors from parents to offspring during breeding. The existence of high significant variations and heritability among the agronomic characters showed that selection can be made in the early generations for these traits. High broad sense heritability estimate also indicates low influence of the environment and that the

variation observed was mainly under genetic control this may also be attributed to uniform environmental conditions during the conduct of the experiment (Fekadu *et al.*, 2003). The high heritability obtained from days to 50% flowering, plant height, panicle length, panicle weight, grain weight, 1000-grain weight, and grain yield agreed with the findings of Ekebil *et al.* (1977); Totok (1997); Aba *et al.* (2001) and Biswas *et al.* (2001). High narrow sense heritability observed for most traits in both crosses indicates the importance of additive genetic variation. Estimates of genetic advance help in understanding the type of gene action involved in the expression of polygenic characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh and Narayanan, 1993). Heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates (Johnson *et al.*, 1955). High heritability associated with high genetic advance of mean was observed for days to 50% flowering in both crosses this corroborates the report of Deepalakshmi and Ganesamurthy (2007).

Plant height, panicle weight, 1000 grain weight and grain yield showed high heritability associated with high genetic advance of mean in both crosses, this corroborates with the report of Deepalakshmi and Ganesamurthy (2007) and Jain and Patel (2012) who revealed high heritability accompanied with high genetic advance (GA) as per cent of mean for plant height, panicle weight, 1000 grain weight and grain yield indicating that these traits are under the influence of additive gene action in their expression and selection of genotypes based on phenotypic performance would be useful in a breeding program and selection may be effective in early generations for these traits, hence, selection in the segregating generation would be fairly effective for them. In the present study, panicle length showed high heritability combined with low genetic advance in SAMSORG 17 × SAMSORG 14, this is in corroboration with the report of Umakanth *et al.* (2004) and Umakanth and Kuriakose (2005) who reported that estimates of variance

indicated predominance of non-additive gene action for panicle length may indicate that the trait is governed by non-additive genes hence heterosis breeding would be recommended for improvement of this trait.

CONCLUSION

High heritability was realized for days to 50% flowering, plant height, panicle length, panicle weight, grain weight, 1000-grain weight, and grain yield in this study. So also, broad sense heritability estimates was high for PVA in the

two crosses studied. High heritability with high to moderate estimates of genetic advance recorded PVA and all the agronomic traits studied when carefully selected may lead to improvement for these traits. Hence, this may provide better opportunity for selecting sorghum genotypes useful for production and for use as breeding lines and for enhanced nutrition in diets using fortified sorghum genotypes.

REFERENCES

- Aba, D. A., Nwasike, C. C., Yeye, M. and Zaria, A. A. (2001). Studies on Genetic Variations in sorghum Variety Irradiated with Cobalt-60 (Co60), *Crop Science Journal*, 9:377-384.
- Abu-Gasim, E. H. and Kambal, A. E. (1985) Variability and interrelationship among characters in indigenous grain sorghum of the Sudan. *Crop Science*, 11: 308-309.
- Allard, R.W. (1960). *Principles of Plant Breeding*. New York: John Wiley and Sons. (pp.485).
- Basu, A.K. (1981) Variability and heritability estimate from Inter-season Sorghum Cross. *Indian Journal Agricultural Science*, 41:116-117.
- Bello, D., Kadams, A.M. and Simon, S.Y. (2001). Correlation and Path Coefficient analysis of grain yield and its components in Sorghum. *Nigerian Journal Tropical Agriculture*, A Publication of SAAT, FUT, Yola, Nigeria, 3: 4-9.
- Biswas, B.K., Hasanuzzaman, M. Eltaj, F., Alam, M.S. and M.R. Amin, (2001). Simultaneous selection for fodder and grain yield in sorghum. *Journal Biological Science*, 1: 319-320.
- Chander, S., Guo, Y. Q., Yang, X. H., Zhang, J., Lu, X.Q., Yan, J. B., Song, T. M., Rocheford, T. R. and Li, J.S. (2008). Using molecular markers to identify two major loci controlling carotenoid contents in maize grain. *Theoretical Applied. Genetics*, 116:223-233.
- Deepalakshmi, A. J., and Ganesamurthy, K. (2007), Studies on genetic variability and Character Association in kharif sorghum {*Sorghum bicolor* (L.) Moench. *Indian Journal of Agriculture Research*, 41 (3):177-182.
- Eckebil, J.P., Ross, M.W., Gardner, C. O. and J.W. Maranville, (1977). Heritability estimates, genetic correlation and predicted gains from S. progeny test in three grain sorghum population. *Crop Science Journal* 17: 373-377.
- Ecoport, (2010). Ecoport database. Ecoport. Ecoport. [www http://ecopoert.org](http://ecopoert.org) (*sainfoin conobrychis viciifolia*) srimp meal sorghum grain (general) Tamarugo (*prosopis tamarugo*)
- Egesel, C. O., Wong, J. C., Lambert, R. J., Rocheford, T. R. (2003). Combining ability of maize inbred for carotenoids and tocopherols. *Crop science*, 43:818-823.
- Falconer, D. S. and Mackay, T. F. C. (1996). *Introduction to Quantitative Genetics* 4th ed. Benjamin Cummings, England, ISBN-10:0582243025.
- Fisher, R. A. (1935). *The design of experiments*. Oliver and Boyd, London, 6th Ed., 2U14 pp., (Section 2U).
- Fekadu, M., Ravishankar, H. and Lemma, D. (2003). Study on variability in tomato germplasm under conditions of central Ethiopia. *-Vegetable Crops Research Bulletin*, 58:41-50.
- Feyissa, T., and Zinaw, D. (2014) Genetic Variability, Heritability and Character Association of Twelve Sugar Cane Varieties in Finchaa Sugar Estate West Wolega Zone Oromia Region of Ethiopia. *International Journal of Advanced Research in Biological Sciences*, 1(7): 35-37.

- Fisher, R. A. (1935). The design of experiments. Oliver and Boyd, London, 6th Ed., 2U+4 pp., (Section 2U).
- Hamma, I. L.; Ibrahim, U. and Yusuf, S. M. (2012). Growth and yield of Okra as influence by live mulch in Samaru Zaria. *European Journal of Sustainable Development*, 1(2): pp.11
- Jain, S.K. and Patel, P.R., (2012). Genetic Variability In Land Races of Forage Sorghum {*Sorghum Bicolor* (L) Moench} Collected From Different Geographical Origin Of India. *International Journal of Agriculture Sciences*, 4(2), 182185. <http://dx.doi.org/10.9735/0975-3710.4.2.182-185>.
- Johnson, H.W., Robinson H. E and Comstock R. E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, 47: 314-318.
- Lyman, O., R. and Michael, L. (2010). *An Introduction to Statistical Methods and Data Analysis*. (6th Ed). (pp.) Texas A&M University: Macmillan Publishing Solutions.
- Obilana, A. B. (2011). Role of biotechnology in sorghum breeding: The case for biofortified sorghum in Nigeria. Pp 3.
- Parthasarathy, Rao P., Birthal, B. S., Reddy Belum, V. S., Rai, K. N. and Ramesh, S. (2006). Diagnostics of sorghum and pearl millet grains-based nutrition in India. *International Sorghum and Millets Newsletter*, 47: 93-96.
- Pfeiffer, W. H. and McClafferty, B. (2007). Harvest Plus: breeding crops for better nutrition. *Crop Science*, 47: 88-105
- Robinson, H. F, Comstock, R. E. and Harvey, V. H. (1949). Estimates of heritability and degree of dominance in corn. *Agronomy Journal*, 41: 353-359.
- Roham, E., Samira, S., Monireh, R., and Javid Ojaghi (2011). Genetic Analysis of (13), (14)-D-Glucans in Barley, Azhul × Falcon Cross. *World Applied Sciences Journal*, 14 (8): 1146 - 1153, 2011 ISSN 1818-4952 IDOSI Publications.
- Rutkowski, M. and Grzegorzczuk, K. (2007). Modifications of spectrophotometric methods for antioxidative vitamins determination convenient in analytic practice. *ACTAScientiarum Polonorum Techologia Alimentaria*, 6(3): 17-28.
- Singh, P. and Narayanan, S. S. (1993). Biometrical techniques in plant breeding. 1st ed. Kalayani Publishers, New Delhi, India.
- Taylor, J.R.N. and Dewar, J. (2001). Developments in sorghum food technologies. *Advances in Food Nutrition and Research*, 43: 218 -264.
- Totok, A. D. H., (1997). Estimating heritability values and genetic correlation, in several agronomic characters. *American Journal of Botany*, 87: 145.
- Umakanth, A.V., Madhusudhana, R., Latha., K. M., Rafiq, S. M., Kiran, V. S. S., (2004), Analysis of genetic variation and trait interrelationships in sorghum [*Sorghum bicolor*(L.) Moench]. *National Journal of Plant Improvement*, 6 (2):104-107.
- Umakanth, A. V. and Kuriakose, S. V. (2005). Assessment of sorghum landraces for combining ability. *Agricultural Science Digest*, 25: 272-74.
- Wolie, A., Tadesse, D. and Ketema, B. (2013). Heritability, variance components and genetic advance of some yield and yield related traits in Ethiopian collections of finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes. *African Journal of Biotechnology*, 12(36), pp. 5529-5534, DOI: 10.5897/AJB11.3409
- Wurtzel, E., Rocheford, T., Wong, J., and Lambert, R. (2004). QTL and candidate genes phytoene synthase carotene desaturase associated with the accumulation of carotenoids in maize. *TAG Theoretical and Applied Genetics*, 108(2):349-359. <http://dx.doi.org/10.1007/s00122-003-1436-4>.
- Zaveri, P.P., Phul, P.S and Dillon, B.S. (1989) Observed and predicted genetic gains from single and multi-trait selections using three mating designs in pearl millet. *Plant Breeding Abstract*, 60: 127-132.

