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Genetic Variability, Coefficient of Variance, Heritability and Genetic Advance of Pro-Vitamin A Maize Hybrids

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Abstract **– Vitamin A deficiency (VAD) is a worldwide nutritional problem affecting especially children and pregnant women. A long term solution to VAD and probably much safer is cultivation of biofortified crops through home gardening and commercial production with crops that are high in pro-vitamin A. Breeding for Pro-vitamin A (PVA) maize varieties requires a thorough understanding of the genetic mechanisms governing yield and the PVA trait. Genetic variability for example may influence breeding programmes while heritability studies give important information about traits that are normally transferred from parents to their offspring and their successive generations. The objective of this study therefore was to determine the genetic variability, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability and genetic advance (GA) of pro-vitamin A maize hybrids with the aim of obtaining information for selecting and breeding for PVA maize varieties. The parents for the crosses included Akposoe (Quality Protein Maize (QPM) variety 80-85 days maturity), Aburohemaa (QPM variety 90 days maturity), Honampa (normal orange PVA variety 110 days maturity) and ZM305 (normal orange PVA inbred line 85 days maturity). Field evaluations were conducted in 2014 major and minor seasons in 8 environments. The number of entries was 20 made up of the parents and their crosses. The design was an RCBD with 3 replications. Results from the studies indicated that narrow sense heritability of PVA was high (87%) in the top cross hybrid but very low (6-14%) in the varietal cross hybrids. High narrow-sense heritability coupled with high values of PCV, GCV and GA as a percentage of the mean for PVA content in the top cross hybrid obtained from this study implied that this trait was mostly controlled by additive genes and was highly heritable. Thus, progress in selection for this trait could be achieved more quickly and hybridization as well as synthetic breeding could be recommended.**

Keywords **– Genectic Advance, Genotypic Coefficient of Variance, Phenotypic Coefficient of Variance, Pro-vitamin A.**

I. INTRODUCTION

VAD is a worldwide nutritional problem [32] particularly in Africa, Americas, Eastern Meditarranean, South and South East Asia and Western Pacific [58]. A long term solution to VAD and probably much safer is cultivation of biofortified crops through home gardening and commercial production with crops that are high in pro-vitamin A [50]. Breeding for PVA maize varieties as in other crops requires the understanding of the genetics of yield and other traits as well as the procedures for selection or breeding. Heritability for example is a measure of the extent of resemblance between relatives and it shows the portion of the total variance attributed to breeding value differences [27], [22]. Heritability studies give important information about traits that are normally transferred from parents to their offspring and their successive generations. Such studies help plant breeders to predict a successful cross with high heritability transmission to the progeny and thus are useful in the incorporation of characters into the offspring and early selection in generations [30], [3]. Heritability values normally range from 0-1 because it is a proportion of variances, with the numerator contained in the denominator but this is not always the case since experimental error could lead to estimates outside the stated range [11] and again it has been observed in PVA breeding that, this situation can occur if studies contrast non pro-vitamin A and high pro-vitamin A genotypes [38]. Narrow-sense heritability (h^2n) estimates are classified as high (>50%), medium (30–50%) and low (<30%) [8]. Broad-senseheritability (h^2b) could be classified as high (>30%), medium (10–30%) and low (<10%) [13]. [47] on the other hand classified h^2b as high (>80%), moderately high (60-79%), medium (40–59%) and low (<40%).

Pro-vitamin A concentrations are heritable [57], [19], [34], [23], [38], [9] and may be controlled by additive gene action [18], [38], [49], [28]. Negative heritability estimates could be observed [12], [44], [30], [24], [43]. Robbinson [42] suggested that such estimates were to be assumed as zero but [17] proposed that it should be reported for future references.

Genetic variability influence breeding programmes especially the extent to which it could occur and the relative amount of variation in the different traits and could be measured by determining the genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) [7]. The phenotypic variances and its PCVs could have higher values than the genotypic variances and its GCVs [7], [43] but for most breeding purposes a high proportion GCV to the PCV is mostly desired [32]. The differences between genotypic and phenotypic coefficient of variation indicate the environmental influence [7]. If differences between the PCV and GCV are small it indicates that the environmental effects on selected traits were low. But if PCV is high and GCV is low then it may imply that environmental effects on the selected traits were high [4]. PCV and GCV greater than 20% are regarded as high and values less than 10% are classified as low whereas values that fall between 10 and 20% are regarded as medium [14]. Since heritability may be affected by environmental factors, information of predicted genetic gain will be more helpful in the selection process [37], [7], [43], [56]. Genetic gain is the difference between the mean phenotypic value of the progeny of selected plants and the

mean of the original parental population [35]. Genetic advance (GA) on the other hand refers to the improvement of traits in genotypic value for the new population in comparison with the original population with one cycle of selection at a particular selection pressure [39], [47]. The estimates of GA have the same unit as those of the mean but in the calculations, heritability in the broad-sense must be used for mixture of pure lines or clones or apomictically reproducing crops whilst narrow-sense heritability should be used for segregating populations or sexually reproductive crops [39], [35]. Traits that exhibit high heritability and high GA may be said to be controlled by additive genes and may indicate the extent of gain in a trait obtained under specific selection intensity. Such traits may have less environmental influence [37], [31]. Genetic gain in percentage of the mean (M) may be categorized as low (0–10%), moderate (10–20%) and high (20% and above) [26]. Low GA may indicate that the trait is being governed by non-additive genes and heterosis breeding may be recommended [35].

Studies to estimate heritability, PCV, GVC, GA and GAM in maize by several workers have been reported. For example, 80% broad-sense heritability for grain yield and other parameters are reported [41]. The differences between genotypic coefficients of variance (GCV) and phenotypic coefficients of variance (PCV) could be very low for characters studied, implying that the environmental effects in the development of those parameters were low. GAM for grain yield and other parameters could be high showing that these parameters were under the control of additive genes [41], [40], [7] and effective selection in subsequent generations could be possible for improvement in these traits [7]. This also makes it clearer that larger proportion of phenotypic variance was attributed to genotypic variance and reliable selection for these traits was possible. In addition, selection at an early segregating generation will prove beneficial for selecting superior maize varieties [7]. High heritability coupled with high expected genetic advance as percent of mean obtained for traits indicates the presence of additive gene effects for potential crop improvement through selection of these traits [56]. However, high heritability and low genetic advance may be attributed to non-additive gene action governing such traits and for that matter their improvement through early generation selection may not be desirable. Thus improvement in these characters could be through hybridization and hybrid vigour [7]. Moderate heritability along with high genetic advance provide little chance for its further improvement and low heritability with low genetic advance may indicate non-additive genetic effects governing such traits [7].

Negative values for genetic variance, heritability and heritability coefficient are possible [30] when negative values are obtained for its genotypic variance and heritability [43].

II. Materials and Methods

Study sites (Kwadaso, Fumesua, Ejura, Akumadan, Pokuase, Nyankpala in the major season of 2014 and at Kwadaso and Pokuase in the minor season of the same year representing 8 environments) are described in Table 1.

Table 1. Description of study sites.

Site	Ecological zone	Mean Annual rainfall[§§§] (mm)	Latitude (N)	Longitude (W)	Altitude[†] (m)	Soil Type[†]
Kwadaso	Decidous Forest	1500	6^0 42'[††]	1^0 39'[†††]	268[††]	Coarse sandy-loam, Paleustult
Fumesua	Decidous Forest	1500	6^0 41'[†]	1^0 28'[†]	289[§]	Coarse sandy-loam, Paleustult
Ejura	Transition	1300	7^0 23'[§]	1^0 22'[§]	235[§#]	Fine coarse sandy-loam, Oxisol
Kpeve	Transition	1300	6^0 41'[††]	0^0 20'E[††]	188[††]	Fine coarse sandy-loam, Oxisol
Akumadan	Transition	1300	7^0 24'[††]	1^0 57'[†††]	389[††]	Forest Ochrosols[†††]
Pokuase	Coastal savanna	800	5^0 36'[†]	0^0 10'[†]	78[§§]	Coarse sandy-loam, Dystrochrept
Nyankpala	Guinea Savanna	1100	9^0 24'[††]	0^0 58'[†††]	170[††]	Fine sandy-loam, Alfisol

Source: [†][45],[††][51]-[55],[†††][36],[§][15][§#][16],[§§][20], [§§§][21]

Design, Management of Trials and Data Recording

The design used was a randomized complete block design with 3 replications. The row length was 5m and row spacing was 75 cm x 25 cm but number of rows and plants for data recording differed according to the type of generation in the genetic studies [25] so that samples for data could be representative enough as follows: Parents and F1s= 2 row plot, data on 10 random plants; BC1s and BC2s= 4 row plot, data on 20 random plants; F2s= 8 row plot, data on 30 random plants. Fields in all sites for both trials were harrowed. Three seeds per hill was planted and after establishment thinned to 1 plant per hill to obtain a plant population of 53,333 plants/ha in each trial. Split application of fertilizer was done at a rate of 90 kg N/ha and 60 kg P_2O_5 and 30 kg K per hectare in both trials. Hand weeding was done on all fields when necessary. Data taken included days to 50% silking (no. of days from planting to 50% silking) and anthesis (no. of days from planting to 50% anthesis); anthesis-silking interval (ASI) calculated as the difference between days to silking and pollen shed; plant height (measured in cm from base of plant to last flag leaf near base of tassel) and ear height (measured in cm from base of plant to node bearing the upper ear); field weight (weight in kg of both pollinated and un-pollinated ears harvested using the hanging scale); grain moisture at harvest (determined in percentage using the Dole moisture meter); cob length and cob diameter (measured in cm using calipers). Cob length was measured from the base of the cob to the tip while cob diameter was measured mid-way of the unshelled cob. Grain yield was

expressed in kg/ha at 15% moisture using the formula: Grain yield = (Field weight (kg)/harvested area (m^2) × (10,000m^2 /ha) × (100 – % grain moisture)/85 × 0.8 (shelling %) according to [6]. Controlled pollinations were used in the stated samples for carotenoid analysis in the genetic studies from 5 environments where the pollinations were done. The maize was harvested and placed in clean polyethylene bags for sun drying to a moisture content of 12%. After drying the ears were manually shelled and random samples drawn from each entry and transferred to clean small sized seed envelopes and mailed to IITA, Ibadan, Nigeria for carotenoid analysis.

Determination of total Pro-Vitamin A Content

Total PVA content in µg/g of dry matter was calculated for each sample as the sum of β-carotene + 0.5 (β-cryptoxanthin) [5]. Since PVA values for the white materials were zero the PVA contents obtained were transformed as: PVA value obtained + 0.05 to enable analysis to be done.

Statistical Analysis

Data was entered using Microsoft Office Excel 2007 and analyzed using the GenStat software version 12.1 to obtain the combined analysis means for the various traits. The Statistical Package for Social Sciences (SPSS) version 16 was then used to calculate the Generation mean, standard errors and variances. The variances obtained were used manually to estimate the additive and dominance gene effects as follows:

Additive and Dominance gene effects were estimated according to methods by [33] as follows:

$VF2=\frac{1}{2}A+\frac{1}{4}D+E$……..Equation Eqn 1

where

VF2= Variance for the F2 generation and

A=the contribution to additive genetic variance

D=the contribution to dominance variance

E=Environmental effects

$VE=E=\frac{Vp1+Vp2+VF1}{3}$ and Vp1, Vp2, VF1 are variances for parent 1, parent 2 and the F1 generations respectively.

$V(BC1)+V(BC2)=\frac{1}{2}A+\frac{1}{2}D+2E$……Eqn 2

where

$V(BC1)=\frac{1}{4}A+\frac{1}{4}D+E$

$V(BC2)=\frac{1}{4}A+\frac{1}{4}D+E$ and

Equation 3 was derived from equation 1 by substituting the value for VF2 and also calculating E using values for Vp1, Vp2 and VF1.

Similarly equation 4 was derived from equation 2 and equations 3 and 4 were solved simultaneously to obtain A and D.

$X=\frac{1}{2}A+\frac{1}{2}D$…….Eqn 4

$X=\frac{1}{2}A+\frac{1}{4}D$…….Eqn 3

The broad-sense heritability (h^2b) was calculated as the ratio of VG to VP represented as $h^2b=VG/VP$ where VG= VA+VD and narrow sense heritability (h^2n) was calculated as the ratio of VA to VP represented by $h^2n=VA/VP$ where VP=VA+VD+VE.

Phenotypic coefficient of variation (PCV) was calculated as:

$$PCV\ (\%) = \frac{\sqrt{\delta^2 p}}{\bar{X}} \times 100$$

Genotypic coefficient of variation was calculated as:

$$GCV\ (\%) = \frac{\sqrt{\delta^2 g}}{\bar{X}} \times 100$$

Where δ^2p, phenotypic variance; δ^2g, genetic variance; $\bar{X}$, mean of a particular trait [48]. Genetic advance (GA) was calculated as: $GA=k\ \delta^2p\ h^2$ where; k = 2.06 at 5% selection intensity; δ^2p = Phenotypic standard deviation; h^2 =heritability in the broad-sense [39].

Genetic advance as percentage of the mean (GAM) was calculated as:

$$GAM\ (\%) = \frac{GA}{\bar{X}} \times 100$$ [48].

III. Results and Discussion

Tables 2-5 show the narrow-sense heritability, mean performance of traits, estimates of phenotypic variance, genetic variance, phenotypic coefficient of variation, genetic coefficient of variation, genetic advance and genetic advance as percentage of the mean ofpro-vitamin A contents, yield and other agronomic traits of PVA hybrids studied. Narrow-sense heritability values ranged from 6% in the varietal cross reciprocal to 145% in the top cross reciprocal for PVA contents. Narrow-sense heritability estimates in grain yield and days to mid-silk for all types of crosses were negative. Days to pollen shed was low in the top cross hybrid and but negative in its reciprocal and in the varietal cross hybrid and its reciprocal. ASI was also negative for all crosses with the exception of the top cross reciprocal which was medium. Ear and plant heights were also negative for all crosses with the exception of the top cross hybrid which was medium. Cob diameter was high to medium for all crosses while cob length was all negative with the exception of the varietal cross reciprocal which was high. Seed weight was high in all crosses with the exception of the varietal cross reciprocal which was negative. High heritability values obtained for the top cross and its reciprocal for PVA contents was in agreement with those obtained by [28]. High narrow-sense heritabilities obtained indicated that the PVA contents were mostly controlled by additive genes and were highly heritable. High heritability values obtained indicated that contribution of the genotype was higher than that of the environment in determining the phenotype[57], [19], [34], [23], [38] and synthetic breeding may be recommended [29], [46]. However, the narrow-sense heritability value > than 1 obtained in this study is in confirmation with observation by [38] that heritability can be overestimated if studies contrast non pro-vitamin A and high pro-vitamin A genotypes. The low narrow-sense heritability values observed in the varietal cross and its reciprocal for pro-vitamin A also suggested the importance of dominance effects as compared to additive effects [46] in controlling PVA contents in the varietal cross hybrids. Narrow-sense heritability is

considered to be of importance to breeding programs, because only additive genetic variability is carried on to the next generation [10]. Thus traits with high narrow-sense heritability values can be selected more quickly with less intensive evaluation than those with low narrow-sense heritability values and are therefore useful in making selection progress estimates in early selection generations [3].

The results from all the crosses depicted that phenotypic variances (σ^2p) and phenotypic coefficient of variation (PCV) were higher than genetic variances (σ^2g) and genotypic coefficient of variation (GCV) for all the characters studied suggesting some environmental influence on the characters studied [4], [56], [7], [43]. PCV was high for PVA contents, grain yield and anthesis-silking interval for all crosses studied and also high for ear height in the top cross hybrid. GCV was high for PVA contents for all crosses studied and also high for anthesis-silking interval in the top cross hybrid. GAM was high for PVA contents, cob diameter and seed weight in the top cross hybrid and also high for PVA contents, anthesis-silking interval and seed weight in the top cross reciprocal. The differences between GCV and PCV were very low for PVA content in all the crosses studied, implying that the environmental effects in the development of PVA content was low [4], [56], [7], [43]. High values of heritability, PCV, GCV and GAM obtained for PVA contents in the top cross hybrid showed that this trait was under the control of additive genes and effective selection could be possible for improvement in this trait using this type of cross [41], [40], [7], [4], [1]. However, low heritability with high PCV and GCV values for PVA contents and anthesis-silking interval coupled with low GAM for these traits in the varietal cross hybrid and its reciprocal showed that though this type of trait may be additive, the additive nature probably was masked by this type of cross and selection for this trait may not be effective and as such heterosis breeding or hybridization may be recommended [7], [35].

Negative heritability with high PCV and high GCV coupled with negative GAM for anthesis-silking interval in the top cross hybrid may indicate non-additive gene effects governing this trait with limited scope of improvement for this trait which is complex and is mostly influenced by environment [7]. This result is in disagreement with [7] who observed moderate heritability along with high genetic advance for anthesis-silking interval. Negative heritability with high PCV coupled with negative GAM for grain yield in all the crosses may also indicate non-additive genetic effects governing this trait in this particular study as the crosses were not selected for high grain yield per se. The results is also in disagreement with [41] and [7] who indicated more than 80% broad-sense heritability for grain yield with high values of PCV and GCV. Medium heritability with high PCV coupled with medium GAM in the ear height for the top cross hybrid may also be indicative of non-additive gene effect. Again the results is in disagreement with [41] and [7] who indicated high broad-sense heritability for ear height with high values of PCV and GCV [41] and [7]. Differences in these results could also have arisen probably because of differences in the genotypes used by these workers and those used in this present study.

PCV was medium for days to pollen shed, plant height and seed weight in the top cross hybrid and medium for days to pollen shed, days to mid-silk, ear height, plant height and seed weight in its reciprocal. PCV was also medium for ear height, plant height and seed weight in the varietal cross hybrid and also medium for ear height and plant height in its reciprocal. GCV was medium for only seed weight in the top cross hybrid, anthesis-silking interval in both the top cross hybrid and varietal cross hybrid. GAM was moderate for ear height and plant height in the top cross hybrid and seed weight in the varietal cross hybrid and cob diameter and cob length in the varietal cross reciprocal.

PCV was low in all crosses studied for cob diameter and cob length. PCV was also low for days to mid-silk in the top cross hybrid. PCV was low for days to pollen shed and days to mid-silk in the varietal cross and its reciprocal and was also low in the varietal cross reciprocal for cob diameter, cob length and seed weight. GCV was low for days to pollen shed, plant height and cob diameter in the top cross hybrid and also low for days to pollen shed, days to mid-silk and seed weight in its reciprocal. GCV was low for cob diameter in the varietal cross hybrid and again low for anthesis-silking interval, cob diameter and cob length in the varietal cross hybrid reciprocal. GAM was low for days to pollen shed in the top cross hybrid and also low for cob diameter in its reciprocal. GAM was low for PVA contents and cob diameter in the varietal cross hybrid. The results indicated differences in response regarding the traits and the various crosses. Generally, most of the traits studied had low and negative heritabilities with low GAMs in the various crosses indicating non-additive gene action for these traits with the type of genotypes and crosses used. There was considerable influence from the environment and improvements for these traits using these types of crosses may be done through hybridization or heterosis breeding [41], [7], [4] and particularly for PVA improvement, backcross breeding could be used where the level of heritability is not of much consequence to the expected progress except the actual trait under transfer [2].

No GCVs were observed for grain yield and ear height in all the crosses studied. There were no GCVs for plant height in all the crosses except the top cross hybrid. Also days to mid-silk, had no GCV in the top cross hybrid and no GCV for cob diameter in its reciprocal. There were no GCVs for cob length in all the crosses except the varietal cross reciprocal. There were no GCVs for days to pollen shed, days to mid-silk and seed weight in the varietal cross hybrid and its reciprocal. No GCVs were obtained for these traits in the various crosses because genotypic variances for these traits were negative [30], [43].

Negative GAMs were obtained in all crosses for grain yield and days to mid-silk. Negative GAMs were also obtained for anthesis-silking interval for all crosses except the top cross reciprocal. Negative GAMs were again obtained for days to pollen shed, ear height, plant height in

all the crosses except the top cross hybrid and similarly negative GAMs were obtained for cob length in all crosses except varietal cross reciprocal. Seed weight also had negative GAM values in the varietal cross hybrid reciprocal. Negative GAM values obtained was due to the fact that heritability values for these traits were negative [43].

Table 2. Mean performance of traits and estimates of phenotypic variance, genetic variance, environmental variance, heritability, phenotypic coefficient of variation, genetic coefficient of variation, environmental coefficient of variation, genetic advance and genetic advance as percentage of the mean ofpro-vitamin A contents, yield and other agronomic traits of top cross hybrid (Akposoe x ZM305).

Trait	Mean	δ^2p	δ^2g	δ^2e	h^2 (%)	PCV (%)	GCV (%)	GA	GAM
Pro-vitamin A contents	2.30	0.80	0.48	0.31	87.00	38.86	30.27	1.60	69.65
Grain yield	2420.00	698700.00	-224733.33	923433.33	-169.10	34.54	-	-2911.76	-120.32
Days to Pollen shed	48.00	30.79	2.89	27.90	3.80	11.56	3.54	0.43	0.90
Days to mid-silk	51.00	22.22	-2.30	24.52	-64.35	9.24	-	-6.25	-12.25
Anthesis-silking interval	3.00	1.72	0.94	0.78	-6.40	43.72	32.32	-0.17	-5.76
Ear height	74.50	280.22	-53.93	334.15	40.70	22.47	-	14.03	18.84
Plant height	160.00	742.50	97.26	645.24	44.30	17.03	6.16	24.87	15.54
Cob diameter	4.08	0.16	0.08	0.08	113.00	9.80	6.93	0.93	22.82
Cob length	12.60	1.07	-0.43	1.50	-77.60	8.21	-	-1.65	-13.12
Seed weight	290.00	1811.00	1292.16	518.84	118.00	14.67	12.40	103.44	35.67

δ^2p, phenotypic variance; δ^2g, genetic variance; δ^2e,environmental variance; h^2, narrow- sense heritability; PCV, phenotypic coefficient of variation; GCV, genotypic coefficient of variation; ECV,environmental coefficient of variation; GA, genetic advance; GAM, genetic advance as percentage of the mean

Table 3. Mean performance of traits and estimates of phenotypic variance, genetic variance, environmental variance, heritability, phenotypic coefficient of variation, genetic coefficient of variation, environmental coefficient of variation, genetic advance and genetic advance as percentage of the mean ofpro-vitamin A contents, yield and other agronomic Traits of Top cross hybrid reciprocal (ZM305 x Akposoe).

Trait	Mean	δ^2p	δ^2g	δ^2e	h^2 (%)	PCV (%)	GCV (%)	GA	GAM
Pro-vitamin A contents	2.29	1.68	1.38	0.30	145.00	56.63	51.25	3.87	169.17
Grain yield	2610.00	760500.00	-536266.67	1296766.67	-333.00	33.41	-	-5982.20	-229.20
Days to Pollen shed	48.00	32.70	5.66	27.04	-7.03	11.91	4.96	-0.83	-1.73
Days to mid-silk	51.00	29.41	5.37	24.04	-3.50	10.63	4.54	-0.39	-0.77
Anthesis-silking interval	3.00	1.13	0.13	1.00	35.40	35.43	12.02	0.78	25.84
Ear height	75.10	214.68	-60.95	275.63	-38.60	19.51	-	-11.65	-15.51
Plant height	159.00	502.28	-138.91	641.19	-30.40	14.10	-	-14.04	-8.83
Cob diameter	4.17	0.06	-0.03	0.09	33.30	5.87	-	0.17	4.03
Cob length	12.70	0.55	-1.17	1.72	-238.00	5.84	-	-3.64	-28.63
Seed weight	284.00	1265.00	413.38	851.62	112.00	12.52	7.16	82.06	28.89

δ^2p, phenotypic variance; δ^2g, genetic variance; δ^2e,environmental variance; h^2, narrow-sense heritability; PCV, phenotypic coefficient of variation; GCV, genotypic coefficient of variation; ECV, environmental coefficient of variation; GA, genetic advance; GAM, genetic advance as percentage of the mean.

Table 4. Mean performance of traits and estimates of phenotypic variance, genetic variance, environmental variance, heritability, phenotypic coefficient of variation, genetic coefficient of variation, environmental coefficient of variation, genetic advance and genetic advance as percentage of the mean ofpro-vitamin A contents, yield and other agronomic traits of varietal cross hybrid (Aburohemaa x Honampa)

Trait	Mean	δ^2p	δ^2g	δ^2e	h^2 (%)	PCV (%)	GCV (%)	GA	GAM
Pro-vitamin A contents	2.18	0.35	0.22	0.25	14.50	26.94	21.56	0.18	8.05
Grain yield	3480.00	1315000.00	-630666.67	1945666.67	-165.00	32.95	-	-3897.75	-112.00
Days to Pollen shed	51.00	22.27	-4.29	26.56	-30.53	9.25	-	-2.97	-5.82
Days to mid-silk	54.00	18.50	-2.83	21.33	-18.97	7.97	-	-1.68	-3.11
Anthesis-silking interval	3.00	1.27	0.31	0.96	-11.80	37.56	18.56	-0.27	-9.13
Ear height	92.50	203.20	-74.84	278.04	-79.80	15.41	-	-23.43	-25.33
Plant height	175.00	444.63	-145.49	590.12	-89.90	12.05	-	-39.05	-22.31
Cob diameter	4.28	0.12	0.06	0.06	45.00	8.09	5.58	0.32	7.50
Cob length	13.20	0.51	-0.30	0.78	-145.00	5.41	-	-2.13	-16.16
Seed weight	282.00	948.30	-72.62	1020.92	88.83	10.92	-	56.35	19.98

δ^2p, henotypic variance; δ^2g, genetic variance; δ^2e,environmental variance; h^2, narrow-sense heritability; PCV, phenotypic coefficient of variation; GCV, genotypic coefficient of variation; ECV, environmental coefficient of variation; GA, genetic advance; GAM, genetic advance as percentage of the mean.

Table 5. Mean performance of traits and estimates of phenotypic variance, genetic variance, environmental variance, heritability, phenotypic coefficient of variation, genetic coefficient of variation, environmental coefficient of variation, genetic advance and genetic advance as percentage of the mean ofpro-vitamin A contents, yield and other agronomic traits of varietalcross hybrid reciprocal (Honampa x Aburohemaa).

Trait	Mean	δ^2p	δ^2g	δ^2e	h^2 (%)	PCV (%)	GCV (%)	GA	GAM
Pro-vitamin A contents	1.97	0.56	0.40	0.16	6.42	38.02	32.13	0.10	5.03
Grain yield	3350.00	1095000.00	-817666.67	1912666.67	-247.00	31.24	-	-5324.41	-158.94
Days to Pollen shed	51.00	25.43	-4.94	30.37	-16.80	9.89	-	-1.75	-3.42
Days to mid-silk	54.00	19.31	-5.30	24.61	-26.00	8.14	-	-2.35	-4.36
Anthesis-silking interval	3.00	0.86	0.04	0.82	-32.60	30.91	6.67	-0.62	-20.76
Ear height	93.00	212.40	-88.30	300.70	-191.50	15.67	-	-57.49	-61.82
Plant height	176.00	528.96	-113.35	642.31	-133.00	13.07	-	-63.01	-35.80
Cob diameter	4.29	0.13	0.06	0.07	76.90	8.40	5.71	0.57	13.31
Cob length	13.20	1.05	0.26	0.79	80.00	7.76	3.86	1.69	12.79
Seed weight	290.00	522.62	-321.42	844.04	-56.59	7.88	-	-26.65	-9.19

δ^2p, phenotypic variance; δ^2g, genetic variance; δ^2e, environmental variance; h^2, narrow-sense heritability; PCV, phenotypic coefficient of variation; GCV, genotypic coefficient of variation; ECV, environmental coefficient of variation; GA, genetic advance; GAM, genetic advance as percentage of the mean.

VI. Conclusions

High narrow-sense heritability coupled with high values of PCV, GCV and GAM for PVA content in the top cross hybrid obtained from this study implied that this trait was mostly controlled by additive genes and was highly heritable. Thus, progress in selection for this trait could be achieved more quickly and synthetic breeding could be recommended.

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