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Genetic studies of M_3 mutants of Bambara groundnut (*Vigna subterranea*(L.) Verdc.) populations

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Abstract
The levels of genetic variability, heritability and genetic advance of twenty four agronomic and yield traits in M_3 mutants of Bambara groundnut were evaluated. Field experiments were conducted for three years (2018, 2019, 2020) in University of Nigeria, Nsukka, Nigeria using randomised complete block design (RCBD) with five replicates. Estimates of genetic variability components, broad-sense heritability and genetic advance were computed for each trait. Only petiole length and 100-seed weight showed significant genotypic differences while eleven traits showed no significant genotypic differences. Environmental variance was significant for plant height, number of leaves, terminal leaflet length, petiole length, internode length, number of pods per plant, number of seeds per plant, seed yield, 100-seed weight, number of nodes per stem, plant spread and terminal leaflet width. Phenotypic coefficients of variation were higher than the corresponding genotypic coefficients of variation for all the traits. Broad- sense heritability ranged from 14.3% for number of nodes per plant and 18.9% for petiole length. The genetic advance was high (25.3%) for yield, medium (21.3%) for number of pods and low for the other traits.

Key Words: *Broad-sense heritability, genotypic coefficient of variation, phenotypic coefficient of variation, genetic advance.*

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I. Introduction

The evaluation of available genetic diversity is a pre-requisite for genetic improvement in crops for example in Bambara groundnut (Olukolu *et al*., 2012). Bambara groundnut is an annual crop, which resembles groundnut (*Arachis hypogaea*) in both cultivation and habitat. It is one of the five most important protein sources for many Africans (Chittaranjan, 2007). Adu-Dapaah and Sangwan, (2004), reported that the seed is regarded as a completely balanced food because it is rich in iron 4.9-48 mg/100 g, compared to a range of 2.0-10.0 mg/100 g for most food legumes, protein 18.0-24.0% with high lysine and methionine contents, ash 3.0-5.0%, fat 5.0-7.0%, fibre 5.0-12.0%, potassium 1144-1935 mg/100 g, sodium 2.9-12.0 mg/100 g, calcium 95.8-99 mg/ 100 g, carbohydrate 51-70%, oil 6-12% and energy 367-414 kcal/100 mg. Bambara groundnut landraces have recognisable morphological features, such as seed testa colour, that can be used to identify them. Commonly, landraces have names based on the colour of the testa and the place where they are grown or from where they have been collected. Such informal methods of classification may lead to one landrace having more than a single name as a consequence of seed introductions to or from other places or the historical movement of people and their crops across the African continent without documentation. The most recent description by Massawe *et al*. (2005) defines a landrace as 'a variety with a high capacity to tolerate biotic and abiotic stress, resulting in high yield stability and an intermediate yield level under a low input agricultural system'. From the definitions given by other researchers (Zeven, 1998) and references therein), landraces can be described as a mixture of genotypes with highly diverse populations both between and within them. This is clearly the case with bambara groundnut landraces where growers either save their own seed for the next season or buy seed from the market and the mixing of seeds (of similar or different testa colour) results in a completely different population.

Mutation techniques have been used to derive many varieties of food crops including bambara groundnut. These methods have proved useful in obtaining new traits, creating genetic variability and supplementing conventional breeding (Sangsiri *et al*., 2005; Anbarasan *et al*., 2013). This genetic variability is what is required for crop improvement (Novak and Burnner, 1992; Aliero, 2006; Bolbhat *et al*., 2012) as

variability existing in all organisms including our crop plants which has been generated by mutation and subsequent recombination.

Ethyl methane sulphonate (EMS) is often used in chemical mutagenesis to produce random mutations by nucleotide substitution; that is point mutations. Although mutation induction with radiation causes large-scale damage such as DNA deletions and reduces viability, it remains the most frequent method for developing mutant cultivars, M_0 seeds are those to be treated with a mutagen, while the first generation after induced mutagenesis is termed M_1 and seeds from it and developing into plants are known as the M_2 generation. Mutant selection is the process to identify mutants with a target phenotype. It includes the screening and verification or confirmation of such putative mutants. Induced mutation may unmask novel alleles for further use in developing new cultivars (Mba, 2013). Ethyl methane sulphonate is considered very effective and its effectiveness has largely been demonstrated in cereal crops such as rice (Bhan and Kaul, 2003), wheat (Bozzini and Mugnozza, 2003), and barley (Nicoloff, 2003) as well as in *Arabidopsis thaliana* (Jacobs, 2005). Recently, this mutagen has also been used to treat seeds and in vitro propagules of many species (Latado, *et al.,* 2004; Luan *et al*., 2007; Basu *et al*., 2008). The objective of the present study was to induce mutations in *Caro* bambara groundnut on different concentration level 0.01%, 0.1%, 0.25%, 0.5% and durations 6hours, 12 hours, 24 hours.

II. Materials And Methods

Plant Establishment

Field evaluation involving mutant M_3 generation from ethyl methane sulphonate mutated Bambra groundnut were conducted in the 2020 cropping season at the research field of the Department of Crop Science, University of Nigeria Nsukka, Nigeria (Latitude 06^o 52`N; Longitude 07$^o$24`E, and altitude of 447.2 above sea level). Nsukka is in the derived savannah agro-ecological zone with vegetation predominantly of grass interspersed with trees. The Bambara groundnut landrace, *Caro* seeds were exposed to five doses of ethyl methane sulphonate (0, 0.01%, 0.1%, 0.25% and 0.5 %) and exposed to three soaking durations(6, 12, 24 hours). After each stipulated immersion period (6, 12 or 24 hours), the seeds were washed with distilled water five times and dried on a filter paper. The treated and untreated seeds were sown in nursery basket in a greenhouse, watered and maintained for optimal performance during the rainy season in 2018 to raise M_1 generation. Each M_1 plant was harvested separately and the seeds were sown in the next season in plant progeny rows, to raise M_2 generation in a randomized block design with three replications. The mutated and untreated (control) seeds were planted in the field to generate M_3 generation in 2020. Sowing was made in research field on a well tilled soil at spacing of 0.5mx1m in a Randomised Complete Block Design (RCBD) with three replications. Each treatment plot consisted of 5 rows of Bambara groundnut at a depth of 3-5cm, spaced 0.5m apart. Blocks containing replicates of treatments were separated by 1m. Manual weeding was done at 2 and 6 weeks after planting (WAP). Compost manure was applied before planting at the rate of 12.5tonns/ha. Insect control was done at 2 week-interval from 4WAP with foliar sprayer of KOMBAT 2.5EC of insecticide at 2ml liter^{-1} of water. Rodents were checked by watch in the field.

Data Analysis

Collected data were subjected to ANOVA for RCBD using GenStat Release 10.3 Discovery Edition (PC/Windows; VSN International, Hemel Hempstead, Hertfordshire, UK). Means were used to calculate genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV), genotypic variance, phenotypic variance, environmental variances, coefficient of variation (CV), and genetic advance to show variability among genotypes.

Genotypic Coefficient of Variation (GCV)

$$GCV = \sqrt{\frac{\sigma^2 g}{\times}} \times 100$$

Phenotypic coefficient of Variation (PCV)

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

Where $\sigma^2 g$ =genotypic variance, $\sigma^2 p$=phenotypic variance and x=grand mean for the trait.

The GCV and PCV were considered low when less than 10%, moderate when 10 to 20% and high when greater than 20% as explained by Deshmukh *et al*.,(1986). Genotypic and Environmental variances were tested against error variance for significant.

Broad-sense heritability and standard errors were estimated by Johnson *et al*, (1955) and Hallauer et al,(2010) using the following equations:

$h^2\% = \frac{\sigma^2 g}{\sigma^2 g + \sigma^2 e}$ x 100 Where σ^2g = genotypic variance, σ^2 = environmental variance,

$\sigma^2 p = \text{phenotypic variance} = \sigma^2 g + \sigma^2 ge$, e = number of environments and SE = standard error. Heritability estimates were categorized into low (less than 40%), medium (40-50%), moderately high (60-79) and very high (80% and above) as described by Singh (2001)

Genetic advance (GA) was estimated using the formula by Singh and Chaudhary (2004)

GA = iσp h^2

Where i = 1.40 (Selection intensity at 20%), σp = phenotypic standard deviation of the mean performance of treated populations, h^2 = heritability (broad –sense).

Genetic advance expressed as percentage of the mean was estimated as described by Souza *et al.*(2009) as follows:

GA (%) = $\frac{GA}{\overline{X}}X100$

Where $\overline{x}$ = grand mean of all mutants for the trait.

GA == Genetic advance

GA was categorised into low (less than 10%), moderate (10-20%) and high (above20%) according to Johnson *et al*., (1955)

Table1: Growth and yield characters used in the analysis and methods of measurement.

S/No	character	Description of measurement according to IPGRI BAMNET(2000)
1	Days to emergence	Counted as number of days from sowing to the day half of the seedlings has emerged.
2	Days to first flowering	Obtained as number of days from sowing to first flower production.
3	Days to 50% Flowering	Obtained as number of days from sowing to the day half of the plants flowered.
4	Plant height	Obtained using a measuring tape from the base to the tip of the terminal leaflet.
5	Peduncle length	Measured with a ruler from the stalk to the point of attachment of the flower.
6	Number of flowers per plant	By counting at two weeks after first flowering.
7	Number of leaves	By counting at two weeks after first flowering
8	Terminal leaflet length	Measured with ruler from the point of attachment to the tip of the leaflet.
9	Terminal leaflet width	Measured with ruler from one point to another across the leaflet.
10	Petiole length	Measured with ruler from the base of a plant to area of attachment of the leaf.
11	Plant spread	Measured with ruler the widest length between two opposite points.
12	Internode length	Measured with ruler the length of fourth internode
13	Number of nodes per plant	By counting at harvest
14	Number of stems per plant	By counting at harvest
15	Number of days to maturity	By counting from the day of sowing to the day of maturity.
16	Number of branches per stem	By counting at harvest
17	Pod length	Measured within two months after harvest from down to top.
18	Pod width	Measured in cm within two months after harvest from one point to another across the pod.
19	Seed length	Measured with ruler within two months after harvest.
20	Seed width	Measured with ruler within two months after harvest.
21	Number of pods/ plant	By counting within two months after harvest
22	Number of seeds/ plant	By counting within two months after harvest
23	Seed yield/plant	Collected within two months after harvest. Weighed in grams.
24	100-seed weight	100-seed weight collected within two months after harvest. Weighed in grams.

III. Results

Table 2: Mean values of selected M_3 growth and yield characters over concentration rates

Concs of EMS	Demegc	DFF	D50%F	PTHT	Ped lengt	NFPP	NL	TLL	TLWIDT	PEL	PS	INTE L	NNPP	NSPP	NDPM	NBPP	POD L	PODWIDT	SL	SWIDT	NPPP	NSEEDPP	YIELD	100-seed
0	7.40	38.00	49.60	1.82	1.2	1.20	39.40	8.56	4.50	19.06	23.34	2.64	4.80	10.00	104.0	17.20	3.10	2.02	1.72	1.04	41.4	46.2	28.8	42.3
0.01	7.20	38.00	50.00	1.76	1.15	1.40	39.80	7.84	4.12	18.96	24.10	2.54	6.60	11.40	104.0	19.80	3.14	2.06	1.72	1.06	46.0	50.2	32.6	55.8
0.1	7.20	38.00	50.00	1.84	1.98	1.60	49.20	7.80	3.92	17.32	21.52	2.84	6.20	11.00	104.0	20.40	2.98	2.04	1.80	1.14	60.4	76.0	46.8	51.9
0.25	7.40	38.00	50.00	1.78	1.59	1.20	46.40	8.52	3.96	16.00	20.62	2.70	6.20	10.80	106.0	20.20	3.20	2.04	1.76	1.06	47.4	53.6	34.8	52.1
0.5	7.20	38.00	50.00	1.80	1.23	1.20	50.40	7.86	4.86	20.08	21.72	2.84	6.00	11.00	106.0	19.60	2.94	2.06	1.72	1.06	93.0	106.4	76.4	78.9
LSD	0.68	ns	0.53	1.47	0.17	0.39	4.28	0.54	0.57	1.11	2.18	0.15	1.09	1.33	7.76	2.42	0.42	0.07	0.15	0.08	17.1	25.14	16.71	56.2

Conc = concentration, Demegc = days to emergence, DFF= days to first flowering, D50%F = days to 50% flowering, PTHT = plant height, Ped lengt = peduncle length, NFPP = number of flowers per plant, NL = number of leaves, TLL = terminal leaflet length, TLWIDT = terminal leaflet weight, PEL = petiole length, PS = plant spread, INTE L = internodes length, NNPP = number of nodes per plant, NSPP = number of stems per plant, NDPM = number of days to maturity, NBPS = number of branches per plant, POD L = pod length,SL = seed length, SWIDT = seed width, NPPP = number of pods per plant, NSEEDPP = number of seeds per plant, YIELD =seed yield.

The mean of growth and yield characters for M_3 mutants are shown in Table 2. The mean performance of the concentrations indicated that 0.01% concentration caused the highest mean value for PS, NNPP, NSPP while 0.25% concentration caused highest mean value for POD L. Concentration 0.1% resulted to the maximum mean value for Ped length, SL, SWDT and NBPP. Concentration 0.5% caused the maximum mean value for NL, TLWIDT, PEL, NPPP, NSEEDPP, YIELD and 100-seed. Concentration 0.5% with NDPM recorded the highest mean value. Concentration 0.5% caused the highest seed yield while control recorded lowest seed yield. The mean 100-seed had maximum value with the support of concentration 0.5% of EMS treatment. Days to first flowering had no significant ($p > 0.05$)effect.

Table 3: Mean performance, standard deviation, range and coefficient of variation for selected agronomic and yield traits of bambara groundnut evaluated in Nsukka.

Traits	Mean±SE	SD	Range	CV (%)
Internode length	2.7± 0.0	0.2	2.54-2.84	10.7
Number of leaves	45.0±2.0	11.5	39.40-50.40	25.6
Number of nodes per plant	5.9±0.5	1.5	4.80-6.60	25.6
Number of pods per plant	57.6±8.0	46.9	41.4-93	81.4
Number of seeds per plant	66.5±11.8	56.1	46.2-106.4	84.5
Petiole length	18.2±0.5	3.6	16.0-20.0	19.7
Plant height	27.1±0.6	2.5	25.40-28.20	9.3
Plant spread	22.2±1.0	3.1	20.62-24.10	14.2
Terminal leaflet length	8.1±0.2	0.8	7.80-8.56	10.6
Terminal leaflet width	4.2±0.2	0.8	3.92-4.86	20.9
Seed yield	43.9±7.8	43.3	28.8-76.4	98.7
100-seed weight	56.2±3.5	30.5	42.3-78.9	54.2

SE =Standard error, SD= standard deviation, CV= coefficient of variation.

Mean performance of populations

The populations evaluated showed a wide range in values for the twelve traits assessed (Table3). The ranges for the twelve traits were 2.54 to 46.2. The least range value was for internodes while highest range value 46.2 was for number of seeds. There was significant variation for all the studied traits which also revealed possible amount of variability among the landrace (Table 3). All traits showed larger estimate of variation coefficients except for plant height (Table3). Seed yield had the largest estimate of variation coefficients. The mean performance of the parameter indicates that the number of seeds had the maximum mean value while internodes had the least mean value.

Table 4: Estimates of genetic parameters of 24 selected agronomic and yield traits of Bambara groundnut populations in Nsukka

Trait	σ^2g±SE	σ^2e ±SE	σ^2p	GCV	PCV	H^2%	GA%
Internode length	0.01±0.08	0.06±0.16	0.08	4.37	10.72	16.66	2.50
Number of leaves	24.75±3.14	109.19±6.60	133.94	11.04	25.69	18.47	6.64

Number of nodes per plant	0.33±0.36	2.005±0.89	2.34	9.71	25.66	14.31	5.14
Number of pods per plant	407.9±12.77	1794.6±26.89	2202.5	35.06	81.47	18.51	21.12
Number of seeds per plant	561.3±14.98	2596.78±32.22	3158.1	35.62	84.50	17.77	21.02
Petiole length	2.46±0.99	10.56±2.05	13.03	8.59	19.75	18.94	5.23
Plant height	1.05±0.65	5.43±1.47	6.49	3.78	9.37	16.26	2.13
Plant spread	1.48 ±0.77	8.61±1.85	10.10	5.47	14.27	14.72	2.94
Terminal leaflet length	0.11±0.21	0.63±0.50	0.75	4.22	10.68	15.60	2.33
Terminal leaflet width	0.12±0.22	0.67±0.52	0.80	8.23	20.97	15.41	4.52
Seed yield	344.74±11.74	1534.26±24.77	1879.0	42.29	98.74	18.34	25.36
100-seed weight	180.05±8.48	751.08±17.33	931.13	19.57	54.29	19.34	14.69

SE= Standard error, $\sigma^2 g$ = genotypic variance, $\sigma^2 e$ = environmental variance, $\sigma^2 p$ = phenotypic variance, GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, H^2 = broad-sense heritability, GA = genetic advance

Estimates of variance components, heritability and genetic advance

Genotypic variance($\sigma^2 g$) and environmental variance($\sigma^2 e$) were significant for petiole length,100-seed and plant height per plant, number of leaves per plant, terminal leaflet length, terminal leaflet width, petiole length, plant spread, internodes length, number of nodes per stem, number of pods per plant, number of seeds per plant, seed yield, 100-seed weight respectively (Table 4).The estimates of genotypic variances were lower than the corresponding environmental variances for all traits. The observed differences among the mutants for most of the traits were therefore more due to environmental than genetic causes. The PCV estimates in this study were higher than the corresponding GCV for all the traits. The PCV and GCV were high for number of leaves, number of pods per plant, number of seeds per plant, seed yield and 100-seed whereas only PCV was high for number of nodes per stem, petiole length, plant spread, terminal leaflet length and terminal leaflet width. The GCV for number of leaves, 100-seed weight and PCV for internodes length, petiole, terminal leaflet length, plant spread and terminal leaflet width were moderate respectively. All other traits manifested low GCV and PCV values. The range in values of GCV and PCV were 4. 22 terminal leaflet lengths to 42.29 yield and 9.37 plant height to 98.74 seed yield respectively (Table 4).

Heritability refers to the ratio of the total variation of phenotypic traits in each population between the individuals due to genetic variation. It has been emphasized that without genetic advance, the heritability values would not be of practical importance in selection based on phenotypic appearance. So, genetic advance should be considered along with heritability in coherent selection breeding program. Estimates of broad-sense heritability ranged from14.3% for number of nodes to19.3% for 100-seed weight. The heritability estimates were low for all the traits (Table 4). Genetic advance expressed as a percentage of the mean ranged from 2.50 for internodes and 25.36 for yield.

The estimates of all other variables were low GA, 100-seed showed moderate while number of pods, number of seeds and seed yield showed high GA (Table 4). Low heritability with low genetic advance values was found for all traits except for number of pods, number of seeds and seed yield GA. This indicates slow progress through selection for traits. The reasons for the low heritability for these traits are as a result of some variances constituting the environmental variance.

IV. Discussion

Mean square from Anova revealed highly significant difference ($P<0.01$) among the characters measured indicating the presence of substantial variability among the concentrations and this is similar to the findings reported by Rao *et al.(*1976, 1998); Maestri *et al*.(1998) and Danshiel (1993) in soyabean. The maximum days to first flowering was observed at all level of the concentrations. It may be due to the inhibition effect of both the mutagens on floral hormones and the same was observed in control and the same type of results were also observed previously in sesame by Menash *et al*. (2007), in cowpea, Pavadai and Dhanavel (2004), in Mungbean by Khan and Wani (2005) and Bhendi (Sasi *et al*., 2005). The mean of the total number of leaves had maximum on plant supported with 0.5%concentration of EMS treatment. Similar results were also observed in soybean (Balakrishnan, 1991; Geetha, 1994; Padmavathi *et al*., 1992 Cheng and Chandlee, 1999; Pavadai and Dhanavel l994 & 1995; Pavadai 1996) which recorded total number of leaves maximum at 0.5%concentration. Similar observations were made in other plants like black gram (Deepalakshmi and Anandakumar, 2004 and Arulbalachandran, 2006). The mean of the yield had maximum value at 0.5% concentration. Similar results were observed by Dhole *et al*., 2003; Pavadai and Dhanavel, 2004 and 2005; Pavadai, 2006) in soybean.

There was significant variation for all the studied traits which also revealed possible amount of variability among landrace. This indicates that a sufficient range of variability in all the traits exists among the populations. The presence of variability could be a consequence of the differences in the ability of the mutagen concentration involved in the development of *caro* bambara groundnut populations to improve the population

(Butron *et al*., 2008; Entringer *et al*., 2017) as well as a reflection of the influence of environment on the expression of the traits.

The estimates of phenotypic variance were greater in extent as compared with their corresponding genotypic variance and environmental variance for most of characters evaluated. This agrees with Tanimu and Aliyu (1997) and Tanimu *et al*. (1990) in Bambara groundnut.

In this study, the choice of selection method specified for the improvement of yield in bambara groundnut was based on the measure of the amount of variation that exists in the gene pool of the crop, estimates of heritability and genetic advance. This is in line with the report of previous studies on heritability, which observed that the selection made for the improvement of a character is not only dependent on available genetic variation but also on the extent of heritability of such variations (Umar *et al*., 2014; Langat *et al*., 2019). Further, the estimates of heritability together with genetic advance provide profound advantage over the use of heritability alone (Shukla *et al*., 2006; Asfaw *et al*., 2017).

The extent of variation coefficients might indicate that mutants and progenies had exploitable genetic variability for yield characters under investigation. However, these results partially coincided with earlier findings of Riaz and Chwodhry (2003); this is perhaps due to differences in mutating material or variation in environment or interaction.

The slightly higher PCV than GCV for traits in this study indicate that the expressions of the traits were influenced, though to a limited extent, by the environment and there is the possibility of improvement using phenotypic selection. Therefore, selection for the improvement of any of these characters should be delayed until genetic influence improves either through hybridization, selection and backcross. The result of this study is in line with the reports of other workers (Ashok *et al*., 2000; Uguru 2000; Adebola *et al*., 2001). Similar results indicating higher PCV than GCV for traits were reported by 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. The PCV for all the traits were more than twice the GCV, an indication of limited chance for selection for the traits in the populations studied. Also the estimates of phenotypic coefficient of variation for data were greater in magnitude as compared with their corresponding genotypic coefficient of variation for most characters evaluated. Similar results were reported by Agbo and Obi (2005), Vanaja and Luckins (2006), Uguru (1995), Adebisi *et al.,* (2004), Kadams and Sajo (1998). The high GCV exhibited by number of pods, number of seeds and seed yield shows that the traits are less affected by environmental fluctuations, which guarantees selection progress for the traits. High GCV estimates are indicative of low amenability of traits to environmental changes (Hefny, 2011). Emphasis on number of pods, number of seeds and seed yield are therefore necessary in the development of mutant from the present genetic materials. Typically, characters with reasonable variation offers a wide range of opportunity for selection for their improvement (Fakuta *et al*., 2014), On the other hand, characters that recorded low GCV and PCV values showed low variability among the bambara groundnut lines. They cannot be effectively used to discriminate among the collections, and again offer little or no opportunity for selection for crop improvement. Almost all the agronomic characters evaluated in this study had low heritability alongside with low genetic advance values. However, this is contrary to (Nwakuche *et al*., 2019) who reported high heritability with high genetic advance. The reasons for the low heritability for these traits are as a result of some variances constituting the environmental variance. Collaku (1994) reported in wheat study that low heritability is as a result of drought stress. Similarly, it was resulted that heritability for yield traits in faba bean was higher in well-watered treatment than drought stress condition (Link *et al*., 1998; Toker, 2004). Johnson *et al*., (1955) classified heritability estimates as low for 0 to 30%, moderate for values from 30 to 60%, and high for values above 60%.

The GA expressed as a percentage of the most mean accompanying these estimates were recorded low. The 100-seeds were recorded moderate. Number of pods, number of seeds and seed yield were high. This suggests that genetic control of the traits was predominantly non-additive which could be exploited through heterosis breeding. Further explanation by Sardana Sardana *et al*.(2007) suggested that high heritability may not necessarily lead to increased genetic gain, unless sufficient genetic variability existed in the germplasm. Johnson *et al*. (1955) and Jilo *et al*. (2018) on sweet corn had previously suggested the simultaneous consideration of heritability estimates and GA because high heritability may not always be associated with high GA. These traits may respond to phenotypic selection (Bello *et al*., 2012; Nzuve et al. 2014) on sweet Corn. Number of pods, number of seeds and seed yield manifested high PCV suggesting a strong influence of environment on its expression.

V. Conclusion

The slightly higher PCV than GCV for traits in this study indicate that the expressions of the traits were influenced, though to a limited extent, by the environment and there is the possibility of improvement using phenotypic selection. Therefore, selection for the improvement of any of these characters should be delayed until genetic influence improves either through hybridization, selection and backcross.

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