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Genetic Analysis of Morpho-metric Traits and Correlations of Yield Parameters in Soybean (*Glycine max* L. Merr)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Top crosses comprising 2 testers and 8 lines were made in the screen house using Line × Tester model. Observations were made on days to flowering, pod maturity, harvest, pods per plant, branching pattern, seeds per pod, 100 seed weight and yield/ha; crude protein, crude fiber, carbohydrate, moisture, ash and oil, as well as trypsin, tannins and phytate. Data collected were subjected to Analysis of Variance and the means separated using Duncan Multiple Range Test (DMRT), at 5% probability level. Genetic component analysis was carried out on the traits using Analysis of Genetic Design (AGD-R) package, to determine heritability, General Combining Ability (GCA) and Specific Combining Abilities (SCA). Results of the study revealed that, positive GCA values were recorded by TGM954 (0.01), TGM120 (0.07), TGM553 (0.70), TGM555 (0.58), TGM574 (0.19), TGM584 (0.14) and TGX1904-6F (0.12) for 100 seed weight; TGM954 (76.83) and TGM584 (12.54) for seed yield. Generally, TGM954 was a better general combiner than TGM951, because it combined well with other varieties for yield and yield-related traits. High heritability estimates were recorded for 100 seed weight (84.10%), number of branches (86.61%), days to flowering (91.69%), pods per pod (88.48%) and seed yield (86.07%). It can be concluded, that, crosses using Line × Tester model is encouraged for trait transfer and enhancement of soybean seed yield.

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Keywords: Correlations; crosses; line by testers; yield; antinutritional factors.

1. INTRODUCTION

"Soybean has many nutritional benefits, for man, livestock, as well as other industrial and commercial uses. It is classified as an oilseed, containing significant amounts of all the essential amino acids, minerals and vitamins for human nutrition. It is therefore an important source of human dietary protein with an average of 40% content, 30% carbohydrate and oil content of 20%" [1]. "Soybean contains some anti-nutritional substances that reduce the nutritional value of the beans and are dangerous to health and therefore, need to be removed before they can be consumed" [2]. "These bioactive compounds, with toxic antinutritional properties can alter the body metabolism of consumers and exert a negative impact on the nutritional quality of the seed protein" [3]. "Prominent among the antinutritional factors found in soybean are trypsin inhibitors (protease inhibitors), tannins and phytic acid" [4]. "In soybean, stigma is receptive to pollen approximately 24 hours before anthesis and remains receptive 48 hours after anthesis. The anthers mature in the bud and directly pollinate the stigma of the same flower. As such, soybeans exhibit a high percentage of self-fertilization and cross pollination is conversely, usually less than one percent" [2]. A soybean plant can produce as much as 400 pods, with two to twenty pods at a single node. Each pod may contain one to five seeds. Being a short day plant, soybean flowers more quickly under short days. Number of pods and seeds per pod are the most important yield components of soybean.

"Knowledge of diversity patterns will allow breeders to better understand the evolutionary relationships among accessions, to sample germplasm in a more systematic fashion and to develop strategies in incorporating useful diversity in their breeding programs" [5]. "Among the different kinds of usefulness, hybridization is the most widely and commonly used technique in most of the crop species including soybean. For creating desirable variability, parents should be carefully selected and some biometrical tools can be used" [6]. "Breeding strategies need to exploit existing variation within germplasm to broaden the genetic base of currently used cultivars" [7]. [8] indicated that "the estimations of genetic distance might help in identifying suitable germplasm for introgression into breeding stocks. Knowledge of genetic diversity in a crop species is fundamental in its improvement".

"Collection of germplasm and assessment of genetic variability is a basic step in any crop improvement program. Yield, being a complex character, is influenced by a number of yield contributing characters controlled by polygenes and also influenced by environment" [8]. "So, the variability in the collections for these characters is the sum total of heredity effects of concerned genes and influence of the environment. Hence, it becomes necessary to partition the observed variability into heritable and non-heritable components measured as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance expressed as per cent mean. Breeders can make number of crosses among inbred parents to determine type of gene actions and also proportions of genetic variances attributable to additive and dominant genes for various plant characters" [9].

"Good combining ability confers on the parent ability to produce superior progeny when combined with another parent" [10], "while the general combining ability (GCA) provides an evaluation of the degree of mainly additive gene action and specific combining ability (SCA) refers to the performance of two particular lines in a specific cross, thus reflecting non-additive types of gene interaction" [11]. "General and specific combining abilities effects are meaningful biometrical techniques which aid in framing the breeding scheme for any crop, particularly when the intension is to produce a hybrid of choice. Earlier studies led to the selection of inbred with high GCA, predominance of non-additive gene action for major yield components and oil contents. It has been proved experimentally that parental lines with high GCA produce higher yielding hybrids than lines with low GCA in sunflower" [12,13]. "Mating design in plant breeding (in theory and practice) refers to the procedure of producing progenies with both vigour performance and stability traits, with subsequent effect on yield. The right choice of mating design in any breeding programme is very important because it helps to provide information on the gene actions affecting the traits under investigation to generate the breeding population to be used as a basis for the selection and development of potential varieties. It is expected that such choice will enhance the chances of estimation of genetic gains and also

provide necessary information for evaluating the parents used in the breeding programme" [14,15].

"The line by tester mating design involves hybridization between wide-based lines (M) and testers (F) in a one by one crossing method, thereby generating F x M = FM hybrids" [16]. "It is the simplest mating design that provides both full-sibs and half-sibs simultaneously. It provides specific combining ability (SCA) of each cross, while providing the GCA of lines and the testers also, because the line and tester are different sets of genotypes" [16]. "Wherein, assessment of improvement in quantitative characters is usually based on progeny/floating performance" [17].

"Combining ability or productivity of crosses is the combination of potential lines concerning the transmission of desirable genes to their offspring. The aptitude of combination between two parents has been classified into general combining ability, defined as the average performance of a line in a series of crosses, and specific combining ability is referred to as performance of inbred parents in specific combination" [18,19]. introduced "line x tester analysis method estimating the combining ability effects useful in selecting desirable parents and crosses for interpretation the pedigree".

"Information on the combining ability status of the genotypes will give an indication as to how well they will combine with a given genotype to produce productive populations. In this direction, the concept of general (GCA) and specific combining ability (SCA)" [18,20] helps the breeder to decide upon the choice of parents for hybridization and to isolate promising genotypes from the segregating population and also gives vital information on gene action, which helps in understanding the nature of inheritance of the characters. The research work is designed to assess prominent antinutritional factors present in selected Soybean genotypes, undertake hybridization among the best performing soybean genotypes for yield improvement and antinutritional factors reduction and develop low ANF soybean genotypes from screen house crosses

2. MATERIALS AND METHODS

2.1 Experimental Site

Crosses between the selected best performer soybean varieties, was conducted during the 2018 planting season (between June and November), in the Screen house facility and field demonstration plots, at the Teaching and Research Farms of the Federal University Wukari, Taraba State, Nigeria. Wukari lies at latitude $7^0$52'17.00^{0}N and longitude $9^0$46'40.30E, with an average annual rainfall of 1058mm-1300mm and relative humidity dropping to about 15%, alongside annual temperature of 28^0C and 30^0C, Situated in guinea savannah of North-eastern Nigeria.

2.2 Collection of Planting Materials

Seeds of the ten soybean varieties used were obtained from the previous season's harvest, through the process of selection. Selection was based on yield, earliness to maturity, seed coat colour, resistance to shattering, antinutritional factor content and pest-disease incidence/ tolerance. There were 8 varieties (TGM111, TGM120, TGM553, TGM555, TGM574, TGM577, TGM584 and TGX1904-6F) designated as lines (subsequently referred to as females), while 2 other varieties (TGM951 and TGM954) were designated as testers (subsequently referred to as males). Crosses were made to produce 16 F_1 hybrids, following the line × tester mating design developed by Kempthorne (1957), during the 2018 planting season. The 16 hybrids and 10 parents were subsequently evaluated in the field during the 2019 planting season, using the Randomized Complete Block Design (RCBD), with three replications.

2.3 Experimental Design

The screen house experiment was set up on raised platforms inside the screen house. Seeds of selected parents (at two seeds/hole) were sown into average-sized black polythene bags (filled with rich top soil), arranged in a Randomized Block Design (RBD). Thinning into one plant per bag was carried out at 2WAP. Bags were placed at 40cm×60cm intra row and inter row spacing, to create sufficient space that would enhance convenience at the point of pollination. Required cultural practices such as regular watering and removal of weeds were performed in due course, as contained in the IITA handbook of Soybean production. For assessment of morphometric traits and yield of hybrids, the 16 hybrids and 10 parents arising from the Line × Tetser crosses in the previous season were grown in the field during the 2019 planting season. The experimental field was laid out in Randomized Complete Block Design

(RCBD), with three replications, for each of the 26 soybean genotypes. Beds of dimensions 2×5m were horizontally aligned, with 50cm distance between beds, 1m demarcation between replications and 2m border row across the length and breadth of the experimental field. At the experimental site, planting distance of 50cm intra-row and 75cm inter-row spacing was used, thus there were 35 soybean plant stands per bed. Thus, the dimension of each of the experimental fields was 96m×26m (2,496m^2) and the total number of soybean plant stands per field was 5,180. Soybean seeds were sown directly into the raised bed, by placing seeds inside the shallow holes of about 2cm depth and covered with soil.

2.4 Artificial Pollination of Soybean

Recommended procedures for artificial hybridization of soybean were applied to flower buds of designated female parents at about one to two days before regular opening of the flowers. Hand-held microscope (magnifying lens) was used to prepare flowers of female parents. Sepals, petals and the ring of anthers were removed by thin forceps. Whenever an anther could be detected precociously releasing pollen to the stigma, the respective flower was discarded. Flowers of male parents containing mature anthers were collected at full bloom and whole flowers were used to pollinate a female stigma after removal of the corolla. Pollination was done immediately after emasculation in the early hours of the day. Only one to two flower buds per raceme were used for hybridization. All manipulations were carried out with the naked eyes. Two to three weeks after pollination, all additional flowers and flower buds except those crossed were removed. At maturity, the tagged pods from crosses were identified by their lack of sepals and dry seeds were harvested.

2.5 Data Collection

A minimum of five plants (exempting the border plants), were randomly selected and tagged from each variety and each of the replications for the purpose of data collection. Observations were made on various characters following the descriptors of the Biodiversity International. Also, in order to determine the General Combining Ability (GCA) and Specific Combining Ability (SCA) of the crossed varieties and the progenies (hybrid seeds) obtained, data were collected on the following traits;

Seed coat and hilum colour: The seed coat and hilum colour were observed under the broad day light and classified into different colour groups, using the standard colour chart.

Seed shape: The seed shape was determined through visual observation and classified into standard shape forms such as spherical, ovoid or elongated and so on.

Seed coat texture and luster: Seed coat texture and luster were determined through observation under the natural broad day light and hand feel.

Seed biometric characters: The seed length (cm) and seed width (cm) were measured, using the vennier caliper.

100 seed weight: The weight [in grams (g)] of 100 seeds was taken, using sensitive electrical balance/scale.

Plant growth habit: At the maturity stage, the nature of plant stem, height of the plant and life form was determined as erect, semi-erect or horizontal.

Plant height: At full maturity, prior to harvesting, the plant height was measured as the length of the plant from the base of the plant, just above the soil surface to the tip of the main stem. It was expressed in Centimeters (cm).

Plant pubescence: The plant stem was carefully observed under the broad day light, at physiological maturity to confirm the presence or absence of pubescence, by hand feeling.

Total number of primary branches per plant: The total number of primary branches was determined by counting the number of branches on the main stem of the selected soybean plant, just before harvesting.

Total number of secondary branches per plant: The total number of secondary branches was determined by counting the number of branches that emanate from the primary branches of the selected plant, just before harvesting.

Leaf shape: The leaf shape was determined by visual observation and grouped into triangular, pointed ovate, rounded ovate, or lanceolate.

Leaf colour: The leaf colour was determined through visual observation, in a broad day light, at about 50% flowering stage and classified as dark green, light green, or green.

Days to flowering: The date at which selected plants reached flowering was recorded and expressed as the number of days to flowering.

Flower colour: The flower colour was determined through careful observation under a broad day light and the observed pigmentation was compared with the standard colour chart for confirmation.

Flower form: The flower form description was through careful observation of the flowers at full bloom and classification was based on full-formation or malformation.

Pubescence on pod: At maturity, pods were assessed to determine the presence or otherwise of pubescence on them.

Pod colour: Colour of the matured soybean pods was visually observed under the broad day light and the observed colour was compared with the standard colour chart, to determine the pod colour.

Pod shattering attribute: After ten days of attainment of pod physiological maturity, shattering was observed in the different varieties and scored as shattering tolerant (ST) or shattering susceptible (SS).

Number of pods per plant: At the attainment of physiological maturity, the total number of pods borne on individual plant was counted and averaged.

Pod length: At harvesting, the pod length was measured (in cm), using the measuring tape.

Number of seeds per pod: After harvesting**,** the total number of soybean seeds obtainable from each pod of a particular plant was counted and averaged.

Days to physiological maturity of pods: This was estimated as the number of days between the emergence and expression of signs of physiological maturity by the pods, that is, taking on of brown colour by pods for example.

Days to harvest: This was estimated as the number of days between the emergence of seedling and when the pods turn from green to slightly brown/golden colour, with corresponding reduction in moisture content of the pod.

Seed yield (kg/ha): After harvesting, total seed obtained from each of the experimental plots was weighed and converted into kg/ha using the expression below;

$$Seed\ yield\ (kg/ha) = \frac{Seed\ yield\ obtained\ (kg)}{Plot\ size} x\ 10000$$

Analysis and Quantification of Anti-nutritional Factors Content

The determination, analysis and quantification of the antinutritional factors in the different soybean varieties used for the purpose of this research work was carried out by the following procedures;

Analysis of trypsin inhibitor, (Prokopet and Unlenbruck, 2002)
Materials: Grinder/blender, conical flasks, Centrifuge and Spectrophotometer
Reagents: Trypsin inhibitor standards, Sodium Chloride (NaCl)

Procedure:

1. 1g of dry well blended dried soybean sample was weighed into a flask
2. 50ml of 0.5M NaCl was added to the blended sample
3. The solution thus obtained was then stirred for 30 minutes and centrifuged at 1500rpm for 5 minutes
4. The solution was thereafter decanted and the filtrate kept. 10ml of filtrate was pipette and put into another flask
5. Next, 2ml of standard trypsin solution of known concentration (2mg/l) was added to the 10ml filtrate
6. Absorbance was measured at 410nm using 10ml of same substrate (the sample filtrate) as blank
7. Also prepare 1mg, 2mg, 4mg, 6mg, 8mg, and 10mg/l standard trypsin inhibitor were also prepared and their absorbencies measured at 410nm.
8. A standard graph of absorbance against concentration was then plotted
9. Extrapolation was achieved by tracing the absorbance of the sample down the

concentration axis to obtain the trypsin inhibitor concentration of the sample

Calculation:

$$\text{Trypsin inhibitor content (mg/kg)} = \frac{\text{Conc. obtained in mg/l x volume of sample x DF}}{\text{Sample weight}}$$

DF: Dilution factor. If not diluted, then DF = 1

Analysis of tannin, using the Folin Ceocalteu Method

Materials: Blender, Conical flasks, Centrifuge

Reagents: Folin Ceocalteous reagent, Na_2CO_3 (saturated), Tannic acid standard

Procedure:

1. 1g of dry well blended soybean sample was weighed into a conical flask
2. 10ml of distilled water was then added, the mixture agitated and left for 30 minutes at room temperature
3. The mixture was centrifuged at 2500rpm for 15min
4. 2ml of supernatant was measured into a 10ml volumetric flask and 1ml of folin-ceocalteu reagent was added to it
5. Then 2ml of saturated $Na2CO_3$ solution was added to the mixture and the solution was diluted to 10ml with distilled water
6. The solution was then incubated for 30min at room temperature

2.6 Preparation of Standard Tannic Acid

7. The procedure 1 to 6 was repeated for tannic acid standards 20, 40, 60, 80, 100, 120mg/l from a stock of 500ppm (50mg of Tannic acid standard dissolved in 100ml of distilled water) excluding centrifugation (procedure 3)
8. Absorbance of the above Tannic acid concentrations was read off at a wavelength of 725nm and a calibration curve for the tannic acid standards was drawn. That is, absorbance against concentration
9. Extrapolation was done by tracing the absorbance of the sample down the concentration axis to obtain the tannic acid concentration of the sample

Calculation:

$$\text{Tannic Acid content (mg/kg)} = \frac{\text{Conc. obtained in mg/l x volume of sample x DF}}{\text{Sample weight}}$$

DF: Dilution factor. If not diluted, then DF = 1

Determination of phytate (phytic acid), following the Eskin's methologies.

Materials: Conical flask, Filter paper, Pipette, Beaker and Titrating apparatus

Reagents: Hydrochloric acid (HCl), Ammonium thiocyanate and Iron iii chloride ($FeCl_{3)}$

Procedure:

1. 2g of dry finely ground sample of soybean was weighed into a 250ml conical flask
2. 100ml of 2% concentrated HCl was added and allowed to soak for 3 hours and then filtered
3. 50ml of the filtrate was pipette into a 250ml beaker and 107ml of distilled water was added to improve acidity
4. 10ml of 0.3% ammonium thiocyanate solution was added as indicator
5. Titration with standard iron iii chloride ($FeCl_3$) solution which contain 0.00195g iron/ml until a brownish yellow colour appear and persist for 5min
6. The phytic acid content was calculated as shown below:

$$Phytic\ acid\ g/kg = \frac{0.00195\ x\ volume\ of\ FeCl3\ consumed\ x\ DF}{Sample\ wt}$$

DF: Total volume of extraction solvent added/volume of aliquot taken for the titration

*****Determination and analyses of the ANFs were carried out at the Precision Laboratory, Ibadan, Nigeria

Determination of mineral element composition using methods of Association of Analytical Chemists.

Moisture content:

One gram of sample in pre-weighed crucible was placed in an oven (at 105^0C) for 24 hours, allowed to cool and then re-weighed. The percentage moisture was thus calculated as follows;

$$Moisture\ content\ (\%) = \frac{W_{2-W_3}}{W_{2-W_1}} \times 100$$

Where: W_1 is the weight of the crucible

W_2 is the weight of the crucible after drying at 105^0C and sample and

W_3 is the weight of the crucible and the sample after cooling in airtight desicators

2.7 Determination of Ash Content

Two grams of sample was added into a pre-weighed crucible and incinerated in muffle furnace at 600^0C, with the value calculated as follows;

$$\text{Ash content (\%)} = \frac{W_2 - W_3}{W_2 - W_1} \times 100$$

Where: W_1 is the weight of cleaned, dried, ignited and cooled crucible

W_2 is the weight of the crucible and sample after incinerating at 600^0C and

W_3 is the weight of the crucible and the sample after cooling in airtight homogenized vessel

2.8 Fat and Oil Content

The fat and oil content was estimated using Tecatoy Soxtec (Model 2043[20430001]; Hilleroed, Denmark). A quantity of 1.5g sample mixed with 2.3g anhydrous sulfate was weighed into a thimble and covered with absorbent cotton, while 40ml of petroleum ether (40 – 60^0C Bpt) was added to a pre-weighed cup. Both thimble and cup were attached to the Extraction Unit. The sample was extracted using ethanol for 30 minutes and rinsed for 90 minutes. Thereafter, the solvent was evaporated from the cup to the condensing column. Extracted fat in the cup was then placed in an oven at 105^0C for 1 hour, allowed to cool and weighed. Percentage Fat/oil was then calculated as;

$$\text{Lipid} = \frac{\text{Initial cup weight} - \text{Final cup weight}}{\text{Weight of sample}} \times 100$$

2.9 Crude Protein

The crude protein content was determined using the micro-Kjeldahl method, as described by Pearson (1976). A volume of 10mL H_2SO_4 added to 3g of sample was digested with a digestor (model Bauchi 430) for 90 minutes. A volume of 40mL water was added and distilled using a Kjeldahl distillation Unit (model unit B – 316) containing 40% concentrated sodium hydroxide and Millipore water. Liberated ammonia was collected in 20mL boric acid with bromocresol green and methyl red indicators and titrated against 0.04N H_2SO_4. A blank (without sample) was likewise prepared. Percentage protein was thus calculated as;

$$\text{Crude protein (\%)} = \frac{\text{Sample titer} - \text{blank titer} \times 14 \times 6.25}{\text{Sample weight}} \times 100$$

Where: 14 is the molecular weight of nitrogen and 6.25 is the nitrogen factor

2.10 Crude Fiber Content

A weighed crucible containing 1g of defatted sample was attached to the extraction unit (in Kjeldahl, D-40599; Behr Labor-Technik GmbH, Dusseldorf, Germany) and into this 150mL of hot 1.25% H_2SO_4 was added and digested for 30 minutes, then the acid was drained and sample washed with hot distilled water for 90 minutes. The crucible was removed and oven-dried overnight at 105^0C, allowed to cool down, weighed and incinerated at 550^0C in a muffle furnace (MF-1-02; PCSIR Labs, Lahore, Pakistan) overnight and reweighed after cooling. Percentage extracted fiber was thus calculated as;

$$\text{Crude fiber (\%)} = \frac{\text{Weight of digested sample} - \text{Weight of ashed sample}}{\text{Weight of sample}} \times 100$$

2.11 Carbohydrate Content

The carbohydrate content was determined by the difference, that is, addition of all the percentages of moisture, fat, crude protein, ash and crude fiber was subtracted from 100%. This gave the amount of nitrogen free extract otherwise known as carbohydrate. The value is calculated as; Carbohydrate (%) = 100 – (%moisture + %Fat + %Ash + %crude fiber + %crude protein).

2.12 Statistical Analysis

The experimental data were statistically analyzed with the SPSS (23^{rd} edition) statistical package, using the randomized complete block design (RCBD), at 5% probability level and mean separated using the Duncan Multiple Range Test (DMRT). Genetic component analysis was carried out on the traits using Analysis of Genetic Design (AGD-R), by International Maize and Wheat Improvement Center-CIMMYT, 2012 package.

3. RESULTS

3.1 Mean, Estimate of Variance Components, Heritability and Genetic Advance

The mean, estimates of Genotypic Variance (σ^2g), Phenotypic Variance (σ^2p), Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), Broad Sense Heritability (H_B) and Genetic Advance as a percentage of Mean (GAM) are presented in Table 1. The genetic variance ranged from 0.04, for number of days to emergence to 23956.76, for seed yield per hectare, while values for the phenotypic variance varied from 0.004 to 27834.22, for seed width and seed yield per hectare respectively. The GCV values were within the range of 3.12, for number of days to emergence to 41.99, for seed yield per hectare. Meanwhile, PCV ranged from 4.68 to 45.26, for number of days to harvesting and seed yield per hectare respectively.

Plant height at maturity, number of pods per plant, primary branches, number of seeds per plant and seed yield per hectare recorded high GCV. Conversely, moderate GCV were observed for 100 seed weight, seed width and inter-node distance, while low values were recorded for days to emergence, pod length, number of days to flowering, number of seeds per pod, days to pod maturity and days to harvest. High PVC values were recorded for plant height at maturity, number of pods per plant, number of primary branches, number of seeds per plant and seed yield per hectare. Also, medium PCV values were observed for 100 seed weight, pod length, number of days to flowering, number of seeds per pod, seed width and inter-node distance. Low PCV values were recorded for number of days to emergence, number of days to maturity and number of days to harvest.

In most cases PCV was observed to be relatively higher than GCV for all traits measured but close for number of days to flowering, number of days to pod maturity and number of days to harvest (indicating the high contribution of genotypic effect for expression of such traits). In other measured traits (e.g. days to emergence, number of pods per plant, number of seeds per plant inter-node distance and seed yield per hectare), there were wider differences in the estimates of PCV and GCV, which is an indication of the contribution of environmental factors in addition to genotypic effects for expression of the traits.

Values recorded for broad sense heritability ranged from 35.04%, for number of days to emergence to 96.36%, for number of days to pod maturity. The heritability estimate for number of days to emergence is low, at 35.04, also the value recorded for inter-node distance is medium, at 74.81%, while heritability values for all other traits studied were very high. The genetic advance as a percentage of mean for the traits measured ranged from 6.45% to 86.49% for number of days to emergence and seed yield per hectare respectively.

3.2 Mean Performance of Selected Traits of Soybean Parents and Hybrids

The mean performance of eight lines and two testers used as parents in the line × tester crosses (Tables 2 and 3) showed that single parental genotypes exhibited superiority over the testcross hybrids with respect to certain traits. That is, mean values of the hybrids were within the mean value range of the parents. Highest values for 100 seed weight (12.63g), number of pods per plant (184.50), number of seeds per pod (2.93) and number of seeds per plant (491.23) were recorded for TGM553, TGM954, TGM951 and TGM954 respectively. TGM954 × TGM584 (hybrid) recorded the highest value for seed yield per hectare (845.08kg/ha), indicating yield superiority over any of the single parents. However, there existed significant differences in all the measured values.

Also, single parental genotypes recorded the least values for ANF (Tannins, Trypsin and Phytate) contents, relative to the values obtained from their hybrid counterparts. From the table, TGM951 recorded a significantly lower value for Tannins (580.13g/kg), while there was no significant difference in the values obtained for Trypsin and Phytate, in both single parental genotypes and the hybrids.

Line × Tester analysis, estimate of general combining ability, specific combining ability and variance components.

Table 1. Mean and estimate of variance components and genetic advance of soybean varieties

TRAIT	MEAN	δ_g^2	δ_p^2	δ_e^2	GCV (%)	PCV (%)	H_b (%)	GAM (%)
Days to emergence	6.17	0.04	0.11	0.04	3.12	5.29	34.04	6.45
100 seed weight (g)	10.53	1.17	1.39	0.22	10.25	11.18	84.10	21.09
Plant height at maturity (cm)	56.34	118.16	128.60	10.45	20.38	21.26	91.88	41.98
Pods per plant	110.63	1966.68	2222.66	255.98	40.09	42.62	88.48	82.58
Primary branches	3.05	0.50	0.58	0.08	23.22	24.96	86.61	47.84
Pod length (cm)	3.41	0.11	0.13	0.02	9.76	10.62	84.41	20.11
Days to flowering	36.40	12.74	13.89	1.16	9.81	10.24	91.69	20.20
Seeds/pod	2.45	0.05	0.06	0.01	9.13	10.13	81.30	18.82
Seeds/plant	232.58	9116.54	10343.01	1226.26	41.05	43.73	88.14	84.57
Days to pod maturity	87.51	22.18	23.02	0.84	5.38	5.48	96.36	11.09
Days to harvesting	100.77	20.93	22.23	1.30	4.54	4.68	94.17	9.35
Seed width (cm)	0.40	0.03	0.05	0.05	13.61	14.71	85.71	28.04
Internode distance (cm)	3.42	0.33	0.44	0.11	16.76	19.38	74.81	34.54
Seed yield (kg/ha)	368.65	23956.76	27834.22	3877.47	41.99	45.26	86.07	86.49

δ_g^2 = Genotypic variance, δ_p^2 = Phenotypic variance, δ_e^2 = Error variance, GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, H_b = broad sense heritability, GA = genetic advance and GAM = genetic advance as a percentage of mean

Table 2. Mean performance of selected traits in soybean parents

Variety/Traits	100Swt (g)	P/Plant	S/Pod	S/plant	S.yield (kg/ha)	Tannins (g/kg)	Trypsin (g/kg)	Phytate (g/kg)
TGM951	9.42^{efg}	119.32^{abcde}	2.93^{a}	333.45^{abcd}	468.85^{cdefg}	580.13^{d}	439.29^{ab}	41.29^{ab}
TGM954	10.67^{bcdef}	184.50^{a}	2.81^{ab}	491.23^{a}	793.50^{ab}	629.87^{cd}	410.50^{b}	42.79^{a}
Mean (Testers)	**10.05**	**151.91**	**2.87**	**412.34**	**631.18**	**605**	**424.90**	**42.04**
TGM111	10.10^{cdefg}	87.38^{a}	2.51abcd	189.64^{cd}	288.06^{efg}	656.31^{cd}	668.75^{ab}	38.24^{abc}
TGM120	10.75^{bcdef}	119.73^{abcde}	2.70^{abc}	254.00^{bcd}	418.50^{efg}	587.50^{d}	694.61^{a}	28.40^{e}
TGM553	12.63^{a}	88.06^{cde}	2.37^{bcde}	178.16^{cd}	336.75^{efg}	799.02^{abc}	538.18^{ab}	28.47^{de}
TGM555	12.28^{ab}	76.78^{de}	2.50^{abcd}	174.85^{cd}	329.10^{efg}	610.29^{cd}	669.23^{ab}	35.06^{abcde}
TGM574	11.10^{abcde}	79.00^{de}	2.14^{de}	156.11^{d}	247.24^{fg}	688.97^{cd}	631.48^{ab}	36.03^{abcde}
TGM577	8.75^{g}	68.10^{e}	2.52^{abcd}	145.31^{d}	191.26^{g}	841.53^{ab}	608.04^{ab}	33.13^{abcde}
TGM584	10.88^{bcde}	158.23^{ab}	2.09^{e}	343.70^{abcd}	560.08^{abcde}	939.81^{a}	457.08^{ab}	39.94^{abc}
TGX1904-6F	10.88^{bcde}	72.31^{de}	2.33^{cde}	181.87^{cd}	312.69^{efg}	581.73^{d}	538.89^{ab}	33.75^{abcde}
Mean (Lines)	**10.92**	**93.70**	**2.40**	**202.96**	**335.46**	**713.15**	**600.78**	**34.13**

Means within each column followed by the same alphabet are not significantly different from one another based on the 0.05 probability level of LSD

Table 3. Mean performance for selected traits in soybean hybrids of line × tester crosses

Variety/Traits	100Swt (g)	P/Plant	S/Pod	S/plant	S.yield (kg/ha)	Tannins (g/kg)	Trypsin (g/kg)	Phytate (g/kg)
TGM951×TGM111	9.76^{defg}	103.35^{bcde}	2.72^{abc}	261.54^{bcd}	378.45^{efg}	618.22^{cd}	554.02^{ab}	35.06^{abcde}
TGM951×TGM120	10.09^{cdefg}	119.53^{abcde}	2.81^{ab}	293.73^{bcd}	443.68d^{efg}	583.82^{d}	566.95^{ab}	30.14^{cde}
TGM951×TGM553	11.03^{bcde}	103.70^{bcde}	2.65^{abc}	255.81^{bcd}	402.80^{efg}	595.21^{cd}	554.26^{ab}	33.47^{abcde}
TGM951×TGM555	10.85^{bcde}	98.05^{bcde}	2.71^{abc}	254.15^{bcd}	398.97^{efg}	595.21^{cd}	554.26^{ab}	33.47^{abcde}
TGM951×TGM574	10.27^{cdefg}	99.16^{bcde}	2.53^{abcd}	244.78^{bcd}	358.05^{efg}	635.55^{cd}	535.38^{ab}	33.95^{abcde}
TGM951×TGM577	9.09^{fg}	93.71^{bcde}	2.72^{abc}	239.38^{bcd}	330.05^{efg}	710.83^{cd}	523.67^{ab}	37.96^{abcde}
TGM951×TGM584	10.15^{cdefg}	138.78^{abcd}	2.51^{abc}	338.58^{abcd}	758.21^{abc}	759.97^{abcd}	448.19^{ab}	35.91^{abcde}
TGM951×TGX1904-6F	10.15^{cdefg}	95.82^{bcde}	2.63^{abc}	257.66^{bcd}	390.77^{efg}	580.93^{d}	489.09^{ab}	32.82^{bcde}
TGM954×TGM111	10.39^{cdefg}	135.94^{abcd}	2.66^{abc}	340.43^{abcd}	540.78b^{cdef}	643.06^{bcd}	539.87^{ab}	40.51^{ab}
TGM954×TGM120	10.71^{bcdef}	152.11^{abc}	2.75^{abc}	372.61^{abc}	729.00^{abcd}	608.66^{cd}	552.56^{ab}	35.60^{abcde}
TGM954×TGM553	11.65^{abc}	136.28^{abcd}	2.59^{abc}	334.69^{abcd}	565.13^{abcde}	714.42^{bcd}	474.34^{ab}	35.63^{abcde}
TGM954×TGM555	11.48^{abcd}	130.64^{abcde}	2.66^{abc}	333.04^{abcd}	540.78^{abcde}	620.05^{cd}	539.87^{ab}	38.93^{abc}
TGM954×TGM574	10.89^{bcde}	131.75^{abcde}	2.47b^{cde}	323.67^{abcd}	520.37^{bcdef}	659.39^{cd}	520.99^{ab}	39.41^{abc}
TGM954×TGM577	9.71^{efg}	126.30^{abcde}	2.66^{abc}	318.27^{abcd}	492.38^{cdefg}	735.67^{bcd}	509.27^{ab}	37.96^{abcde}
TGM954×TGM584	10.78^{bcdef}	171.36^{a}	2.45b^{cde}	417.46^{ab}	845.08^{a}	784.81^{abcd}	433.79^{ab}	41.37^{ab}
TGM954×TGX1904-6F	10.78^{bcdef}	128.41^{abcde}	2.57^{abc}	336.55^{abcd}	553.10^{abcdef}	605.77^{cd}	489.09^{ab}	38.27^{abcd}
Mean (Line × Tester)	**10.49**	**122.81**	**2.63**	**307.65**	**515.48**	**653.22**	**517.85**	**36.28**
Grand Mean	**10.59**	**116.09**	**2.58**	**283.49**	**468.99**	**667.95**	**536.22**	**36.06**

Means within each column followed by the same alphabet are not significantly different from one another based on the 0.05 probability level of DMRT

Table 4. Line × Tester analysis

Source of variation	Mean Square							
	DF	100Swt (g)	NoP/P	S/pod	S/Plant	Seed yield (kg/ha)	Tannin (g/kg)	Trypsin (g/kg)	Phytate (g/kg)
Genotype	25	4.16**	5027.47**	0.18**	35576.81*	173677.60**	17637.52*	11021.24*	28.71*
Lines	1	0.76*	2006.86*	0.02^{ns}	16874.17^{ns}	57859.58*	822.70**	276.29*	39.68*
Testers	7	5.82*	3730.23*	0.17*	17118.80*	50706.46**	35052.75**	13572.40**	34.61**
Line × Tester	7	3.55**	4006.26^{ns}	0.07^{ns}	21265.02^{ns}	184118.94**	9006.40^{ns}	3565.52^{ns}	20.52^{ns}
Error	14	1.46	2139.46	0.09	19260.47	46641.60	7165.56	12304.46	16.46

*** = Significant at 0.01 probability level, * = Significant at 0.05 probability level, ns = not significant, 100Swt = 100 seed weight, NoP/P = Number of pods per plant and S/Pod = Number of seeds per plant*

Table 5. Estimate of general combining ability (GCA) effects

Genotype	100 Swt	Pod/Plant	Seed/pod	Seed/plant	Seed yield	Tannins	Trypsin	Phytate
TESTERS								
TGM951	-0.10	0.36	0.09	1.23	-1.93	-0.94	-0.64	-0.15
TGM954	0.01	7.63	0.06	5.74	76.83	-0.07	-0.27	0.17
LINES								
TGM111	-0.14	-3.20	-0.01	2.88	-28.43	-0.14	0.83	0.12
TGM120	0.07	0.41	0.01	-1.04	-8.78	-0.87	1.00	-0.30
TGM553	0.70	-3.12	-0.01	-3.21	-21.10	1.38	-0.01	-0.29
TGM555	0.58	-4.38	-0.01	-3.30	-22.25	-0.62	0.84	-0.01
TGM574	0.19	-4.13	-0.03	-3.84	-34.58	0.21	0.60	0.029
TGM577	-0.59	-5.35	-0.01	-4.14	-43.01	1.83	0.44	-0.09
TGM584	0.12	4.70	-0.03	1.52	12.54	2.87	-0.53	0.20
TGX1904-6F	0.12	-4.88	-0.02	-3.10	-24.72	-0.93	-0.01	-0.07
Grand mean	10.53	116.06	2.60	290.38	476.82	667.91	535.66	35.49
Standard error	0.47	10.14	0.09	15.18	65.72	9.58	5.64	0.73

Table 6. Estimates of specific combining ability (SCA) effects

Genotype	100 S. wt	Pod/Plant	Seed/pod	Seed/plant	Seed yield	Tannins	Trypsin	Phytate
TGM951×TGM111	-0.26	-0.82	0.02	-18.46	-27.49	-0.20	1.33	0.16
TGM951×TGM120	-0.05	0.15	0.06	5.73	-0.37	-0.40	1.79	0.12
TGM951×TGM553	0.11	-0.60	0.06	-15.02	-21.43	-0.03	1.33	0.01
TGM951×TGM555	-0.01	-0.57	0.01	-13.15	-19.42	-0.33	1.34	0.01
TGM951×TGM574	-0.09	-0.47	-0.02	-12.84	-20.8	-0.11	0.66	0.11
TGM951×TGM577	-0.47	-0.52	0.01	-13.31	-24.82	0.33	0.24	0.13
TGM951×TGM584	-0.16	-0.11	-0.01	1.33	24.32	0.61	-2.46	0.08
TGM951×TGX1904-6F	-0.42	-0.89	-0.01	-17.24	-27.64	-0.41	-1.00	0.19
TGM954×TGM111	0.06	0.18	-0.01	3.27	2.75	-0.06	0.81	0.09
TGM954×TGM120	0.27	1.16	0.01	27.45	29.86	-0.25	1.27	0.09
TGM954×TGM553	0.43	0.41	-0.01	6.57	8.81	0.35	-1.52	--0.21
TGM954×TGM555	0.30	0.44	0.01	8.58	10.81	-0.19	0.82	-0.21
TGM954×TGM574	0.38	0.11	-0.02	1.25	2.59	0.04	0.15	-0.01
TGM954×TGM577	-0.15	0.49	0.01	8.42	5.42	0.47	-0.27	0.02
TGM954×TGM584	0.16	0.90	-0.01	23.06	54.91	0.75	-2.97	-0.07
TGM954×TGX1904-6F	-0.11	0.12	-0.01	4.49	2.59	-0.27	-1.51	0.14
Grand Mean	10.40	122.76	2.66	318.84	528.21	653.16	516.93	35.94
Standard Error	0.41	3.90	0.02	26.44	59.22	5.01	7.65	0.62

3.3 100 Seed Weight (g)

All traits were significant for genotypes except for number of seeds per pod and seeds per plant, while other traits were significant for testers. Similarly, line × tester was significant for all traits, except number of pods per plant, seeds per pod and Tannin. Highly significant mean squares were recorded for 100 seed weight among crosses due to line effect, tester effect and their interaction (Table 4). Highest GCA value (Table 5) was observed in parental line TGM553 (0.70), while the least value was recorded for line TGM577 (-0.59). TGM954, TGM120, TGM553, TGM555, TGM574, TGM584 and TGX1904-6F are good combiners for100 seed weight, because they had positive GCA values. SCA was positive for TGM951×TGM111, TGM951× TGM120, TGM951× TGM553, TGM951× TGM555, TGM951× TGM574, TGM951× TGM577, TGM951× TGX1904-6F, TGM954× TGM553, TGM954× TGM555, TGM954× TGM574, TGM954× TGM577 and TGM954× TGX1904-6F hybrids, indicating that they are good combiners for the trait (Table 6).

3.4 Number of Pods per Plant

As presented in Table 4, mean square was only significant in line effect and tester effect for number of pods per plant but, was negative for their line × tester effect. Also, value for GCA was highest in tester TGM954 (7.63) and line TGM577 recorded the least value (-5.35). With positive GCA values (Table 6), parents TGM951, TGM954, TGM120 and TGM5847 would be good combiners, useful for the developing new varieties. With the exception of TGM954× TGM120, TGM954× TGM555, TGM954× TGM574, TGM954× TGM577 and TGM954× TGM584, other hybrids recorded positive SCA values (Table 6), revealing their ability as good specific combiners.

3.5 Number of Seeds per Pod

Mean square values for number of seeds per pod were significant in genotype effect and tester effect (Table 5), while the line effect and line × tester effect showed no significant difference. With parent lines and tester TGM951, TGM954 and TGM120 exhibiting potential of good general combiners (Table 6), the highest GCA value (0.09) was recorded by TGM951 and TGM584, the lowest (-0.03). TGM951×TGM111, TGM951× TGM120, TGM951× TGM553, TGM951× TGM555, TGM951× TGM577, TGM954× TGM120, TGM954× TGM555 and TGM954× TGM577, bearing positive values (Table 6) were good specific combiners that could be used in soybean improvement programmes to develop new hybrids.

3.6 Number of Seeds per Plant

Calculation of mean square values (Table 5) was highly significant in genotype effect and tester effect for number of seeds per plant but, showed no significant difference for line effect and line × tester effect. TGM954 scored the highest (5.74) GCA value, and the lowest value (-4.14) was recorded by TGM577 (Table 6). TGM951, TGM954, TGM111 and TGN584 had positive values and are regarded as good general combiners. From Table 6, it could be seen that TGM951× TGM120, TGM951× TGM584, TGM954× TGM111, TGM954× TGM120, TGM954× TGM553, TGM954× TGM555, TGM954× TGM574, TGM954× TGM577, TGM954× TGM584 and TGM954×TGX1904-6F recorded positive SCA values (Table 6), thus could be valuable in the development of new varieties. However, the highest value (27.45) was recorded by TGM954×TGM120, while TGM951×TGM553 had the least value (-15.02).

3.7 Seed Yield (kg/ha)

Highly significant (at 1% probability level) mean square was observed for crosses due to line effect, while it was relatively significant (at $P \leq 0.005$) for genotype effect, tester effect and line × tester effect (Table 4). Only TGM954 (76.8286) and TGM584 (12.54) recorded positive GCA values, with the former having the highest value (Table 4). This is indicative of their ability as good general combiner for seed yield. Meanwhile, the lowest value for the same trait (-43.01) was observed in TGM577. In Table 6, the highest SCA value was recorded for TGM954 × TGM584 (54.9045), while TGM951 × TGX1904-6F recorded the least value (-27.64). However, TGM951 × TGM584, TGM954 × TGM111, TGM954 × TGM120, TGM954 × TGM553, TGM954 × TGM555, TGM954 × TGM574, TGM954 × TGM577, TGM954 × TGM584 and TGM954 × TGX1904-6F recorded positive values and are, as such, regarded as good specific combiners.

3.8 Tannins (g/kg)

The mean square values obtained for Tannins were only significant for genotype effect, line

effect and tester effect, while it was insignificant for the line × tester effect (Table 4) for Tannin content. TGM584 recorded the highest GCA value of 2.8663 and the lowest value (-0.94) was observed in TGM951. Only four varieties (i.e. TGM553, TGM574, TGM577 and TGM584) were found to bear positive values, portraying them to be general good combiners for the trait under study (Table 6). TGM951 × TGM577, TGM951 × TGM584, TGM954 × TGM553, TGM954 × TGM574, TGM954 × TGM577 and TGM954 × TGM584 recorded positive SCA values, conferring on them the ability of good specific combiner for the trait. Highest SCA value (0.75), however, was recorded for hybrid TGM954 × TGM584, while TGM951 × TGX1904-6F has the least value (-0.41).

3.9 Trypsin (g/kg)

Highly significant mean squares were recorded for genotype effect and line effect, while the tester effect was only significant at the 5% probability level for Trypsin content. However, the obtained mean square value was not significant for line × tester effect (Table 4). In Table 6, the highest (1.00) and lowest (-0.64) SCA values were observed for TGM120 and TGM951 respectively. Besides, TGM111, TGM120, TGM555, TGM574 and TGM577 recorded positive GCA values. TGM951 × TGM111, TGM951 × TGM120, TGM951 × TGM553, TGM951 × TGM555, TGM951 × TGM574, TGM951 × TGM577, TGM954 × TGM111, TGM951 × TGM120, TGM951 × TGM555 and TGM951 × TGM577 recorded positive SCA values, and could be regarded as good specific combiner for trypsin. Trypsin content (Table 6), 1.7876 being the highest SCA value was recorded for TGM951 × TGM120, while the lowest (-2.46) was observed in TGM951 × TGM584.

3.10 Phytate (g/kg)

In Table 5, highly significant mean square values were estimated for genotype effect and line effect for phytate content. However, the value was relatively significant (5%) for tester effect, while it was not for the line × tester effect. TGM584 scored the highest GCA value (0.20), while the lowest value (-0.30) was observed for TGM120. TGM954, TGM111, TGM574 and TGM584 recorded positive GCA values are could be said to be good general combiners for the trait . TGM951 × TGM111, TGM951 × TGM120, TGM951 × TGM553, TGM951 × TGM555, TGM951 × TGM574, TGM951 × TGM577, TGM951 × TGM584, TGM951 × TGX1904-6F, TGM954 × TGM111, TGM954 × TGM120, TGM954 × TGM577 and TGM954 × TGX1904-6F recorded positive SCA values (Table 6), revealing them to be specific good combiners for the trait and that could be explored for improvement programmes, targeted at developing new varieties. However, the highest SCA value (0.19) was recorded by TGM951 × TGX1904-6F and the least value (-0.21) was recorded by TGM954 × TGM553.

4. DISCUSSION AND CONCLUSION

“Estimates of heritability values are useful in predicting the expected progress to be achieved through the process of selection. Heritability values greater than 80% are regarded as very high, values between 60% and 79% are classified as moderately high, while values between 40% and 59% are regarded as medium and values less than 40% are low” [21]. “Traits with very high heritability estimates reflect a relatively little influence or contribution of the environmental factors to its phenotype and selection for such traits could be made easy, due to high additive effect. High estimates of broad sense heritability was also reported in other crops for height, stem diameter, days to flowering, days to harvest, fruit length and fruit” [22-24].

“The knowledge of heritability and genetic advance is imperative, because heritability alone does not indicate the amount of improvement that would result from selection. Genetic advance (GA) under selection refers to the improvement of traits in genotypic values, for the new population, compared with the base population, under a single cycle of selection, at specific selection intensity” [21]. “As such, genetic advance is important in predicting the expected genetic gain from one cycle of selection” [25]. Estimates of genetic advance for seed yield per hectare recorded the highest value, at 318.847kg, indicating that when a 5% high yielding genotype is selected, the mean seed yield per hectare could be improved greatly. That is, the mean genotypic value of the new population for seed yield per hectare will be improved from the initial 368.645kg to 687.492kg. Likewise, the number of seeds per plant will be improved from 323.584 to 429.272 and number of pods per plant will improve from 110.627 from the base population to 201.981.

GAM values are categorized as high when greater than 20%, moderate when the estimated value is between 10% - 20% and low when it is below 10% [26]. As such, the GAM values for number of days to emergence and number of days to harvesting were considered to be low, number of seeds per pod and number of days to pod maturity as moderate, while GAM estimates for other traits measured are regarded as very high. According to [10], "high heritability estimate coupled with high genetic advance as a percentage of mean is considered more useful over heritability alone, in predicting gain under selection".

"High heritability estimate along with high genetic advance as percentage of mean are recorded for 100 seed weight, plant height at maturity, number of pods per plant, number of primary branches, pod length, number of days to flowering, number of seeds per pod, seed width, inter-node distance and seed yield per hectare, indicating the presence of additive gene action, for the expression of these traits, which are transferrable to next generations. Thus, it is ideal to base selection in the next population on these traits". [10] also reported high heritability coupled with high genetic advance for yield per plant in bell pepper.

For traits such as number of seeds per pod and number of days to pod maturity; having high heritability values with moderate values for genetic advance as percentage of mean, the estimates suggest that improvement of these traits could yield benefits. This also reveals the greater role of non-additive gene action in their pattern of inheritance. It was also reported by [24], "that plant height and days to flowering traits exhibited high heritability and moderate genetic advance in cultivated plants".

"When GCV and PCV values are greater than 20%, they are regarded as high, while values between 10% and 20% are classified as medium and values less than 10% are considered to be low" [10,27]. "High GCV and PVC values recorded by plant height at maturity, pod per plant, primary branches, number of seeds per plant and seed yield per hectare indicate the existence of substantial variability for such traits, upon which selection for improvement can be based. Similar findings were earlier reported in pepper fruits, fruit weight, fruit length, fruit girth and yield per plant" [16]. "It also agrees with report on days to flowering and days to maturity in pepper, by" [27,16].

"The genotypic coefficient of variation provides information on the genetic variability present in quantitative characters in a population but, it is not possible to determine the amount of the variation that was heritable solely from the genotypic coefficient of variation. A combination of the genotypic coefficient of variation and the heritability estimates would give more precise amount of advance to be expected from selection" [28]. Therefore, the heritable portion of the variation is more useful with the help of heritability estimates.

"The significant variances obtained for 100 seed weight, number of pods per plant, seeds per pod and seeds per plant indicate that they exact a strong positive influence on final seed yield, agreeing to the findings by" [27,24] who reported strong positive relationship of grain weight with final grain yield and yield components in maize. Positive SCA values recorded by TGM954, TGM120, TGM553, TGM555, TGM574, TGM584 and TGX1904-6F (for 100 seed weight); TGM951, TGM954, TGM120 and TGM584 (pods per plant); TGM951, TGM954 and TGM120 (seeds per pod); TGM951, TGM954, TGM111 and TGM584 (seed per plant); TGM954 and TGM584 (seed yield) are indicative of their potential, as parents for hybrid formation. Generally, TGM954 was a better specific combiner than TGM951, as it combines well with many of the lines for yield and yield related traits studied. [13] posited that "breeder always try to find out new combinations with high yielding, hybrid stability with outstanding performance in various features for a crop while experiments by" [12], has proven that parental lines with high GCA produce higher yielding hybrids than lines with low GCA.

"Over-dominant gene action is reported for plant height, head diameter, oil contents, 100-seed weight, seed and oil yield, to estimate GCA and SCA as well as genetic variance components for different agronomic traits in sunflower inbred lines" [29]. "However, additive gene action for these traits has also been reported [23]. Estimates of GCA and SCA indicating additive effects were more important for oil contents [30]. Additive gene action has the greatest effect on flowering" [31].

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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