

Genetic Advance and Heritability Analysis of Linextester of Four Cowpea Crosses

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Abstract: A line x tester analysis was undertaken using 4 lines (TVu3629, TVu1509, TVu14019 and TVu15687) and 1 tester (TVu1) resulting in 4 hybrids of cowpea with a view to study genotypic and phenotypic coefficient of variation (GCV and PCV), heritability and genetic advance in four crosses of cowpea made. The pot experiment was laid out in completely randomized design with six replications at Research plot, Department of Agricultural Technology, Federal College of Forestry, Ibadan, Nigeria during rainy season 2018. Data collection and analysis were conducted on days to flowering, pod length, number of seeds per pod, 100-seed weight and seed yield per plant to estimate broadsense heritability and genetic advance. The high phenotypic and genotypic coefficient of variation was observed for days to flowering and seed yield per plant, while lowest GCV and PCV was observed for pod length, number of seeds per pod and 100 seed weight.

High magnitude of broad sense heritability along with moderate to high genetic advance as percentage of mean recorded for days to flowering, pod length, number of seeds per pod, 100 seed weight and seed yield per plant obtained in crosses indicated that these characters can be improved through selection in advanced generations using linextester method.

Keywords: Heritability, Genetic Advance, Genotypic Variation, Phenotypic Variation, LinexTester, Improvement

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I. Introduction

The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding programme, Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Rita *et al.*, 2009).

Cowpea plays a significant role in the livelihood of millions of people in Africa and other parts of the developing world where it is a major source of dietary protein that nutritionally complements low-protein staples like cereal and tuber crops (SARI, 1996 and 1997). Improving cowpea against constraints without farmer/consumer preference may result in the rejection of such varieties by farmers since farmer/consumer choice is very significant in utilization of cowpea in Nigeria and the world at large. Considering the farmer/consumer preference of early maturity, colour and seed yield makes cowpea improvement programme more complex and as such no single variety can be suitable for the farmer/consumer preference. Thus, there is need to develop varieties suitable for a specific region and or use. However, production is constrained by low and variable grain yield, seed quality, susceptibility to diseases and pests and the absence of improved cultivars. Under such circumstances genetic diversity is of great importance and plays a crucial role in focusing crop improvement. Hence this study was carried out to estimate the broad sense heritability and genetic advance in cowpea crosses using the linextester mating design.

II. Materials And Methods

Location of Study

The experiment was conducted in the Research plot of Department of Agricultural Technology, Federal College of Forestry, Jericho, Ibadan, Nigeria. Five cowpea lines as shown in Table 1 were collected from International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. Four (4) lines (TVu3629, TVu1509, TVu14019 and TVu15687) were crossed to a tester (TVu1) to generate F₁, F₂ and F₃ generations of all four crosses. The evaluation of the five generations was evaluated in pot experiments. Each block contains the five

generations of each cross. A single replication had one row each of the parents and F₁ generation, two rows of F₂ generation and three rows of F₃ generation. There were ten plants in a row. The inter and intra row spacing 50cm and 20cm was used. The pot experiment was laid out in completely randomized design with six replicates. Plastic pots of 25cm diameter filled with garden soil weighing 4.5kg. Two seeds were planted and later thinned to one plant per pot was done at two weeks after planting.

Cultural practices such as daily watering was carried out for potted plants, while hand weeding and spraying were carried out when necessary in the pot and field experiments. Pest control was achieved by using insecticides Cypermethrin with application rate of 600 ml/ha and Lara-Force® (Lambda-cyhalothrin) with the application rate of 1000 ml/ha for pre- and post-flowering insect pests control respectively. Vertebrates pest were controlled using scarecrows and wire nettings to cover the experimental plot.

Table 1: Cowpea lines used in the study and their characteristics

S/No.	LINES	SOURCE	SEED COLOUR	FLOWER COLOUR	MATURITY
1	TVu3629	IITA	Brown	White	Medium (75-90 days)
2	TVu14019	IITA	White	White	Medium (75-90 days)
3	TVu15687	IITA	Cream	White	Late (> 100 days)
4	TVu1509	IITA	Cream with brown eye	White	Early (60-70 days)
5	TVu1	IITA	Red	Purple	Early (60-70 days)

*IITA= International Institute of Tropical Agriculture, Ibadan, Nigeria.

Data Collection

Data were collected on:

- A. Days to flowering
- B. Number of seeds/pod
- C. Pod length
- D. 100-seed weight
- E. Seed yield/plant

Data Analysis

Data collected was analyzed using TNAU STAT statistical package (Manivannan, 2014) to determine the mean performance, phenotypic and genotypic coefficient of variation, broad sense heritability and genetic advance as percent of mean on each of the parameters.

III. Results And Discussion

Table 2: Mean performance of P₁, P₂, F₁, F₂ and F₃ generations for five agronomic traits in cross TVu1 x TVu3629, TVu1 x TVu1509, TVu1 x TVu14019 and TVu1 x TVu15687

TRAITS	CROSS	P ₁	P ₂	F ₁	F ₂	F ₃
DF	I	38.00	45.00	39.30	42.55	41.90
	II	38.00	48.40	36.50	43.40	44.10
	III	38.00	47.20	38.30	42.75	42.73
	IV	38.00	55.00	44.20	48.05	49.93
PL	I	13.12	13.50	15.60	14.93	12.89
	II	13.12	12.68	13.82	14.03	13.85
	III	13.12	12.06	14.52	12.71	12.27
	IV	13.12	14.62	15.22	14.74	14.81
NSP	I	12.00	11.80	13.80	13.05	11.43
	II	12.00	12.40	12.90	12.80	12.27
	III	12.00	10.80	14.30	11.45	11.27
	IV	12.00	13.20	14.40	13.80	13.90
100SW	I	10.12	14.50	12.58	10.77	11.15
	II	10.12	5.44	7.87	7.54	8.15
	III	10.12	17.18	14.18	13.83	13.11
	IV	10.12	12.44	12.68	10.72	11.17
SYP	I	47.47	55.59	58.46	52.92	53.40
	II	47.47	32.48	56.07	48.38	46.96
	III	47.47	58.55	61.94	56.21	54.22
	IV	47.47	53.30	57.12	53.06	54.51

DF= Days to Flowering, PL= Pod Length, NSP=Number of Seeds/Pod, 100SW=100-Seed Weight, SYP= Seed Yield/Plant, Cross I=TVu1 x TVu3629, Cross II= TVu1 x TVu1509 Cross III= TVu1 x TVu14019 and Cross IV= TVu1 x TVu15687 F₁= First filial generation, F₂= Second filial generation, F₃= Third filial generation

Mean Performance

The mean performance of the four crosses is presented in Table 2. Parent lines used in this study showed difference from the tester parent (TVu1) in days to flowering, pod length, number of seeds per pod, 100 seed weight and seed yield per plant. The tester parent have the earliest days to flowering and have lower mean values than the line parents in seed yield/plant and 100 seed weight but has better performance than TVu1509 in pod length, 100 seed weight and seed yield/plant. The mean performance in the F₁ generation of the four crosses in days to flowering, TVu1 x TVu1509 (36.50 days) flowered earlier than the tester parent (38.00 days). In pod length, number of seeds/pod and seed yield/plant, all the F₁ crosses performed better than the line parents and tester parent. In the F₂ generation, mean performance recorded showed that all the crosses flower later than the tester parent, while the cross of TVu1 (tester) to TVu3629 and TVu1509 have better performance in pod length and number of seed/pod while all the crosses produced better than the tester parent in seed yield/plant. The mean performance of the F₃ generation for the five traits studied showed that the hybrid performance in the segregating generation were between the line parents and tester parent (TVu1) in days to flowering and 100 seed weight, however the cross TVu1 x TVu15687 have better performance than parental lines in pod length and number of seeds/pod. The differences among the analyzed generations were sufficient to perform generation mean analysis on the five generations.

Table 3: Estimates of Heritability (%) and Genetic Advance as per cent of mean for various characters in TVu1 x TVu3629, TVu1 x TVu1509, TVu1 x TVu14019 and TVu1 x TVu15687 crosses of cowpea.

TRAITS	CROSS	GV	PV	Herit %	Gen Adv.	Gen Adv. %	Mean
DF	I	2.27	3.03	74.92	2.69	6.44	41.72
	II	11.41	12.35	92.38	6.69	15.64	42.74
	III	5.03	6.24	80.59	4.15	9.84	42.14
	IV	14.17	16.49	85.96	7.19	14.93	48.14
PL	I	1.29	1.52	84.81	2.15	15.46	13.92
	II	0.06	0.17	35.77	0.30	2.21	13.76
	III	0.60	0.74	80.84	1.43	11.21	12.76
	IV	0.21	0.28	75.52	0.82	5.58	14.71
NSP	I	0.64	1.04	61.72	1.29	10.52	12.30
	II	0.07	0.11	58.53	0.41	3.24	12.50
	III	1.18	1.40	84.21	2.06	17.46	11.77
	IV	0.29	0.39	73.68	0.95	6.88	13.76
100SW	I	1.22	1.42	86.03	2.11	18.53	11.41
	II	0.91	1.06	85.58	1.82	23.05	7.88
	III	2.16	2.43	88.98	2.86	21.09	13.54
	IV	0.61	0.71	86.49	1.50	13.3	11.27
SYP	I	9.54	12.27	77.73	5.61	10.39	54.00
	II	47.29	52.01	90.94	13.51	28.29	47.75
	III	18.97	22.13	85.71	8.31	14.80	56.11
	IV	7.25	9.01	80.45	4.98	9.24	53.85

DF=Days to Flowering, PL= Pod Length, NSP=Number of Seeds/Pod, 100SW=100-Seed Weight, SYP= Seed Yield/Plant, Cross I= TVu1 x TVu3629, Cross II= TVu1 x TVu1509, Cross III= TVu1 x TVu14019 and Cross IV= TVu1 x TVu15687
 GV= Genotypic Variation, PV= Phenotypic Variation, Herit %= Heritability (%), Gen Adv.= Genetic Advance, Gen Adv. %= Genetic Advance as percentage of mean,

Heritability and Genetic Advance

The quantitative traits are highly heritable. High or low heritability is not rigidly defined but the following values were used in categorizing the broad sense heritability as developed by Robinson *et al.* (1949) and Stansfield (1969).

- i. Low heritability: < 20%
- ii. Moderate heritability: 20 to 50%
- iii. High heritability: > 50%

The value of expected genetic advance as percentage of mean for various characters is classified into three categories viz, low, moderate and high as follows (Johnson *et al.*, 1955).

- (i) Low genetic advance as percentage of mean: < 10%
- (ii) Moderate genetic advance as percentage of mean: 10 to 20%
- (iii) High genetic advance as percentage of mean: > 20

The results obtained on these aspects for different characters studied in all the crosses are discussed under.

Days to flowering

All the crosses revealed high broad sense heritability for this trait that ranged from 74.92 (TVu1 x TVu3629) and 92.38 (TVu1 x TVu1509) also the predicted genetic advance as percentage of mean ranged from 6.44 to 15.64 same as in the broad sense heritability. The high broad sense heritability coupled with moderate genetic advance in crosses TVu1 x TVu15687 and TVu1 x TVu1509 will allow for better opportunity for

selecting superior genotypes. The present findings are in close agreement with the results obtained by Patil and Bhaviskar (1987), Siddique and Gupta (1991), Sharma and Singhania (1992) and Rocha *et al.* (2003) of high broad sense heritability for days to flowering.

Pod length

For the pod length characteristics in the crosses made the broad sense heritability ranged from 35.77 (TVu1 x TVu1509) to 84.81 (TVu1 x TVu3629). The predicted genetic advance as percentage of mean ranged from 2.21 (TVu1 x TVu1509) to 15.46 (TVu1 x TVu3629). The crosses that exhibited moderate genetic advance as percentage of mean were TVu1 x TVu3629 and TVu1 x TVu14019 can be improved through selection. The high broad sense heritability coupled with moderate genetic advance in crosses TVu1 x TVu3629 and TVu1 x TVu14019 will allow for better opportunity for selecting superior genotypes. This was reported by Aryeetey and Laing (1973), Leleji (1975), Tikka *et al.* (1977), Apte *et al.* (1987) and Siddique and Gupta (1991).

Number of seeds per pod

All the crosses revealed high broad sense heritability for this trait that ranged from 58.53% (TVu1 x TVu1509) to 84.21 (TVu1 x TVu14019). The predicted genetic advance as percentage of mean were low in crosses TVu1 x TVu15687 and TVu1 x TVu1509 while the remaining crosses exhibited moderate genetic advance. The crosses with moderate genetic advance can be improved through selection while the low genetic advance have little possibility of improvement of this trait by straight selection. The high heritability of this trait in cowpea was reported by Tikka *et al.* (1977), Jana *et al.* (1982), Apte *et al.* (1987), Gowda *et al.* (1991), Siddique and Gupta (1991) and Ram and Singh (1997).

100 Seed weight

The estimates of broad sense heritability for this trait obtained in the present study showed that all the four crosses exhibited high heritability values that ranged from 85.58 (TVu1 x TVu1509) to 88.98 (TVu1 x TVu14019), while the genetic advance as percentage of mean of this trait were moderate and high. The crosses with high broad sense heritability and high genetic advance were TVu1 x TVu14019 and TVu1 x TVu1509 implies that there is close correspondence between genotypic and phenotype values due to relatively smaller contribution of environmental effect on this trait and better opportunity for selection of better genotypes in segregating generations for improvement of the trait the present findings are in close agreement to the findings of Boradia *et al.* (1973), Lakshmi and Gouel (1977), Tikka *et al.* (1977), Jana *et al.* (1982), Apte *et al.* (1987), Siddique and Gupta (1991), Pal *et al.* (2003), Kumar and Sangwan (2000) and Rocha *et al.* (2003).

Seed yield per plant

All the crosses exhibited high broad sense heritability, the estimates of this trait ranged from 77.73 (TVu1 x TVu3629) to 90.94 (TVu1 x TVu1509) while the genetic advance as percentage of mean ranged from 9.24 (TVu1 x TVu15687) to 28.29 (TVu1 x TVu1509). The high heritability of this trait was reported by Siddique and Gupta (1991), Biradar *et al.* (1993) and Damarany (1994). TVu1 x TVu1509 was the only cross with high heritability and high genetic advance. This selection of genotypes in the segregating generations will be effective.

IV. Conclusion

High magnitude of broad sense heritability along with moderate to high genetic advance as percentage of mean recorded for days to flowering, pod length, number of seeds per pod, 100 seed weight and seed yield per plant obtained in crosses indicated that these characters can be improved through selection in advanced generations. High heritability estimates along with high genetic advance as per cent was noticed in 100 seed weight and seed yield per plant in crosses of TVu1 (tester parent) with TVu1509. The high heritability coupled with genetic advance reveals the presence of lesser environmental influence and prevalence of additive gene action in their expression. Hence seed yield per plant can be improved by selection in further generation. The effectiveness of selection for any character will depend not only on the extent of genetic variability but also on extent to which it will be transferred from one generation to the next generation. High heritability of any character will give greater genetic advance under selection and accordingly a breeder will make his breeding strategies. Genetic advance gives magnitude of improvement per cycle in the base population by selection. That is heritability and genetic advance helps in determining the influence of environment in the expression of characters and the extent to which improvement is possible after selection.

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References

- [1]. Apte, U.B.; Chavan, S.A. and Jadhav, B.B. 1987. Genetic variability and heritability in Cowpea. *Indian Journal of Agricultural Sciences*. 57: 596-598.
- [2]. Aryeetey, A.N., and Laing, E. 1973. Inheritance of yield components and their correlation with yield in cowpea *Vigna unguiculata* (L.)Walp. *Euphytica* 22, 386-392.
- [3]. Biradar, B.D.; Goud, J.V. and Patil, S.S. 1993. Components of variance, heritability and genetic gain in cowpea (*Vigna unguiculata* (L.) Walp). *Annals of Agricultural Research*. 14(4): 434-437.
- [4]. Bordia, P.C.; Yadavendra, J.P. and Kumar, S. 1973. Genetic variability and correlation studies in cowpea (*Vigna sinensis* L. savi ex Hassk.). *Rajasthan Journal of Agricultural Science*. 4(1): 39-44.
- [5]. Gowda, T.H.; Hiremath, S.R. and Salimath, P.M. 1991. Estimation of genetic parameters in intervarietal crosses of cowpea (*Vigna unguiculata* (L.) Walp.) and their implication in selection. *Legume Research*. 14(1): 15-19.
- [6]. Jana, S.; Som, M.G. and Das, N.D. 1982. Genetic variability and correlation studies in Cowpea. *Vegetable Science*. 9: 96-106.
- [7]. Johnson, H.W., Robinson, H.F. and Cornstock, R.E. 1955. Estimates of genetic and environmental variability in soybeans. *Agron. J.*, 47:314-318.
- [8]. Kumar, R. and Sangwan, R.S. 2000. Genetic variability and heritability in cowpea [*Vigna unguiculata* (L.) Walp.]. *Annals of Biology*. 16(2):81-183.
- [9]. Lakshmi, P.V. and Goud, J.V. 1977. Variability in cowpea (*Vigna sinensis* L.). *Mysore Journal of Agricultural Sciences*. 11(2): 144-147.
- [10]. Leleji, O.I. 1975. Inheritance of three agronomic characters in cowpea [*Vigna sinensis* L. (Savi.)]. *Madras Agricultural Journal* 62, 95-97.
- [11]. Manivannan, N. 2014. TNAU STAT-Statistical package. Retrived from <https://sites.google.com/site/tnaustat>.
- [12]. Pal, A.K.; Maurya, A.N.; Singh, B.; Ram, D. and Kumar, S. 2003. Genetic variability, heritability and genetic advance in cowpea [*Vigna unguiculata* (L.) Walp]. *Orissa Journal of Horticulture*. 31(1): 94-97.
- [13]. Patil, R.B. and Bhaviskar, A.P. 1987. Variability studies in cowpea. *Journal of Maharashtra Agricultural Universities*. 12(1): 63-66.
- [14]. Ram, D. and Singh, K.P. 1997. Variation and character association studies in cowpea (*Vigna unguiculata* (L.) Walp.). *Horticultural Journal*. 10(2): 93-99.
- [15]. Rita B., A.K. Sarawgi And S. B. Verulkar. 2009. Study Of Heritability, Genetic Advance And Variability For Yield Contributing Characters In Rice. *Bangladesh J. Agril. Res.* 34(2) : 175-179.
- [16]. Robinson, H.F., Comstock, R.E., and Harvey, P.H., 1949, Estimates of heritability and degree of dominance in corn. *Agronomy Journal*, 41 : 353 -359.
- [17]. Rocha de M.M.; Campelo, J.E.G.; Freire Filho, F.R.; Ribeiro, V.Q. and Lopes, C. 2003. Estimates of genetic parameters in white coat cowpea genotypes. *Revista Científica Rural*. 8(1): 135-141.
- [18]. Sharma, C.D. and Singhania, D.L. 1992. Performance of Cowpea genotypes for fodder traits. *Annals of Arid Zone*. 31: 65-66.
- [19]. Siddique, A.K.M.A.R. and Gupta, S.N. 1991. Genotypic and phenotypic variability for seed yield and other traits in Cowpea. *International Journal of Tropical Agriculture*. 9: 144-148.
- [20]. Stansfield, W.D. 1969. Theory and problems of Genetics. Publ. by McGraw Hill Book Company, New York.
- [21]. Tikka, S.B.S., Jaimini, S.N., Asawa B.M. and Mathur, J.R. 1977. Genetic variability, interrelationships, and discriminant function analysis in cowpea [*Vigna unguiculata* (L.) Walp.]. *Indian Journal of Heredity* 9, 1-9.

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