# Generation Mean Analysis Of Linextester Cross Of Four Cowpea Crosses

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*Abstract: A line x tester analysis was undertaken using 4 cowpea lines (TVu14019, TVu1509, TVu15687 and TVu3629) and 1 tester cowpea line (TVu1) to generate 4 hybrids with a view to study the gene effects in crosses of cowpea. 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 were recorded and analysed to estimate for their mean performance, scaling tests and gene effects on days to flowering, pod length, number of seeds per pod, 100-seed weight and seed yield per plant*

*Scaling tests revealed the presence of one or more kinds of epistatic effects for almost all the agro-morphological traits. There was significant complementary and duplicate epistatic gene effect in days to flowering, pod length, number of seeds per pod in the cross involving TVu1 with TVu15687, TVu3629 and TVu14019 while the cross with TVu1509, there was additive effect which ensures the improvement in 100 seed weight and seed yield per plant in the cross.*

*The present investigation indicated that both additive and non-additive types of gene actions were important in governing all the traits with preponderance of non- additive gene action for seed yield and its components and inbreeding depression could be utilized advantageously for improving yield through heterosis breeding. The result obtained also indicated that the possibility of improving cultivated varieties with biparental mating hybridization while still maintaining their preference traits.*

*Keywords: Additive effects, Non-additive effects, Epistasis, Generation Mean Analysis, Gene effect, Inheritance.*

## I. INTRODUCTION

Cowpea (*Vigna unguiculata* L.) is an important legume widely cultivated in tropics and subtropics for forage, green pods and grains (Ali *et al*., 2004). Cowpea is usually better adapted to drought, high temperatures and other biotic stresses compared with other crops (Kuykendall *et al*., 2000; Martins *et al*., 2003). However, growth and development of many cowpea cultivars are affected by drought and high temperatures, especially during floral development (Dadson *et al*., 2005). Protein content of cowpea seed is among the the

highest in cultivated legumes (Aremu *et al*., 2007) and can serve as an excellent source of dietary protein in animal feeds (Igbasan and Guenter, 1997). The mature grain contains 20 to 25% of protein (Kay, 1979), 1.3 to 1.5% lipid and 5.1 to 5.8% crude fibre (Tshovhote *et al*., 2003).

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.

The prime objective the crop improvement programme is to improve genotypes /hybrids or population of genotypes to develop crop varieties that are superior in one or more aspects than the cultivated best varieties/hybrids in the crop. In a self-pollinating crop like cowpea, variability is often created through hybridization between carefully chosen parents. The scope of exploitation of hybrid vigour will depend on the direction and magnitude of heterosis, biological feasibilities and the type of gene action involved. The information of such estimates is essential to plan efficient breeding programme for the improvement of the crop. One of the common approaches followed to understand the nature of gene effects by growing different generations and carrying out the generation mean analysis, using first-degree statistics was employed in the present study. The purpose of the present study was to evaluate the cowpea varietal differences and assess through generation mean analysis the genetic control of five yield traits; so that the yield output can be genetically improved.

## II. MATERIALS AND METHODS

### LOCATION OF STUDY

The experiment was conducted in the Research Experiment 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 lines were crossed to a tester (TVu1) to generate $F_1$, $F_2$ and $F_3$ 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 $F_1$ generation, two rows of $F_2$ generation and three rows of $F_3$ 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.

| 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*

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

### DATA COLLECTION

Data were collected on:
- ✓ Days to flowering
- ✓ Number of seeds/pod
- ✓ Pod length
- ✓ 100-seed weight
- ✓ Seed yield/plant

### DATA ANALYSIS

Data collected was was analyzed using Generation mean 5 parameter statistical programme of TNAUSTAT statistical package (Manivannan, 2014) to determine the gene effects and scaling effects. The estimation of gene effects determined were computed on mid parental value (m), additive gene effects (d), dominance gene effects (h), additive x additive (epistatic) interaction effect (i) and dominance x dominance (epistatic) interaction effect (l) using the five parameter module developed by Hayman (1958).

The scaling test was estimated in the crosses at the C and D scales to determine if the values were significant to show epistatic interaction in the five characters studied. The scaling test developed by Hayman (1958) was used to determine C and D

Where
$$C = 4\bar{F}_2 - \bar{F}_1 - \bar{P}_1 - \bar{P}_2$$
$$D = 4F_3 - 2F_1 - P_1 - P_2$$

Where $P_1$ = mean of Parent 1
$P_2$ = mean of parent 2
$F_1$ = mean of $F_1$
$F_2$ = mean of $F_2$
$F_3$ = mean of $F_3$

And where significance of any one of these scales was taken to indicate the presence of epistasis.

## III. RESULTS AND DISCUSSION

| 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 |

| Trait | Cross | P1 | P2 | F1 | F2 | F3 |
|---|---|---|---|---|---|---|
| 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*
*F$_1$= First filial generation, F$_2$= Second filial generation, F$_3$= Third filial generation*

*Table 2: Mean performance of P$_1$, P$_2$, F$_1$, F$_2$ and F$_3$ generations for five agronomic traits in cross TVu1 x TVu3629, TVu1 x TVu1509, TVu1 x TVu14019 and TVu1 x TVu15687*

## MEAN PERFORMANCE

The mean performances of the four crosses are 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 F$_1$ 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 F$_1$ crosses performed better than the line parents and tester parent. In the F$_2$ 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 F$_3$ 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 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.

| Traits | Cross | m | d | h | i | l | C | D |
|---|---|---|---|---|---|---|---|---|
| DF | I | 42.50* | -3.10* | -0.43 | -4.03 | -12.13 | 7.80* | -1.30 |
|  | II | 43.40* | -4.80* | -6.47* | -8.97* | -14.67* | 13.40* | 2.40 |
|  | III | 42.75* | -4.20* | -2.92 | -6.22* | -11.96 | 8.40* | -0.57 |
|  | IV | 48.05* | -8.10* | -7.59* | -21.09 | -0.22 | 1.00 | 9.83* |

| Trait | Cross | m | d | h | i | l | C | D |
|---|---|---|---|---|---|---|---|---|
| PL | I | 14.94* | -0.19 | 5.91* | 3.24* | -9.15* | 1.92 | -4.94* |
|  | II | 14.03* | 0.22 | 0.34 | -0.14 | -1.50 | 2.66* | 1.54 |
|  | III | 12.71* | 0.53* | 2.37* | 1.50 | 2.52 | -3.40* | -1.51 |
|  | IV | 14.74* | -0.75* | 0.11 | -2.74* | 1.71 | 0.76 | 2.04* |
| NSP | I | 13.05* | 0.10 | 4.81* | 3.11* | -6.62 | 0.80 | -4.17* |
|  | II | 12.80* | -0.20 | 1.49 | 0.39 | -2.58 | 1.00 | -0.93 |
|  | III | 11.45* | 0.60* | 2.39* | 0.69 | 6.62 | -5.60* | -0.63 |
|  | IV | 13.80* | -0.60* | 0.13 | -2.87* | 2.13 | 1.20 | 2.80* |
| 100SW | I | 10.77* | -2.19* | 0.18 | -4.46* | 6.86* | -6.68* | -1.54 |
|  | II | 7.54* | 2.34* | -1.43 | 3.16* | 4.19 | -1.16 | 1.98 |
|  | III | 13.83* | -3.53* | 2.15 | -5.44* | -2.87 | -0.36 | -2.52 |
|  | IV | 10.72* | -1.16* | 0.11 | 3.61* | 7.62* | -5.04* | 0.67 |
| SYP | I | 52.92* | -4.06* | 2.42 | 12.62* | 17.32 | -8.31 | 4.68 |
|  | II | 48.38* | 7.50* | 8.90 | 7.81 | 12.95 | 1.43 | 11.14 |
|  | III | 56.21* | -5.54* | 9.13 | -10.88* | 4.67 | -5.06 | -1.56 |
|  | IV | 53.06* | -2.91* | -1.16 | -13.72* | 18.55 | -2.77 | 11.14* |

*= significance at 5% level of probability
*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*
*m= mid parent, d= additive gene effects, h= dominance gene effects  i= additive x additive gene effects l= dominance x dominance gene effects*

*Table 3: Estimates of scaling tests and gene effects for days to flowering, pod length(cm), number of seeds/pod, 100 seed weight(g), seed yield/ plant (g) of TVu1 x TVu3629, TVu1 x TVu1509, TVu1 x TVu14019, TVu1 x TVu15687 crosses in cowpea*

## GENE EFFECTS AND SCALING TEST ESTIMATES

The results of the generation mean analysis provide estimates of the main and first order interaction gene effects (Table 3). The gene effects of mid parent (m), additive (d), dominance (h) gene effects, interaction effect of additive x additive (i) and dominance x dominance (l) on the five traits studied in the four crosses of cowpea.

## DAYS TO FLOWERING

There were significant differences for this character in all the four crosses. As such they were subjected to scaling test and estimates of gene effects for respective generation. The highly significant values of mid parent (m) values from the generation mean analysis in all the four crosses showed that the five generations differed from each other with respect to this traits. The significant estimates of scaling tests for all the four crosses indicated that the crosses exhibited the presence on non-allelic interaction for this trait. The estimation of gene effects revealed that all the crosses were negatively significant in additive (d) gene effects while cross TVu1 x TVu1509 and

TVu1 x TVu15687 were also negatively significant for dominance (h) gene effects. For the interaction effect, the additive x additive gene effects revealed that all the crosses were negative and significance was obtained in all the crosses except in TVu1 x TVu3629 while in the dominance x dominance (l) gene effects all the crosses were negative and significance was obtained in TVu1 x TVu1509. From the result, the negative values of dominance (h) indicates that shorter days to flowering is completely or partially dominant to longer days to flowering in all the crosses. In the test of adequacy, the same sign between dominance (h) and dominance x dominance (l) gene effects indicates that the days to flowering is controlled by complementary epistasis. This finding was supported by the report of Ojomo (1971) and Mak and Yap (1980). The complementary epistatic interaction was not in accordance to the report of Ubi *et al.*, (2001), Ishiyaku *et al.* (2005), Rashwan (2010) reporting duplicate epistasis.

## POD LENGTH

There were significant differences for this character in all the four crosses. As such they were subjected to scaling test and estimates of gene effects for respective generation. The highly significant values of mid parent (m) values from the generation mean analysis in all the four crosses showed that the five generations differed from each other with respect to this trait. The dominance (h) estimates is positive in all the crosses thus indicating that long pod length is completely or partially dominant to short pod length. The significance of additive gene effects in all the crosses except in TVu1 x TVu3629 and TVu1 x TVu1509 suggests that selection within earlier generations leading to isolation of homozygous lines having desired pod length could be achieve through selection. The significant estimates of scaling tests in all the four crosses exhibited the presence of non-allelic interaction for this trait. The complementary type of epistatic interaction was recorded in TVu1 x TVu1509 and TVu1 x TVu14019 while it was duplicate type of epistatic interaction in TVu1 x TVu3629 and TVu1 x TVu15687.This result is in agreement of the reports by Chaudhari *et al.* (1998) and Ubi *et al.* (2001).

## NUMBER OF SEEDS PER POD

There were significant differences for this character in all the four crosses. As such they were subjected to scaling test and estimates of gene effects for respective generation. The highly significant values of mid parent (m) values from the generation mean analysis in all the four crosses showed that the five generations differed from each other with respect to this traits. In the number of seeds per pod, the gene effect of the four crosses made showed additive, dominance and epistatic interaction. There were significant estimates of the scaling tests in the crosses TVu1 x TVu3629 and TVu1 x TVu15687 exhibiting duplicate type of epistatic interaction while complementary epistatic interaction was exhibited in cross TVu1 x TVu14019. There was no epistatic interaction in the cross TVu1 x TVu1509.

The present findings are in conformity to the results of Singh *et al.* (2006) Lal *et al.* (2013) and Thakare *et al.* (2016) who reported that additive, dominance and epistatic effect occurred in the inheritance of seeds per pod in cowpea thereby suggesting that homozygous elite recombinants could be developed following inter-crossing of desirable segregants.

The involvement of both additive and non-additive gene effects in the genetic control of this trait suggested that recombinants could be developed following inter-crossing of desirable segregants.

## 100 SEED WEIGHT

There were significant differences for this character in all the four crosses. As such they were subjected to scaling test and estimates of gene effects for respective generation. The highly significant values of mid parent (m) values from the generation mean analysis in all the four crosses showed that the five generations differed from each other with respect to this traits. The result obtained for this trait in all four crosses showed the highly significant values of mid parent values (m) thus implying that the mean of the five generations differed from each other. The estimates of the gene effects revealed that additive, additive x additive gene effect were highly significant in all the crosses. The significant opposite signs of dominance and dominance x dominance effects indicated the presence of duplicate epistasis in the inheritance of this trait in TVu1 x TVu3629 and TVu1 x TVu15687. These results of duplicate and complementary epistatic inheritance were in agreement to the findings of Sherif and Damarany (1992) and El-Ameen (2008) who have reported both non-allelic gene interaction in their studies. Therefore with additive and non-additive interaction involved in this trait breeding methods involving high volume crossing like biparental, recurrent and diallel selective mating designs seemed more promising.

## SEED YIELD PER PLANT

There were significant differences for this character in all the four crosses. As such they were subjected to scaling test and estimates of gene effects for respective generation. The highly significant values of mid parent (m) values from the generation mean analysis in all the four crosses showed that the five generations differed from each other with respect to this traits. The dominance (h) values were positive in all the crosses except in cross TVu1 x TVu15687 thus implying that high seed yield is completely or partially dominant to low seed yield on the crosses. In all the crosses, additive gene effect was significant which is in agreement of the finding of Patel *et al.* (1994) and Mehata and Zaveri (1997) who reported predominance of additive gene effects. The duplicate epistatic gene interaction was registered based on the different sign on dominance (h) and dominance x dominance (l) in the crosses and also as indicated by the significance exhibited in the C and D scaling test. Therefore with the result of the findings, biparental or multiple crossing may be employed for the improvement of this trait in cowpea.

## IV. CONCLUSION

The nature and magnitude of gene effects have essentially been obtained by employing generation mean analysis. This

provides the estimates of different non-allelic interactions operating in the inheritance. The non-allelic interactions could inflate the measure of additive and dominance components. It is therefore important to identify and estimate components of epistasis along with the additive and dominance components so that the fixable components can be exploited by simple selection. On the other hand, if dominance gene effect is predominant in the population. The emphasis should be given for the development of hybrids and creating variability for further selection.

Since different gene effects were responsible for the inheritance of the same character in different crosses and for the different characters in the same cross specific handling of individual crosses for different characters would be advantageous for the improvement of these characters. The characters controlled by both additive and non-additive gene effects can be successfully improved by utilizing hybrid vigour or biparental mating method of breeding.

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