Diallel Analysis of Cowpea Cultivar Ife Brown and its Mutants

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Abstract— The present investigation of using half diallel analysis in Cowpea cultivar Ife Brown and its three mutants was conducted at Research plot of Department of Agricultural Technology, Federal College of Forestry, Ibadan, Nigeria during the rainy season of 2017. Four parents were used in this study consisting of three (3) mutants (Ife BPC, Ife Brown Yellow, Ife Brown Crinkled) and one (1) putative parent (Ife Brown) that were derived from the Department of Crop Protection and Environmental Biology, University of Ibadan, Ibadan, Nigeria. The present study involves four parents and their seven resultant crosses were grown in a completely Randomized Design with five replications. Analysis of variance for general and specific combining ability(GCA and SCA) revealed that only SCA variances were significant for all the characters. Whereas, comparison of the error mean square of GCA in days to flowering, 100 seed weight and seed yield/plant was higher than the error mean square of SCA thus implying that additive gene action played a more important role in the inheritance of these traits than the non-additive (dominance and epistasis) gene action. Among the parents Ife BPC was observed to be the best general combiner for days to flowering and seed yield/plant. Among the crosses the crosses involving Ife Brown Yellow with Ife Brown in pod length and number of seeds/pod while with Ife Brown Crinkled for days to flowering were recorded. It is evident from present investigation that the hybrid combinations exhibited the high per se performance and sca effect for seed yield per plant and highly promising even in respect of other characters could be advanced by selecting desirable segregants and recombinants in each generation for funneling the new genotype or for using further advanced breeding programme.

The present study based on two biometrical analysis (combining ability and genetic components of variances) revealed that the additive and non-additive were involved with preponderance of non-additive gene effects in the inheritance of seed yield and its attributes. It is, therefore, suggested that biparental mating, intermatting of elite segregants and selection at later generations should be followed which meets the requirement of utilizing both types of gene actions.

Keywords— Cowpea, Yield, Mutants, Diallel, Combining Ability, Gene Action, Inheritance.

I. INTRODUCTION

Cowpea *Vigna unguiculata* (L) Walp, is an annual crop grown as a pulse, vegetable or for fodder throughout the tropics and the sub-tropics (Steele, 1976). Cowpea is one of the most important food legume crops in the semi-arid tropics covering Asia, Africa, southern Europe and Central and South America. In Nigeria, apart from being a key staple food, cowpea provides more than half the plant protein needed in human diet. Cowpea serves as a source of dietary protein, carbohydrates, vitamins and minerals both in the rural and urban communities of the semi and humid tropical regions of Africa. It is eaten in form of dry seeds, green pods and young leaves which serve as vegetable (Brader *et al.*, 2002). A drought tolerant and warm weather crop, cowpea is well adapted to the drier regions of the tropics, where other food legumes do not perform well. It is also important in the traditional cropping system. It contributes to the sustainability of cropping systems in marginal lands of semi-arid areas and helps in soil improvement through its nitrogen fixing ability due to a symbiotic association with *Bradyrhizobium* spp. (Evans *et al.*, 2003). On account of its ability to fix nitrogen in the soil it is grown in monoculture, in rotation with cereals or intercropped with maize, sorghum or millet. Cowpea is also highly compatible with a wide range of root and fibre crops like cassava and cotton (Rachie, 1985).

Choice of parents is considered as an important aspect in any breeding programme aimed at improving yield and its related attributes because the high yielding parent may not necessarily transfer its superiority to the progenies in the crosses. Land races are primitive varieties, which had evolved without a systematic and sustained plant breeding efforts. They are store houses of genetic variability and ordinarily, are adapted to the local soil type, climatic conditions etc. They are sources of many valuable genes including those for adaptation. It is therefore, necessary to identify promising lines, land races and involve them in crosses with appropriate mating design.

In the crop improvement programme, the nature of gene action depends on the genetic structure and divergence between populations involved in hybridization. It may happen that high yielding genotypes may not be able to transmit their superiority in cross combinations and vice– versa. Therefore, a breeder should know the genetic potential of the parents by estimating their combining ability. Besides, the use of combining ability analysis in the selection of parents elucidates the nature and magnitude of various types of gene action involved in the expression of quantitative characters. Such information is of potential use in formulation and executing an efficient breeding programme for achieving maximum genetic gain with minimum resources and time.

Diallel analysis is a popular experimental method to assess the combining ability of the parents. It also provides, in quantitative characters, estimates of variability in a population. The study of such genetic parameters attempted in this investigation would not only help the breeders in selecting suitable parents for hybridization, but could also contribute towards the evaluation of effective breeding methodology to improve nutritional quality and productivity of one of the most important pulses of the country. With limited scope for further expansion of area under cultivation, increasing demand of cowpea for various purposes and majority of vield components being polygenically controlled, concerted efforts are required on the part of the breeders to address the problems of low productivity and quality simultaneously through suitable breeding strategies. However, the success of cowpea breeding programme depends upon the objectives set forth prior to actual initiation of work, proper choice of parents, mating systems employed, quantity and quality of heritable variability, environmental conditions and finally the breeder's keen judgment in selecting superior genotypes

from the large segregating populations. In addition, the useful gene combinations organized in the form of high combining lines and isolation of superior transgressive segregants also determine the success of any breeding procedure. Some parental lines produce outstanding progenies from crossing with others; while certain others may not yield desirable progenies on crossing. The lines which perform well in several cross combinations are eventually of great importance to plant breeders. Information on combining ability provides guide line to the plant breeder in selecting the elite parents and desirable cross combinations to be used in formulation of systematic breeding programme and hence, investigation on general and specific combining abilities would give very useful information. Also knowledge of gene effects involved in the inheritance of quantitative characters of economic importance is very essential before formulation of efficient breeding strategies for rapid vield improvement. Keeping all these factors in view, the present investigation involving diallel set of mutant genotypes of cowpea with the objective to study the general and specific combining ability effects for the selection of potential parents and effective crosses, respectively for seed yield and its components.

II. MATERIALS AND METHOD

The research was carried out at the Research plot of Department of Agricultural Technology, Federal College of Forestry, Ibadan, Nigeria during the rainy season of 2017. Four parents were used in this study consisting of three (3) mutants and one (1) putative parent that were derived from the Department of Crop Protection and Environmental Biology, University of Ibadan, Ibadan, Nigeria. The seeds of the parents were sown in 5kg soil capacity plastic pots filled with garden soil. The parents were established in three phases with two weeks interval at 4 pots per week making a total of twelve parental stands available for plant to plant pollination using the hand pollination developed by Rachie et al.,(1975). All possible crosses were made except the reciprocals resulting in six (6) cross combinations following the 4x4 diallel crossing pattern. Each cross was tagged for easy identification and at maturity, the F₁ seeds were harvested separately. The parents and their 6 F_1 genotypes were evaluated in pot experiment. The experiment was laid out in completely randomised design with 5 replicates. Each replicates consists the parents and F₁. Data were collected on the days to flowering, pod length, number of seeds per pod, 100-seed weight and seed yield per plant on each plant. Data collected were subjected to analysis of variance and test of significance to meet the pre-requisite for further analysis. Subsequently the means were also analysed for general and specific combining abilities in the parents and the F₁s following mthod II of Griffings (1956). The diallel component analysis for the parents and F1 were obtained according to the Griffings (1956) method using PBTools statistical software package.

Table 1: Mean Performance of the diallel crosses of cowpea ife brown and its three mutants						
lines	DTF	PL	NSP	100SW	SYP	
Ife Brownx Ife BPC	40.00bc	11.87cd	9.33cd	14.41c	13.88cd	
Ife Brown x Ife Brown Yellow	43.33e	12.38ab	12.00a	11.88i	14.71bc	
Ife Brown x Ife Brown Crinkled	38.67ab	12.17bc	11.33ab	11.97h	14.00c	
Ife BPC x Ife Brown Yellow	53.00gh	10.20f	9.33cd	15.16a	14.61c	
Ife BPC x Ife Brown Crinkled	41.33cd	12.63a	12.00a	14.17d	17.55a	
Ife Brown Yellow x Ife Brown Crinkled	49.00f	11.58d	10.67abc	13.68e	15.06bc	
Ife Brown	42.33de	10.26f	8.00d	13.76e	11.36e	
Ife BPC	53.33h	11.66d	11.00ab	14.73b	16.72ab	
Ife Brown Yellow	51.67g	10.84e	10.00bc	12.64f	13.05cde	
Ife Brown Crinkled	37.67a	11.04e	9.33cd	12.40g	11.95de	
sig	*	*	*	*	*	
CV%	2.14	2.33	8.50	0.36	8.38	
SEM	0.56	0.15	0.51	0.03	0.69	

RESULTS

III.

*= significance at 5% level of probability: CV% = Coefficient of Variation percentage: SEM= Standard Error of Mean; DTF= Days to Flowering; PL= Pod Length (cm); NSP= Number of seeds/pod; 100SW= 100 seed weight; SYP= Seed Yield/Plant

Mean Performance

The mean values of all the characters are presented in Table 1 of the parents and their cross combinations in F₁ generation. In the days to flowering, the parent Ife Brown Crinkled was the earliest (37.67 days) while the parent Ife BPC was late (53.33 days). In the cross combinations Ife Brown x Ife Brown Crinkled was early at 38.67 days whereas Ife BPCxIfe Brown Yellow was late at 53.00 days.

For the pod length, among the parents, Ife Brown recorded the lowest length (10.26cm) while Ife BPC had the highest (11.66cm) pod length. Among the crosses, highest pod length was recorded in the cross Ife BPC x Ife Brown Crinkled (12.63cm) and the lowest (10.20cm) was recorded in Ife BPC x Ife Brown Yellow. The parent, Ife Brown had the lowest (8.00) number of seeds/pod whereas the parent Ife BPC expressed the highest (11.00) value. the number of seeds/pod in the F1 ranged from 9.33 (Ife Brown x Ife BPC and Ife BPC x Ife Brown Yellow) to 12.00 (Ife Brown x Ife Brown Yellow and Ife BPC x Ife Brown Crinkled).

The mean parental value for 100-seed weight varied from 12.40g (Ife Brown Crinkled) to 14.73g (Ife BPC) whereas for the cross combinations ranged from 11.88g (Ife Brown x Ife Brown Yellow) to 15.16g (Ife BPC x Ife Brown Yellow).

The mean seed yield/plant of the parents ranged from 11.36g (Ife Brown) to 16.72g (Ife BPC) while the F1 cross combinations ranged from 13.88g (Ife Brown x Ife BPC) to 17.55g (Ife BPC x Ife Brown Crinkled).

Table 2: Estimates of general combining ability effects for seed yield and its components traits in cowpea cultivar ife brown
and its three mutants

lines	DTF	PL	NSP	100SW	SYP	
Ife Brown	-3.08	-0.06	-0.47	-0.27	-1.02	
Ife BPC	2.64	0.12	0.19	0.97	1.34	
Ife Brown Crinkled	-3.47	0.19	0.19	-0.46	-0.16	
Ife Brown Yellow	3.92	-0.25	0.08	0.23	-0.16	
EMS	87.73	0.23	0.61	2.55	5.77	
Estimates	12.60	0.00	0.00	0.29	0.52	
Std Error	22.76	0.19	0.45	0.67	1.57	
Sig	ns	ns	ns	ns	ns	

*= significance at 5% level of probability:DTF= Days to Flowering; PL= Pod Length (cm); NSP= Number of seeds/pod; 100SW= 100 seed weight; SYP= Seed Yield/Plant

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General Combining Ability (GCA)

The analysis of variance of the parent and its mutant in the characters studied revealed that there were no significant difference among the traits of the parent GCA for days to flowering, pod length, number of seed/pod, 100 seed weight and seed yield/plant. The parental line Ife Brown have negative values for all the characters studied while the mutant Ife BPC had positive values in all the traits studied. Ife Brown Crinkled had negative GCA values in days to flowering, 100-seed weight and seed yield/plant while Ife Brown Yellow was negative in pod length and seed yield/plant. The GCA for days to flowering ranged from -3.47 (Ife Brown Crinkled) to 3.92 (Ife Brown Yellow), in pod length it ranged from -0.25 (Ife Brown Yellow) to 0.19 (Ife Brown Crinkled) while in the seed yield/plant it ranged from -1.02 (Ife Brown) to 1.34(Ife BPC).

 Table 3: Estimates of specific combining ability effects for seed yield and its components traits in cowpea cultivar ife brown and its three mutants.

and its infec matants.						
LINES	DTF	PL	NSP	100SW	SYP	
Ife Brown x Ife BPC	-4.59	0.35	-0.69	0.23	-0.73	
Ife Brown x Ife Brown Crinkled	0.19	0.58	1.31	-0.78	0.89	
Ife Brown x Ife Brown Yellow	-2.53	1.23	2.09	-1.10	1.61	
Ife BPC x Ife Brown Crinkled	-2.87	0.86	1.31	0.18	2.08	
Ife BPC x Ife Brown Yellow	1.41	-1.14	-1.24	0.95	-0.86	
Ife Brown Crinkled x Ife Brown Yellow	3.52	0.17	0.09	0.89	1.09	
EMS	12.15	0.97	2.30	0.82	2.66	
Estimates	11.84	0.95	2.16	0.82	2.41	
Std. Error	7.02	0.56	1.34	0.47	1.54	
Sig.	*	*	*	*	*	

*= significance at 5% level of probability:

DTF= Days to Flowering; PL= Pod Length (cm); NSP= Number of seeds/pod; 100SW= 100 seed weight; SYP= Seed Yield/Plant

Specific Combining Ability (SCA)

Based on the analysis of variance, significant differences of characters studied were registered in the specific combining ability of the cross combinations of the four cultivars of cowpea, Ife Brown. The SCA effects for days to flowering ranged from -4.59 (Ife Brown x Ife BPC) to 3.52 (Ife Brown Crinkled x Ife BrownYellow);for pod length it ranged from -1.14 (Ife BPC x Ife Brown Yellow) to 1.23 (Ife Brown x Ife Brown Yellow). In the number of seeds/pod the SCA effects ranged from -1.24 (Ife BPC x Ife Brown Yellow) to 2.09 (Ife Brown x Ife Brown Yellow while in the seed yield/plant it ranged from -0.86 (Ife BPC x Ife Brown Yellow) to 2.08 (Ife BPC x Ife Brown Crinkled). The SCA effects for the cross Ife Brown Crinkled x Ife Brown Yellow registered positive SCA in days to flowering, pod length, number of seeds/pod, 100 seed weight and seed yield/plant.

Tuble 4. Estimates of Generic Variance Components of Cowpea Cattivar ife brown and its three matants						
VARIANCES	DTF	PL	NSP	100SW	SYP	
V _A	50.39	0.00	0.00	1.15	2.08	
VD	47.35	3.79	8.66	3.27	9.63	
h ₂ narrow	0.51	0.00	0.00	0.26	0.17	
H ₂ broad	0.99	0.99	0.98	0.99	0.98	
Dominance Ratio	1.37	#	#	2.38	3.04	

Table 4: Estimates o	f Genetic Va	ariance Compon	ents of cowpea	ı cultivar ife brown	and its three mutants

 V_A = Variance due to additive gene effects; V_D = Variance due to Dominance gene effects; h_2 = narrow sense heritability; H_2 = broad sense heritability; DTF= Days to Flowering; PL= Pod Length (cm); NSP= Number of seeds/pod; 100SW= 100 seed weight; SYP= Seed Yield/Plant

Genetic Variance Components

The estimates of genetic variance components of additive (V_A) and dominance (V_D) gene effects and narrow (h_2) and broad (H_2) heritability for days to flowering, pod

length, number of seeds/pod, 100 seed weight and seed yield/plant as shown in Table 5. For the characters studied, variance due to additive gene effects was highest in days to flowering while it was 0.00 in pod length and

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number of seeds/pod. The variance due to dominance gene effects in the characters studied was highest in days to flowering (47.35) and least in 100 seed weight (3.27). In the heritability estimates, the broad sense heritability is very high in all the traits studied ranging from 0.98 to 0.99. For the narrow sense heritability, it ranged from 0.00 (pod length and number of seeds/pod) to 0.51 (days to flowering).

IV. DISCUSSION

The significance that was registered in the mean performance in days to flowering, pod length, number of seeds/pod, 100 seed weight and seed yield/plant of the parental lines and F_1 cross combinations of half diallel of 4 cowpea Ife Brown cultivars indicating substantial amount of genetic variability among the parents for these characters studied. An overall appraisal of the general combining ability (GCA) effects of the parents used in the present study indicated that Ife BPC was observed to be the best general combiner for days to flowering and seed yield/plant as indicated in the positive values of GCA recorded thus implying that it can be used in cowpea breeding programme to improve days to flowering and seed yield potential.

The error mean square of GCA in days to flowering, 100 seed weight and seed yield/plant was higher than the error mean square of SCA thus implying that additive gene action played a more important role in the inheritance of these traits than the non-additive (dominance and epistasis) gene action. This findings is in accordance with the reports of Zaveri, et al., 1983; Aravindhan and Das, 1996; Hazra, et al., 1996; Jayarani and Manju, 1996; Ponmariamma and Das, 1997; Chaudhari et al., 1998; Singh, et al., 2006; Patel, et al., 2010; Uma and Kalubowila, 2010; Chaudhari, et al., 2013 and Patel, et al., 2013 indicating that both additive and dominance components were important in the inheritance of these traits.

All these crosses involved either good x good, good x average, good x poor, average x poor or poor x poor general combiners. The SCA effects of the crosses did not show any specific trend for good general combining effects of the parents involved in these combinations. However, in majority of crosses, good x good, good x poor and poor x poor combinations resulted in high SCA effects. The SCA represents dominance and epistatic components which are non-fixable variation in nature. High positive SCA obtained in crosses involving Ife Brown Yellow with Ife Brown in pod length and number of seeds/pod while with Ife Brown Crinkled for days to flowering were recorded. These crosses involved a good general combiner parent (Ife Brown Yellow) and poor ones (Ife Brown and Ife Brown Crinkled) hence implying that non-additive gene action plays major role in the inheritance of days to flowering, pod length and number of seeds/pod thus yielding transgressive and stable performing segregants possessing enhanced potential of these traits. These findings are in agreement with earlier findings of Zaveri *et al.* 1983, Aravindhan and Das, 1996, Singh *et al.*, 2006, Patil and Nawale, 2006, Kwaye *et al.*, 2008, Patel *et al.*, 2008, Meena *et al.*, 2010 and Chaudhari *et al.*, 2013.

In addition to knowledge of combining ability, the nature and mode of inheritance of quantitative characters are helpful to formulate a more pragmatic breeding programme. The diallel cross technique has long been used for obtaining information regarding type of gene action involved in the inheritance of different quantitative characters. For the the characterrs studied, the variance due to additive gene effects was higher than the variance due to dominance gene effects in days to flowering while it was 0.00 in pod length and number of seeds/pod thus indicating that pod length and number of seeds/pod showed that they are mostly controlled by dominance (non-additive) gene action. The high broad sense heritability obtained in this study for the characters studied showed that there is not much environmental effects while the low narrow sense heritability recorded in pod length, number of seed/pod and seed yield/plant were as a result of small amount of additive gene effects compared to the dominance gene effects. The low narrow sense heritability estimates indicated a major role of nonadditive gene action in the inheritance of these characters studied and hence there are of limited scope for improvement in these characters through direct selection. This finding is in accordance with by Thiyagarajan et al., 1990; Patel et al., 1994; Sawant et al., 1995; Jayarani and Manju, 1996; Ponmariamma and Das, 1997; Chaudhari et al., 1998; Singh et al., 2006; Patel et al., 2010; Uma and Kalubowila, 2010; Chaudhari et al., 2013 and Patel et al., 2013 for days to flowering, pod length, 100-seed weight and seed yield/plant.

V. CONCLUSION

Selection of parents based on their performance per se alone, may not always be a sound procedure, since phenotypically superior genotypes may yield inferior hybrids and/or poor recombinants in the segregation generations. It is therefore essential that parents are selected on the basis of their genetic worth.

An efficient cowpea breeding programme should involve parents with desirable agronomic traits and good general

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combining ability for seed yield and its components, which in cross combination, may result in high heterosis over the better parent, high heterosis over standard parent, specific combining ability and high per se performance. On the basis of this the cross combination involving Ife Brown Yellow showed the most promising combinations for seed yield per plant and thus can be utilized effectively in the breeding programme. As cowpea is selfpollinated crop, the genetic variability resulting from additive effects can be effectively utilized through selection followed by hybridization in segregating generations. It is, therefore, suggested that biparental mating, intermatting of elite segregants and selection at later generations should be followed which meets the requirement of utilizing both types of gene actions.

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