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Combining Ability of Cowpea (*Vigna unguiculata* (L) Walp) Genotypes for Resistance to Cowpea Bacterial Blight in Uganda

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ABSTRACT

The low productivity of cowpea is partly attributed to a number of constraints including diseases such as cowpea bacterial blight (CoBB). Cowpea bacterial blight has the capacity to cause up to 92% yield loss under severe infections. The objective of this study was to determine the combining ability for resistance to CoBB among cowpea genotypes in Uganda. Nine selected parents were crossed to produce 63 progenies. F1 progenies were evaluated and data gathered included days to 50% flowering, CoBB disease scores and grain yield. The mean squares for rAUDPC due to GCA and SCA effects were significant (P≤0.001) and non-significant respectively. The broad sense coefficient of genetic determination (BCGD) and narrow sense coefficient of genetic determination (NCGD) were 44.3% and 29.1% respectively for rAUDPC. Parents WC 26 (-0.023) and NE 31 (-0.035) had highly significant negative GCA effects for rAUDPC and were therefore good general combiners for this trait. Crosses SECOW 3B x ACC 26 X SECOW 1T and WC 26 x NE 32 had negative significant SCA effect for rAUDPC with a values of -0.073 and -0.06, respectively while Crosses ACC 26 x SECOW 1T x NE 40 (-0.07) and NE 40 x WC 26 (-0.06) had significant negative reciprocal effects for rAUDPC. This study revealed that genetic inheritance for cowpea bacterial blight was controlled predominantly by additive gene effects. Parents WC 26 and NE 31 identified as good general combiners for resistance to CoBB could be utilized as sources of resistance while Crosses SECOW 3B x ACC 26 X SECOW 1T, WC 26 x NE 32, ACC 26 X SECOW 1T x NE 40 and NE 40 x WC 26 that were the best specific combiners for resistance to CoBB could be put under further evaluation as potential varieties.

INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp.), family Fabaceae (2n = 22) (Lonardi *et al.*, 2019), is a vital and economically important indigenous African legume crop to the livelihood of several millions of people in sub-Saharan Africa (SSA) (Carvalho *et al.*, 2017). Cowpea is predominantly cultivated in the drought-prone regions of Eastern, Central and Western parts of Africa (Horn et. al., 2022, Oyewale and Bamaiyi, 2013). The importance of cowpea cuts across its use as a staple food and cash crop (Mbavai *et al.*, 2015). The crop is useful in various ways, for instance, the grains serve as inexpensive and nutritious food to relatively poor urban communities (Silva et. al., 2018). In addition to being sold as green vegetables, cowpea leaves are also utilized as animal fodder in Benin, Cameroon, Ethiopia, Ghana, Kenya, Malawi, Mali, Tanzania and Uganda (Alemu *et al.*, 2019, Pottorff *et al.*, 2012,).

Despite the numerous benefits of cowpea as food and a component of the farming system, the productivity of the crop especially among smallholder farmers has remained very low at 0.5 t/ha (Kebede & Bekeko 2020, Okonya *et al.*, 2014) compared to the potential yield of 3 t/ha reported for improved varieties (Ayalew *et al.*, 2021, Ashinie *et al.*, 2020). In most regions of SSA, the crop is threatened by several diseases, including cowpea bacterial blight (CoBB) caused by *Xanthomonas axonopodis pv. vignicola (Xav)* among other constraints. Cowpea bacterial blight was first reported in the United States of America during the mid-20th century (Nandini, 2012). In Africa, Tanzania first documented the disease in 1964 (Allen, 1981), Nigeria in 1975 (Williams, 1975) while Uganda reported the first occurrence of CoBB in the early 1990s (Edema *et al.* 1997). Most countries where cowpea is grown have recorded cases of CoBB to date (Nandini and Kulkarni, 2016; Bastas & Sahin, 2017; Durojaye *et al.*, 2019). *Xanthomonas axonopodis pv. vignicola (Xav)* affects stems, pods and seeds though the primary effects are on the leaves, and depending on the genotypes' susceptibility, it may result in full defoliation (Claudius-Cole *et al.*, 2014). Therefore with the increasing threat posed by CoBB to cowpea production in Uganda, it is of great importance to breed cowpea varieties with resistance to CoBB and enhanced yield. In the process of developing new plant varieties, it is imperative to understand the mode of gene action involved in the expression of important traits (Boukar *et al.*, 2020). Understanding gene action will help the breeder in selecting suitable parents and choosing appropriate breeding strategy in a breeding program (Owusu *et al.*, 2018, Falconer and Mackay, 1996). The basis for identification of the best parents and their crosses is through combining ability analysis (Pallavi *et al.*, 2018, Muhinyuza *et al.*, 2016, Kwaye *et al.*, 2008). The general combining ability (GCA) gives an indication of the average contribution of a parent to its progeny; it provides an estimation of the parental gametic contribution to its offspring by the mean performance of the progeny (Begna, 2021, Falconer and Mackay, 1996).

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The specific combining ability (SCA) is the deviation from the progeny mean from the expected on the basis of GCA (Mwale, 2017, Bradshaw and Mackay, 1994).

Therefore, genetic variability which is a basis for plant improvement is necessary and can be achieved through hybridization. The diallel cross as a method of hybridization has been defined as the group of all possible crosses among several parental genotypes (Owusu *et al.*, 2020, Griffings 1956). Diallel analysis has been used in cowpea to provide important information on GCA and SCA, determine genetic variances, estimate heritability, and maternal effects (Dieni, *et al.*, 2019, Hazra *et al.* 1994). Therefore, a study of the combining abilities of a set of genotypes, through diallel analysis, will undoubtedly contribute to the achievement of the research objectives. The objective of this study was to determine the mode of inheritance for resistance to Cowpea Bacterial Blight disease among cowpea genotypes in Uganda. This will contribute to the development of CoBB resistant high yielding cowpea varieties.

MATERIALS AND METHODS

Nine cowpea genotypes obtained from the National Semi-Arid Resources Research Institute (NaSARRI) Serere, Uganda were selected and used as parents. Four of the parents were resistant, 2 moderately susceptible and 3 susceptible (Table 1). These genotypes were selected based on their adaptation to wider agro-ecology, preference by farmers and resistance to other biotic and abiotic stresses.

The nine cowpea parental lines were each planted separately in a bucket (4 seeds planted and then thinned to 2 plants per bucket) in February 2021. Each genotype was hand emasculated before pollen shedding and crossed at flowering in all possible combinations following Griffing's (1956) diallel mating design to produce 29 F1 crosses and 34 reciprocal crosses, but there were 9 missing crosses. The F1 crosses and the reciprocals were selfed to produce F2 seeds in a screen house.

Evaluation trials were set up at Makerere University Agricultural Research Institute - Kabanyolo (MUARIK),

Table 1: Characteristics of Parental genotypes used in the study

Genotypes	Cultivar Type	Maturity	Yield (t/ha)	Diseases Response
NE 32	Landrace	Medium	1.7	Resistant
NE 44	Landrace	Medium	1.7	Resistant
WC 32A	Landrace	Late	1.3	Resistant
WC 26	Landrace	Medium	1.9	Resistant
ACC 26 X SECOW 1T	Inbred line	Early	1.8	Moderately susceptible
SECOW 3B	Improved variety	Early	1.4	Moderately susceptible
NE 31	Landrace	Early	1.4	Susceptible
NE 37	Landrace	Late	1.5	Susceptible
NE 40	Landrace	Late	1.9	Susceptible

located in the Central part of Uganda – Wakiso district, 17.3 km North of Kampala (0°28'N and 32°37'E; 1200m above sea level) from March to June 2022. The average rainfall and relative humidity recorded during the first experimental period were 162.8 mm and 69 – 87%, respectively. The evaluation trial was laid out in an alpha lattice design of 8 blocks x 9 plots with three replications and a spacing of 1m x 2m. All the 9 parents were planted with F2 seeds of 29 crosses and 34 reciprocal crosses.

The plants were rated for disease severity at 6 weeks after planting and subsequently at 7 days intervals for 4 weeks (Jackai & Singh, 1988, Shi *et al.*, 2016). Disease severity were scored on 5 selected plants from two middle rows of each plot excluding plants at the beginning and end of rows. Disease severity was evaluated using a disease scale of 1 – 5 by Withanage (2005), with modification to assess the percentage of leaf surfaces covered by the CoBB symptoms, where: 1 = 0% or No symptoms; 2 =1 to 15% (resistant); 3 =16 to 30% (moderately resistant), 4 =31 – 45% (moderately susceptible) and 5 =46% and above (susceptible). For all plots and assessment dates, the relative area under the disease progress curve RAUDPC (Fry, 1978, Lima-Primo *et al.*, 2019) was calculated using the formula in equation 1:

$$rAUDPC = \frac{\sum(T_{i+1} - T_i)*\left(\frac{D_{i+1}+D_i}{2}\right)}{T_{Total}*100} \text{ ---------- Equation 1}$$

Where; T_i is the ith day when an estimation of percent foliar late blight was made

D_i is the estimated percentage of area with blighted foliage at T_i.

T_{Total} is the number of days at which the final assessment was recorded.

Days to 50% flowering was recorded for all genotypes. At maturity, plants were harvested manually from each plot and data on yield was collected.

Combining ability analysis was performed whereby the genetic variance component was partitioned into general and specific combining ability (GCA and SCA) variances according to Griffing's (1956) method III, model 1. The statistical linear model used is shown in equation 2:

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + e_{ij} \text{ ----- Equation 2}$$

Where;

Y_{ij} = observed value from each experimental unit

μ is the grand mean,

g_i and g_j are GCA effects of the ith and jth parents respectively,

s_{ij} is the SCA effect for the combination between the i_{th} and j_{th} parents and eij is experimental error.

Broad and narrow sense coefficient of genetic determination (BS-CGD; NS-CGD) were computed using the formulas (equation 3 and 4) described by Dabholkar (1999). The relative importance of additive versus non-additive gene effects was determined according to the ratio established by Baker (1978) as shown in equation 5.

$$\mathbf{BS-CGD} = \frac{2\times\sigma^2GCA + \sigma^2SCA}{2\times\sigma^2GCA + \sigma^2SCA + \frac{\sigma^2e}{r}} \text{ ----------Equation 3}$$

$$\mathbf{NS-CGD} = \frac{2\times\sigma^2GCA}{2\times\sigma^2GCA + \sigma^2SCA + \frac{\sigma^2e}{r}} \text{ ----------Equation 4}$$

$$\mathbf{BR} = \frac{2\times\sigma^2GCA}{2\times\sigma^2GCA + \sigma^2SCA} \text{ ----------Equation 5}$$

Where; r is number of replications,
σ^2GCA and σ^2SCA are variance components estimates of GCA and SCA, respectively and
σ^2e is the variance due to experimental error.
A two-tailed t-test was performed to test the significance of individual parent GCA and SCA effects of F2 generation crosses using the following formula in equation 6:

$$\mathbf{tGCA_i} = \frac{GCA_i}{S.E\ GCA} \text{ and } \mathbf{tSCA_{ij}} = \frac{SCA_{ij}}{S.E\ SCA} \text{ ----------Equation 6}$$

Where; GCA_i is the GCA effect of the ith parent
SCA_{ij} is the SCA effect of the combination between the ith female and jth male parents,
S.E GCA and S.E SCA are the standard errors of GCA and SCA effects, respectively.

RESULTS

The analysis of variance for combining ability, variance components, Baker's ratio, narrow and broad sense coefficient of genetic determination for rAUDPC, grain yield and days to 50% flowering for F1 progenies are presented in table 2.
Analysis of variance showed significant effects due to GCA (P≤0.001), reciprocals (P≤0.05) and non-significant effects due to SCA for rAUDPC. Grain yield had non-significant effects due to GCA, significant effects due to SCA (P≤0.001) and reciprocals (P≤0.01). For days to 50% flowering, the effects due to GCA, SCA and reciprocals were significant at (P≤0.01), (P≤0.001) and (P≤0.001) respectively.
Baker's ratio as estimated from variance components was 65.8% for rAUDPC, 0.7% for grain yield and 24.9% for days to 50% flowering. The broad sense coefficient of genetic determination (BCGD) analogous to broad sense heritability and narrow sense coefficient of genetic determination (NCGD) which is similar to narrow sense heritability were estimated from variance components were 44.3% and 29.1% respectively for rAUDPC, 65.3% and 0.5% respectively for grain yield and 55.5% and 13.8% respectively for days to 50% flowering.
The results for specific combining ability and reciprocal effects of F1 crosses for rAUDPC, grain yield, and days to 50% flowering are presented in table 3.
Parents WC 26 (-0.023) and NE 31 (-0.035), had highly significant negative GCA effects at (p≤0.01) and (p≤0.001) respectively for rAUDPC while positive significance GCA effects (p<0.001) were observed for parents NE 44 (0.027) and ACC 26 x SECOW 1T (0.039). The remaining five parents had non-significant GCA effects for rAUDPC.
Parent WC 32A (0.23t/ha) had positive significant GCA effects (p≤0.001) for yield while NE 31 (-0.15 t/ha) being negatively significant for yield at (p≤0.05) (Table 6). For days to 50% flowering, parents NE 44 (-1.8 days), NE 40 (-1.2 days) had negative significant GCA effects of (p≤0.05) and (p≤0.01) respectively, while NE 31 (1.7days), NE 37 (1.8 days) and SECOW 3B (1.5days) had positive significant GCA effects at (p≤0.001), (p≤0.01) and (p≤0.01) respectively.
The results for specific combining ability and reciprocal effects of F1 crosses for rAUDPC, grain yield, and days to 50% flowering are presented in table 4.
The crosses SECOW 3B x ACC 26 X SECOW 1T (-0.073) and WC 26 x NE 32 (-0.060) had negative significant SCA effect at (p≤0.01) and (p≤0.05) respectively for rAUDPC, while the cross of NE 44 x ACC 26 X SECOW 1T had significant (p<0.05) positive SCA effect of 0.056 for rAUDPC. The remaining cross combinations had non-significant SCA effects for rAUDPC. Crosses ACC 26 X SECOW 1T x NE 40 (-0.070) and NE 40 x WC 26 (-0.060) had significant (p≤0.05) negative reciprocal effects for rAUDPC while NE 44 x SECOW 3B (0.090), NE 37 x NE 44 (0.075) and NE 40 x NE 44 (0.075) had significant (p≤0.01) positive reciprocal effects for

Table 2: ANOVA for Combining Ability and Heritability Estimates for Raudpc, Grain Yield and Days to 50% Flowering For f1 Progenies.

SOV	DF	rAUDPC	GY	DTF
Crosses	62	0.004***	0.39***	20.06***
GCA	8	0.007***	0.14	21.97**
SCA	28	0.002	0.58***	20.74***
Reciprocal	26	0.003*	0.26**	18.75***
Error	85	0.002	0.13	7.59
NS-CGD (%)		29.1	0.5	13.8
BS-CGD (%)		44.3	65.3	55.5
Baker's ratio (%)		65.8	0.7	24.9

, **, *; significance level at P ≤ 0.05, P ≤ 0.01 and P ≤ 0.001 respectively, DF; degrees of freedom, GCA; general combining ability, SCA; specific combining ability, NS-CGD; narrow sense coefficient of genetic determination, BS-CGD ; broad sense coefficient of genetic determination, rAUDPC; relative area under disease progress curve, GY; grain yield*

rAUDPC. For yield, cross WC 26 x NE 32 had significant (p≤0.001) positive SCA effect (1.31 t/ha) and NE 37 x NE 32 displayed significant (p≤0.01) negative SCA effect (-0.61 t/ha). Additionally, the reciprocal effects showed that ACC 26 X SECOW 1T x WC 32A had the highest significant (p≤0.001) positive reciprocal effect (1.14 t/ha) and NE 40 x NE 44 had the lowest significant (p≤0.05) negative reciprocal effect (-0.55 t/ha).

Crosses NE 40 x NE 31, SECOW 3B x NE 37, WC 26 x NE 31, and WC 26 x NE 32 displayed highest significant (p≤0.05) positive SCA effects (4 days) and SECOW 3B x NE 31 displayed lowest significant (p≤0.01) negative SCA effect (-6 days) for days to 50% flowering. Cross combinations NE 40 x NE 44, NE 37 x NE 44, and NE 32 x SECOW 3B had negative significant reciprocal effects and NE 31 x WC 26, NE 32 x NE 37, NE 40 x SECOW 3B and SECOW 3B x WC 32A had positive significant reciprocal effects for days to 50% flowering.

Table 3: General Combining Ability (GCA) values of parents in rAUDPC, grain yield and days to 50% flowering of the F1 progenies

Parents	rAUDPC	GY	DTF
ACC 26 X SECOW 1T	0.039***	-0.06	-0. 7
NE 31	-0.035***	-0.15*	1.8***
NE 32	-0.004	-0.06	-0. 6
NE 37	-0.006	-0.04	1.8**
NE 40	-0.009	-0.03	-1.2*
NE 44	0.027**	0.00	-1.8**
SECOW 3B	0.007	0.03	1.5**
WC 26	-0.023**	0.07	0.0
WC 32A	0.003	0.23**	-0.7
S.E. GCA	0.01	0.08	0.6

, **, *; significance level at, P ≤ 0.05, P ≤ 0.05 and P ≤ 0.001 respectively, rAUDPC; relative area under disease progress curve, DTM; days to maturity, GY; grain yield*

Table 4: Specific Combining Ability (SCA) and Reciprocal effects of F1 progenies for rAUDPC, yield, days to 50% flowering and days to 50% flowering

Sca Effects	0.024	0.14	3.1	Reciprocal Effects	Raudpc	Gy	Dtm
Ne 31 X Acc 26 X Secow 1t	0.008	-0.07	1.7	Acc 26 X Secow 1t X Ne 31	0.005	-0.45	-1.3
Ne 32 X Acc 26 X Secow 1t	-0.006	0.43	-5.0**	Acc 26 X Secow 1t X Ne 32	0.000	-0.38	-1.5
Ne 32 X Ne 31	-0.047	-0.61**	-1.0	Acc 26 X Secow 1t X Ne 37	0.000	0.00	0.0
Ne 37 X Ne 32	-0.002	-0.14	-0.9	Acc 26 X Secow 1t X Ne 40	-0.070*	-0.19	-1.3
Ne 40 X Acc 26 X Secow 1t	0.015	0.15	4.0*	Acc 26 X Secow 1t X Ne 44	0.036	-0.43	-0.3
Ne 40 X Ne 31	-0.017	0.45*	2.5	Acc 26 X Secow 1t X Secow 3b	0.005	-0.10	1.3
Ne 40 X Ne 32	0.056*	0.03	-4.0*	Acc 26 X Secow 1t X Wc 26	0.000	-0.10	-1.8
Ne 44 X Acc 26 X Secow 1t	-0.023	-0.52*	1.0	Acc 26 X Secow 1t X Wc 32a	-0.045	1.14***	-1.0
Ne 44 X Ne 37	-0.020	-0.19	2.0	Ne 31 X Ne 32	-0.003	-0.45	0.0
Ne 44 X Ne 40	-0.073**	-0.13	0.3	Ne 31 X Ne 37	0.000	0.00	0.0
Secow 3b X Acc 26 X Secow 1t	0.009	0.09	-6.0**	Ne 31 X Ne 40	0.048	-0.34	-0.8
Secow 3b X Ne 31	0.030	-0.43	0.5	Ne 31 X Ne 44	0.000	0.00	0.0
Secow 3b X Ne 32	0.022	0.44	4.0*	Ne 31 X Secow 3b	-0.068	-0.21	-2.3
Secow 3b X Ne 37	-0.032	0.17	0.6	Ne 31 X Wc 26	-0.022	0.40	5.0*
Secow 3b X Ne 40	0.029	0.04	-1.3	Ne 31 X Wc 32a	0.005	-0.05	0.0
Secow 3b X Ne 44	-0.003	-0.45*	-1.6	Ne 32 X Ne 37	0.030	0.33	5.0*
Wc 26 X Acc 26 X Secow 1t	0.003	-0.24	4.0*	Ne 32 X Ne 40	0.048	-0.36	-1.8
Wc 26 X Ne 31	-0.060*	1.31***	4.0*	Ne 32 X Ne 44	0.000	0.00	0.0
Wc 26 X Ne 32	-0.028	-0.28	1.7	Ne 32 X Secow 3b	-0.020	0.06	-6.0**
Wc 26 X Ne 37	0.015	-0.23	-2.8	Ne 32 X Wc 26	0.000	0.00	0.0
Wc 26 X Ne 40	0.007	0.18	-1.3	Ne 32 X Wc 32a	0.000	0.18	3.5
Wc 26 X Secow 3b	-0.019	0.69**	-0.7	Ne 37 X Ne 40	0.000	0.00	0.0
Wc 32a X Acc 26 X Secow 1t	-0.020	-0.39	-1.2	Ne 37 X Ne 44	0.075**	0.12	-5.0*
Wc 32a X Ne 31	-0.011	-0.13	0.2	Ne 37 X Secow 3b	-0.050	-0.22	1.8
Wc 32a X Ne 32	0.044	-0.55	-1.2	Ne 37 X Wc 32a	0.000	0.00	0.0
Wc 32a X Ne 40	-0.007	-0.14	-0.6	Ne 40 X Ne 44	0.075**	-0.548*	-8.0***

Wc 32a X Ne 44	0.008	-0.37	2.8	Ne 40 X Secow 3b	0.013	-0.14	6.0**
Wc 32a X Secow 3b	0.000	-0.48*	0.1	Ne 40 X Wc 26	-0.060*	-0.30	-1.5
Wc 32a X Wc 26	0.025	0.23	1.8	Ne 44 X Secow 3b	0.090**	-0.17	1.0
Se Sca				Ne 44 X Wc 26	0.000	0.00	0.0
				Ne 44 X Wc 32a	-0.045	0.04	-0.5
				Secow 3b X Wc 26	0.027	0.23	-0.8
				Secow 3b X Wc 32a	-0.030	0.24	4.0*
				Wc 26 X Wc 32a	0.043	-0.22	1.0
				Se Reciprocals	0.028	0.26	1.9

, **, *; significance level at, P ≤ 0.05 P ≤ 0.01 and P ≤ 0.001 respectively, rAUDPC; relative area under disease progress curve, DTM; days to maturity, GY; grain yield and SE is standard error.*

DISCUSSION

The significant effects due to GCA and non-significant effect of SCA for rAUDPC suggested that additive gene action was involved in the level of resistance to CoBB disease in these genotypes. More so, non-significant effects of GCA and significant effects due to SCA for grain yield suggested that the inheritance of this trait was controlled by non-additive action. Significant effects due to GCA and SCA observed for days to 50% flowering suggested that both additive and non-additive gene action were controlling the inheritance of this trait and significant effects due to reciprocals for rAUDPC, grain yield and DTF indicated the influence of cytoplasmic factors on these traits. Similar results were reported by Alladassi *et al.* (2017) and Rodrigues *et al.* (1999) who observed significant GCA and non-significant SCA effects for bacterial blight disease in common beans. Romanus *et al* (2008) reported significant GCA and non-significant SCA effects for grain yield and also observed similar results in which significant GCA and SCA effects for days to flowering were observed.

High value of Baker's ratio observed in this study for rAUDPC implied high predictability of a hybrid's performance for resistance to CoBB disease on the basis of the parents' GCA effects (Dabholkar, 1999 and confirmed the relative importance of additive genetic effects over the non-additive effects in this set of crosses for CoBB resistance. The additive genetic effects give a better basis for predicting the breeding value of a parent for hybrids as they represent the transmitted effects from one generation to the next (Hallauer *et al.*, 1988; Rubaihayo, 1996).

Average broad sense heritability estimates for rAUDPC, grain yield and DTF obtained suggested average genetic contribution towards the phenotypic variance of the traits. As a result, a greater percentage of the phenotypic variation for CoBB were due to environmental variance implying that the phenotypes did not greatly reflect the genotypes. The low estimates of narrow sense heritability for rAUDPC (29.1), grain yield (0.5%) and DTF (13.8%) observed among crosses suggested low proportions of the phenotypic variation was due to additive genetic effects.

Parents displaying significant GCA effects in the desired direction for a character of interest are the best for hybridization (Mwale *et al.*, 2017). Parents WC 26 and NE 31 were therefore good general combiners for rAUDPC. However, considering GCA effects for this trait alongside GCA for grain yield and DTF, the best and most suitable general combiner for rAUDPC was parent WC 26 which in addition had desirable GCA effects for other traits. This therefore suggested that parent WC 26 would contribute to increasing CoBB resistance without compromising grain yield and days to 50% flowering and can be used in a breeding program as a source of CoBB resistance.

Positive significant GCA effects are desirable for grain yield improvement while negative GCA effects are desired for introgression of genes for earliness. Therefore, WC 32A was a good general combiner for grain yield while NE 40 and NE 44 were good general combiners for days to 50% flowering suggesting that they are good parents to use in a breeding program to develop high yielding early maturing varieties. Making crosses out of two good general combiners governed by additive x additive gene actions may produce transgressive segregants in the advanced generations for the traits, thereby producing hybrids with good specific combining ability (Ayo-Vaughan *et al.*, 2013).

The F1 progenies WC 26 x NE 32 and SECOW 3B x ACC 26 X SECOW 1T showed desirable negative significant SCA effects for rAUDPC, implying that these progenies performed better than what was predicted based on their parents' GCA effects. The mean performance for rAUDPC of WC 26 x NE 32 and SECOW 3B x ACC 26 X SECOW 1T was above the mean rAUDPC of all the crosses. The dominance of these crosses may be due to complementary and duplicate gene actions (Ceyhan *et al.*, 2014) 1989). As such these crosses are expected to produce desirable segregants and could be exploited in cowpea varietal improvement programs. A large and negative SCA effects for a trait suggests the possibility of transgressive segregation for the trait in later generation of selfing (Ojo, 2003).

CONCLUSION AND RECOMMENDATIONS

This study revealed that genetic inheritance for cowpea bacterial blight and grain yield were predominantly controlled by additive gene effects and non-additive gene effects respectively while days to 50% flowering controlled by both additive gene effects and non-additive gene effects. The inheritance of resistance to CoBB, grain yield and days to flowering were influenced by maternal

effects.

Parents WC 26 and NE 31 were identified as good general combiners for resistance to CoBB and therefore source of resistance. Parents WC 32A and NE 44 were the best general combiners for grain yield and days to flowering respectively and can therefore be used to introgress genes for high yield and earliness respectively.

Crosses SECOW 3B x ACC 26 X SECOW 1T, WC 26 x NE 32, ACC 26 X SECOW 1T x NE 40 and NE 40 x WC 26 were the best specific combiners for resistance to CoBB. Crosses WC 26 x NE 32 and ACC 26 X SECOW 1T x WC 32A were best specific combiners for grain yield. Cross combinations SECOW 3B x NE 31, NE 40 x NE 44, NE 37 x NE 44, and NE 32 x SECOW 3B were the best desired specific combiners for days to flowering. These crosses can be utilized in a breeding program to develop CoBB disease resistant, high yielding and early maturing lines.

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