



Received: 04 July 2018
Accepted: 31 August 2018
First Published: 05 September 2018

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SOIL & CROP SCIENCES | RESEARCH ARTICLE

Gene action and combining ability studies for grain yield and its related traits in cowpea (*Vigna unguiculata*)

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Abstract: Identification of superior genotypes from variability generated via hybridization and understanding the nature of the gene action controlling grain yield and related traits are crucial for cowpea varietal improvement. A field experiment was conducted at the Savannah Agricultural Research Institute, Tamale-Ghana in the 2016 cropping season to examine the combining ability, genotypic and phenotypic correlations for grain yield and other agronomic characters in 25 cowpea genotypes (5 parents and 20 hybrids derived from a diallel cross of the parents). The result indicated that the general combining ability and specific combining ability varied for all characters measured signifying the prominence of both additive and non-additive genetic components in the present study. Non-additive gene action was important for grain yield, canopy width at maturity, plant height (PLHTF), number of seeds per pod, pod weight and days to 50% flowering (DFF). On the other hand, additive gene action was important for days to maturity (DM) and pod length. Parents PADI-TUYA and IT86D-610 were observed to be good general combiners for grain yield and other traits while IT86D-610 × PADI-TUYA, SONGOTRA × PADI-TUYA and IT86D-610 × SARC 57-2 were identified as promising specific combiners for

ABOUT THE AUTHOR

The authors are plant breeders with research focus on the assessment of genetic diversity in crops, particularly grain legumes to enhance genetic improvement of yield as well as towards resilience to climate variability. The group's research activities seek to contribute to food security and poverty alleviation by increasing the production, productivity and utilization of cowpea in Ghana. The authors are experienced in conducting participatory varietal selection, out scaling of improved cowpea varieties, development of climate smart technologies, nutritional sensitization of cowpea, training of Agricultural Extension Agents (AEAs), seed producers and farmers on good agronomic practices for cowpea production.

PUBLIC INTEREST STATEMENT

Cowpea is an important leguminous crops in Ghana because of its crucial role in human diet for proteins, minerals and energy. The potential of cowpea to address food and income security in Ghana is well established. This is the first study that evaluates yield performance and combining ability effects of cowpea genotypes in Guinea and Sudan Savannah agro-ecological zones of Ghana using diallel mating design. The research was designed to elucidate the nature of gene action controlling grain yield and related traits in cowpea. The study revealed that the inheritance of grain yield and its related traits in cowpea is conditioned by both additive and non-additive genetic actions. The information provided in this study is useful to understand the interaction between grain yield and other traits in the cowpea improvement programme. This is expected to boost cowpea production in Ghana through development and deployment of high-yielding climate resilient varieties.

grain yield and related traits. Selection criteria to improve the grain yield of cowpea should focus on plants with long peduncles, high canopy width and many pods per plant as these traits have high genetic correlation with grain yield.

Subjects: Agriculture & Environmental Sciences; Plant & Animal Ecology; Earth Sciences

Keywords: diallel mating design; heterosis; genotypic correlation; *Vigna unguiculata*

1. Introduction

Cowpea (*Vigna unguiculata* L. Walp.) is one of the most important and native grain legume crops in sub-Saharan Africa (SSA) which accounts for about 64% of the annual world production of 7.6 million tonnes (Sivakumar et al., 2013; Timko & Singh, 2008). An average of 143,000 MT is produced annually on about 156,000 ha making Ghana the fifth highest producer of cowpea in SSA (ICRISAT, 2012). In Ghana, the crop is predominantly cultivated by resource limited small holder farmers usually women with an average farm size of 0.5–1.0 ha and yield of 0.5 t ha⁻¹ (Wiggins, 2009; Wiggins and Sharada, 2013). It is essential to develop high-yielding cowpea varieties to help improve production and productivity of the crop in Ghana.

Grain yield is one of the most important but complex traits in crop improvement programmes. It is the result of interaction of the environment with all growth and development processes that occur at vegetative and reproduction stages of the crop (Quarrie et al., 2006). Grain yield in cowpea directly depends on yield components such as number of pod per plant, number of seeds per pod and 100 seed weight, and is highly influenced by both genetic and environmental factors (Hassan et al., 2005; Wattoo et al., 2009). Therefore, selection on the basis of grain yield alone is usually not efficient. Hence, selection along with yield and its associated components can improve the efficiency of selection in plant breeding programs (Romanus et al., 2008).

Different environmental conditions which result in yield variations in cowpea, have led to the development of cowpea improvement programmes that depend on selection of lines developed from potential parents (Romanus et al., 2008). According to Dar et al. (2014), the per se performance of parents is not always a true indicator of its potential to exploit the hybrid combination. The nature and magnitude of gene action controlling quantitative traits is very useful for successful development of crop varieties through proper choice of parents for hybridization programme (Baker, 1978; Falconer, 1989; Griffings, 1956). There is therefore the need to make a proper choice of parents that will provide potential progenies.

Combining ability describes the breeding value of parental lines to produce hybrids. It helps to select the parents and utilize them in the breeding programmes for production of superior hybrids. The concept of combining ability was first proposed by Sprague and Tatum (1942) in maize and has been used successfully in several studies. The general combination ability refers to additive gene action and is used to determine the performance of parents in general terms while specific combining ability effect is determined by dominant gene action and is used to indicate the hybrid performance in specific terms. Breeders use these variance components to determine the gene action and to assess the genetic potentials of parent in hybrid combinations. Diallel (Griffing, 1956) and line × tester (Kempthorne, 1956) matting designs provide reliable information about the general and specific combining ability of parents and their cross combinations. Full diallel analysis is a mating design where selected parents are crossed in all possible combinations and is used in predicting combining ability of the parents.

The knowledge of combining ability and gene action would help cowpea breeders to effectively identify potential parents, breeding strategies and to select promising genotypes from the segregating populations to improve productivity of cowpea.

Table 1. Number of days to pod maturity, potential grain yield, seed coat colour, and growth habit for the parental genotypes used for the study

Genotype	Trait			
	Maturity	Potential yield t/ha	Seed coat colour	Growth habit
Padi-tuya	75 days	2.0	White	Erect with few vines
Songotra	65 Days	2.2	White	Erect
Sanzi	50 Days	0.8	Molted	Creping
IT86D-610	60 Days	2.6	Brown	Semi erect
SARC-1-57-2	60 days	1.8	White	Erect

The objectives of this study were to: (i) determine the nature and the magnitude of gene action controlling yields and its component traits, (ii) identify potential parents for hybridization and selection programme and (iii) determine the genetic relationships among these traits.

2. Materials and methods

The research was conducted during the 2016 cropping season at the Council for Scientific and Industrial Research Savannah Agricultural Research Institute (CSIR-SARI) Tamale. SARI is in the Guinea Savannah agro-ecological zone of Ghana, located on latitude 9°, 25', 41N, longitude 0°, 58', 42W and about 183 m above sea level. The area is characterized by mono-modal rainfall with an average annual rainfall of about 1200 mm (Ndamani & Watanabe, 2013).

The present study examined five cowpea genotypes viz IT86D-610, SARC 1-57-2, Sanzi, Padi-tuya and Songotra. The genetic materials used had phenotypic variation for yield and its related component traits (Table 1). Genotypes IT86D-610 and SARC 1-57-2 are advanced breeding lines from International Institute of Tropical Agriculture (IITA) in Ibadan, Nigeria and CSIR-SARI, Ghana, respectively. Sanzi is a land race while Padi-tuya and Songotra are improved varieties released by CSIR-SARI in 2008. A full diallel cross was made using these five parents. A total of 20 F₁ individuals and their five parents were evaluated in a randomized complete block design with three replications at SARI during the 2016 cropping season. Seeds were planted at a spacing of 100 cm inter-row and 20 cm within row. Each plot was made up of two rows of 2 m length. Parents and F₁'s were randomly assigned to each plot and labelled accordingly. Observations were made on number of days to 50% flowering (DFF), plant height at flowering (cm) (PLHTF), number of branches (NBR), peduncle height (cm) (PEDHT), number of days to first pod maturity (DFPM), number of days to 90% pod maturity (DM), canopy width at maturity (CWM), canopy width at vegetation (CWV), number of pods per plant (PDPL), number of seeds per pod (SDPD), pod length (cm) (PODL), pod weight (t ha⁻¹) (PODWT), 100 seed weight (g) (HSW), and grain yield (t ha⁻¹) (YLD). Five plants were randomly selected from each plot and tagged for phenotypic observations. Before the analysis, the data was subjected to normality test to ensure it conforms to basic assumptions of analysis of variance (ANOVA). All the count data were transformed using the square root transformation method. Consequently, ANOVA was conducted using PROC GLM in Statistical Analysis System (SAS) using a RANDOM statement with the TEST option (SAS Institute, 2011 version 9.3). Genotypes were considered fixed effects whilst replications and blocks were considered random effects. GCA and SCA were estimated using Analysis of Genetic Designs (AGD-R version 3.0) the DIALLEL R program (Rodriguez et al., 2015) following Griffing's Method II and Model I (fixed) of diallel analysis (Griffing, 1956).

3. Results

3.1. Analyses of variance and combining ability estimates for grain yield and other traits

Analysis of variance revealed significant differences ($p < 0.01$; $p < 0.05$) among the cowpea genotypes for grain yield and all the other agronomic traits examined (Table 2). Mean squares

Table 2. Analysis of variance and mean squares for grain yield and other agronomic traits of diallel crosses involving five cowpea lines evaluated during 2016 cropping season

Source	df	NBR	CWV	CWM	DF	DFPM	DM	YLD	HSW	PLHTM	PLHTF	PEDHT	PDPL	PODWT	PODL	SDPD
REP	2	0.16NS	741.76NS	373.76**	0.52NS	0.09NS	0.42NS	0.68**	2.08NS	9.65NS	2.92**	0.61NS	1.62NS	0.09NS	0.39NS	3.21NS
Cross	24	4.50**	9444.17**	6062.27**	17.30**	23.78**	54.64**	7.02**	35.47*	165.73**	123.51**	100.29**	201.11**	9.82**	4.69**	5.11**
GCA	4	3.94**	5643.70**	2960.92**	31.11**	65.01**	170.75**	7.90**	102.16**	424.9**	203.75**	365.49**	63.44NS	6.50NS	13.01**	4.92**
SCA	10	6.75**	15,437.22*	11,259.42**	15.48**	18.96**	25.23**	10.11**	5.57**	114.42**	135.09**	20.50**	323.32**	12.90**	2.54NS	5.13**
Residual	40	0.34	720.8	539.4	0.29	1.46	3.12	0.49	1.22	3.28	4.28	5.44	25.89	2.85	1.37	1.2
%GCA SS		18.92	12.76	9.52	44.57	57.84	73.03	23.82	88.01	59.77	37.63	87.7	7.28	16.77	67.17	27.72
%SCA SS		81.08	87.24	90.48	55.43	42.16	26.97	76.18	11.99	40.23	62.37	12.3	92.72	83.23	32.83	72.28
Heritability (Ha)		0.122	0.077	0.053	0.354	0.454	0.603	0.160	0.783	0.499	0.284	0.766	0.028	0.053	0.386	0.124

**NBR, number of branches; CWV, canopy width at Vegetation (cm); CWM, canopy width at maturity (cm); DF, Days to 50% flowering; DFPM, Days to first pod maturity; DM, Days to maturity; YLD, seed yield (t ha⁻¹); HSW, hundred seed weight (g); PLHTM, plant height at maturity (cm); PLHTF, peduncle height (cm); PEDHT, number of pods per plant; PODWT, pod weight (t ha⁻¹); PODL; pod length (cm); SDPD, number of seeds per pod.

attributable to general combining ability (GCA) and specific combining ability (SCA) were significant for all traits in the present study except for SCA for pod length (PODL) and GCA for number of pods per plant (PDPL) and pod weight (PODWT) (Table 2). The SCA sum of squares as percentage of hybrid sum of squares were larger than GCA sum of squares for grain yield (76.18%), number of branches (NBR) (81.08%), canopy width at maturity (CWM) (87.24%), canopy width at vegetation (CWV) (90.48%), days to 50% flowering (DFF) (55.43%), plant height at maturity (PLHTM) (59.77%), number of pods per plant (PDPL) (92.72%), pod weight (PODWT) (83.23%) and seeds per pod (SDPD) (72.28), whereas GCA sum of squares were larger than SCA sum of squares for days to first pod maturity (DFPM), days to maturity (DM), hundred seed weight (HSW), plant height at flowering (PLHTF), peduncle height (PEDHT) and pod length (PODL) thus 57.84, 88.01, 62.37, 87.70 and 67.17 %, respectively.

The estimates of GCA effects for grain yield varied significantly ($P \leq 0.05$; $P \leq 0.01$) among the five cowpea parents studied except for SONGOTRA (Table 3). Lines PADI-TUYA and IT86D-610 consistently showed highly significant positive GCA effects for most of the traits measured except for PLHTF, PDPL and PODWT. PADI-TUYA exhibited negative but significant GCA for NBR. The GCA effects of SONGOTRA were positive and significant for DFF, DFPM, DM, HSW, PLHTM and PEDHT. Inbred line SARC 57-2 showed highly significant and positive GCA effects for DFF and DFPM and significant negative GCA for PLHTM, PODWT and SDPD. Inbred line IT86D-610 had highly significant negative GCA effects for CWV, CWM and DFF. Also, IT86D-610 had significant positive GCA for NBR, YLD, PLHTM, PEDHT and SDPD. Interestingly, SANZI had significant negative GCA effects for YLD and most of the agronomic traits studied except for CMM and CWV which showed significant positive GCA.

The estimates of SCA of the crosses for the traits examined are presented in Table 4. Of this, three crosses thus SONGOTRA \times PADI-TUYA (low \times high), IT86D-610 \times SARC 57-2 (high \times low) and IT86D-610 \times PADI-TUYA (high \times high) exhibited maximum SCA effects and per se performance for seed yield. Also, cross SANZI \times IT86D-610 (low \times low) was observed to be a good combiner for DFF. Good specific combiners for NBR were IT86D-610 \times SONGOTRA (high \times low) and IT86D-610 \times SARC 57-2 (high \times low). Crosses SANZI \times SONGOTRA (high \times low), SONGOTRA \times PADI-TUYA (low \times high), IT86D-610 \times SARC 57-2 (low \times low) and IT86D-610 \times PADI-TUYA (low \times high) showed high SCA for CWM and CWV. For HSW, high positive SCA effect was displayed by the cross SANZI \times SONGOTRA (low \times high). Also, high positive SCA's were obtained for PLHTM as displayed by crosses SONGOTRA \times PADI-TUYA (low \times high), SARC 57-2 \times PADI-TUYA (low \times high) and SARC 57-2 \times SONGOTRA (low \times high). High SCA for PDPL and PODWT was shown by crosses SONGOTRA \times PADI-TUYA, IT86D-610 \times SARC 57-2, and IT86D-610 \times PADI-TUYA. None of the crosses had positive SCA for PODL and SDPD. However, SANZI \times SARC 57-2 obtained significant but negative SCA for PODL and SDPD.

3.2. Comparison of performance of parents and hybrids for grain yield and other agronomic traits

The mean grain yield (YLD) from the study ranged from 0.73 t ha⁻¹ for PADI-TUYA \times SANZI to 6.33 t ha⁻¹ for IT86D-610 \times PADI-TUYA (Table 5). Many of the hybrids had higher seed yield than most of the parents. Mean days to 50% flowering (DFF) was 38.56, with a range of 34 to 44. DM was ranged from 49.00 to 66.67, with an average of value of 57.89. Mean number of seeds per pod (SDPD) was 7.33, with a range of 3.67 to 9.33. Mean number of pods per plant (PDPL) was 19.75, with a range of 3.33 to 43.67 and PEDHT ranged between 9.67 and 34.33, with a mean of 24.67.

Results of one degree of freedom contrast between the means of the parents and the means of the hybrids revealed highly significant difference ($p < 0.05$) between the parents and hybrids for most of the traits considered except plant height at flowering (PLHTF), plant height at maturity (PLHTM), peduncle height (PEDHT), pod length (PODL), pod weight (PODWT) and hundred seed weight (HSW) (Table 6). The mean of the 15 hybrids was significantly higher than the mean of the 5 parents in YLD, number of branches (NBR), number of pods per plant (PDPL), canopy width at vegetation (CWV) and canopy width at maturity (CWM) by 56.95, 51.01, 60.90, 121.04, 129.26 % respectively (Table 4). It is noteworthy that

Table 3. General combining ability (GCA) effects of five cowpea genotypes for grain yield and agronomic traits during 2016 cropping season

Parent	NBR	CWM	CWV	DF	DFPM	DM	YLD	HSW	PLHTM	PLHTF	PEDHT	PDPL	PODWT	PODL	SDPD
PADI-TUYA	-0.42**	14.35*	13.27*	0.97**	1.78**	2.15**	0.50**	2.12**	6.67**	4.04	1.69**	1.65	0.55	1.20**	0.50**
SONGOTRA	0.1	-3.84	-2.64	0.73**	0.50*	1.68**	0.03	1.12**	-1.95**	-1.15	2.78**	1.31	0.32	0.06	-0.02
SARC 57-2	-0.04	-8.03	-5.83	0.83**	0.78**	1.06	-0.33*	0.17	-0.71*	0.13	0.88	-1.21	-0.80*	-0.23	-0.59*
IT86D-610	0.68**	-21.08**	-15.35**	-0.74**	-0.17	0.01	0.65**	0.27	1.48**	1.37	2.02**	0.65	0.28	-0.04	0.46*
SANZI	-0.32*	18.59**	10.55*	-1.79	-2.89	-4.90**	-0.85**	-3.69**	-5.48**	-4.39	-7.36**	-2.40*	-0.34	-0.99**	-0.35
SE	0.11	5.24	4.53	0.11	0.24	0.34	0.14	0.22	0.35	0.4	0.46	0.99	0.33	0.23	0.21

* P ≤ 0.05; ** P ≤ 0.01

†SE = standard error of the general combining ability effects; NBR, number of branches; CWV, canopy width at Vegetation (cm); CWM, canopy width at maturity (cm); DF, Days to 50% flowering; DFPM, Days to first pod maturity; DM, Days to maturity; YLD, seed yield (t ha⁻¹); HSW, hundred seed weight (g); PLHTM, plant height at maturity (cm); PLHTF, plant height at flowering (cm); PEDHT, peduncle height (cm); PDPL, number of pods per plant; PODWT, pod weight (t ha⁻¹); PODL, pod length (cm); SDPD, number of seeds per pod.

Table 4. Specific combining ability effects of five cowpea crosses for grain yield and agronomic traits during 2016 cropping season

Hybrids	NBR	CWM	CWV	DF	DFPM	DM	YLD	HSW	PLHTM	PLHTF	PEDHT	PDPL	PODWT	PODL	SDPD
PADI-TUYA × PADI-TUYA	-0.54*	-91.02**	-77.33**	2.52**	2.46**	3.65**	-2.00**	0.4	-5.22**	-8.03**	-3.68**	-7.21**	-1.46	0	0.75
SONGOTRA × PADI-TUYA	0.27	99.51**	87.90**	-1.90**	-2.25**	-2.21*	2.31**	0.06	4.40**	5.16**	4.89**	11.79**	2.71**	0.81	-0.06
SARC 57-2 × PADI-TUYA	0.41	26.37	26.10*	-0.67*	-1.21	-1.59	0.14	1.68*	7.83**	7.54**	1.13	-7.02*	-1.97*	-0.57	-0.16
IT86D-610 × PADI-TUYA	0.37	49.41**	51.62**	-0.1	-0.59	-0.87	1.83**	-1.75*	-1.03	1.3	2.65*	8.13**	2.74**	0.24	-0.21
SANZI × PADI-TUYA	0.03	6.75	-10.95	-2.38**	-0.87	-2.63*	-0.28	-0.79	-0.75	2.06	-1.3	1.51	-0.57	-0.48	-1.06
SONGOTRA × SONGOTRA	-1.92**	-77.97**	-67.19**	1.67**	3.03**	2.27**	-0.98**	-0.27	-3.32**	-2.65**	-1.54	-7.54**	-0.67	-0.71	0.46
SARC 57-2 × SONGOTRA	0.89**	6.22	0	0.57	-1.59	-0.44	-0.18	-1.32	6.11**	5.73**	0.37	11.32**	1.72	0.24	-0.3
IT86D-610 × SONGOTRA	2.84**	-52.40**	-40.48**	-1.19**	-1.97**	-2.73*	-2.17**	-0.75	-8.41**	-9.51**	-2.11	-12.54**	-3.16**	-0.62	-0.68
SANZI × SONGOTRA	-0.16	102.60**	86.95**	-0.81*	-0.25	0.84	2.00**	2.54**	4.54**	3.92**	-0.06	4.51	0.06	1.00	0.13
SARC 57-2 × SARC 57-2	-1.30**	-23.92*	-17.48	1.14**	2.46**	2.84*	-0.42	-0.7	-1.79**	-2.22*	-1.73	-4.49	-0.29	0.86	1.60**
IT86D-610 × SARC 57-2	1.32**	49.79**	42.05**	-2.95**	-3.59**	-4.44*	2.26**	1.21	-3.32**	-2.46*	1.46	12.65**	2.16*	0.33	0.22
SANZI × SARC 57-2	-0.02	-34.54*	-33.19**	0.76*	1.46*	0.79	-1.37**	-0.17	-7.03**	-6.37**	0.51	-7.97**	-1.32	-1.71*	-2.97**
IT86D-610 × IT86D-610	-2.40**	-42.49**	-39.76**	-0.05	1.70**	3.60*	-1.52**	0.78	7.49**	7.97**	-2.02	-8.54**	-1.12	-0.52	-0.16
SANZI × IT86D-610	0.27	38.17**	26.33*	4.33**	2.75**	0.84	1.11*	-0.27	-2.22**	-5.27**	2.03	8.84**	0.5	1.1	0.98
SANZI × SANZI	-0.06	-56.49**	-34.57**	-0.95**	-1.54**	0.08	-0.73*	-0.65	2.73**	2.83**	-0.59	-3.44	0.66	0.05	1.46**
S.E	0.23	10.70	9.25	0.22	0.48	0.70	0.28	0.56	0.91	1.04	1.18	2.03	0.85	0.59	0.55

* P ≤ 0.05; ** P ≤ 0.01

†NBR, number of branches; CWV, canopy width at maturity (cm); CWM, canopy width at maturity (cm); DF, Days to 50% flowering; DFPM, Days to first pod maturity; DM, Days to maturity; YLD, seed yield (t ha⁻¹); HSW, hundred seed weight (g); PLHTM, plant height at maturity (cm); PLHTF, peduncle height (cm); PEDHT, peduncle height (cm); PDPL, number of pods per plant; PODWT, pod weight (t ha⁻¹); PODL, pod length (cm); SDPD, number of seeds per pod.

Table 5. Mean grain yield and other traits of the 20 F₁ cowpea hybrids and five parental lines evaluated in Ghana during 2016 cropping season

Cross	YLD	DF	PLHTF	PLHTM	NBR	DIFPM	DM	PDPL	PEDHT	SDPD	CWV	CWM	PODL	PODWT	HSW
PADI-TUYA × SONGOTRA	3.47	39.33	32.00	37.33	2.33	54.00	58.67	20.00	30.33	6.67	87.00	117.00	12.00	5.53	20.00
PADI-TUYA × SARC 57-2	3.60	39.33	27.00	31.67	3.33	54.67	65.00	20.00	25.67	7.33	125.00	155.33	11.67	4.13	20.00
PADI-TUYA × IT86D-610	2.67	38.67	25.67	31.00	2.00	54.00	58.33	10.67	28.33	8.00	40.00	46.00	9.67	3.53	21.00
PADI-TUYA × SANZI	0.73	34.33	19.33	22.00	2.33	50.67	54.67	6.33	17.33	4.00	66.00	75.33	10.67	1.73	16.33
SONGOTRA × PADI-TUYA	6.20	39.00	31.67	36.33	3.67	53.33	60.33	34.33	34.33	8.00	190.00	220.00	14.00	8.40	20.00
SONGOTRA × SARC 57-2	4.87	38.33	20.33	23.33	4.00	52.67	57.67	23.67	32.33	8.00	88.00	98.67	14.00	7.00	20.33
SONGOTRA × IT86D-610	2.53	39.33	23.00	28.00	3.00	54.67	59.00	16.67	23.67	6.00	44.67	48.67	12.00	3.27	18.67
SONGOTRA × SANZI	2.93	36.33	20.33	20.67	4.00	51.67	54.67	24.33	21.67	6.33	131.67	174.67	10.67	7.67	16.00
SARC 57-2 × PADI-TUYA	3.67	40.33	35.33	41.00	3.67	54.67	60.33	13.00	28.67	7.33	125.00	142.67	12.33	2.60	20.67
SARC 57-2 × SONGOTRA	2.87	41.33	28.33	30.67	4.67	53.00	61.00	31.00	29.00	6.67	83.00	104.33	12.00	6.07	16.67
SARC 57-2 × IT86D-610	4.07	37.33	19.33	24.33	4.00	51.00	54.67	27.00	26.33	7.33	71.67	81.00	12.33	5.33	15.67
SARC 57-2 × SANZI	2.33	38.00	13.33	15.67	2.33	49.00	53.00	16.67	15.67	7.67	70.00	85.67	11.67	3.40	11.67
IT86D-610 × PADI-TUYA	6.33	39.33	30.33	34.33	4.33	54.33	60.00	30.00	31.33	8.33	141.00	152.67	13.33	8.40	17.33
IT86D-610 × SONGOTRA	1.87	38.00	14.33	18.33	7.33	51.67	57.67	9.00	27.67	7.33	33.00	32.67	11.33	2.27	17.33
IT86D-610 × SARC 57-2	5.93	36.33	22.67	24.67	5.67	50.33	55.33	31.67	29.33	7.67	112.33	130.67	12.00	6.47	18.33
IT86D-610 × SANZI	3.67	35.00	18.33	22.33	4.00	47.33	51.00	34.67	20.67	8.33	79.67	93.00	12.33	4.47	10.00
SANZI × PADI-TUYA	2.73	36.00	25.33	27.67	3.00	51.33	53.33	20.33	18.00	6.67	104.33	149.67	11.67	4.47	14.33
SANZI × SONGOTRA	4.53	37.33	22.00	24.33	3.33	50.67	56.33	23.00	20.33	7.33	186.33	227.33	12.00	4.87	16.67
SANZI × SARC 57-2	0.80	39.00	13.00	14.00	3.33	52.67	55.67	8.00	19.00	3.67	63.00	86.00	9.00	2.37	13.00
SANZI × IT86D-610	4.27	41.00	15.33	21.00	4.33	53.00	54.67	26.67	21.67	8.67	113.00	145.67	12.00	5.27	13.00
PADI-TUYA	2.37	43.67	23.67	35.33	2.33	59.33	66.67	15.67	24.67	9.33	40.67	47.67	14.33	4.47	21.33
SONGOTRA	2.43	42.33	18.67	20.00	2.00	57.33	64.33	14.67	29.00	8.00	19.00	24.33	11.33	4.80	18.67
SARC 57-2	2.27	42.00	21.67	24.00	2.33	57.33	63.67	12.67	25.00	8.00	62.33	70.00	12.33	2.93	16.33
IT86D-610	3.13	37.67	34.33	37.67	2.67	54.67	62.33	12.33	27.00	8.33	21.00	25.33	11.33	4.27	18.00
SANZI	0.93	34.67	17.67	19.00	3.00	46.00	49.00	11.33	9.67	8.33	78.00	90.67	10.00	4.80	8.67

(Continued)

Table 5. (Continued)

Cross	YLD	DF	PLHTF	PLHTM	NBR	DFPM	DM	PDPL	PEDHT	SDPD	CWV	CWM	PODL	PODWT	HSW
Mean	3.25	38.56	22.92	26.59	3.48	52.77	57.89	19.75	24.67	7.33	87.03	105.00	11.84	4.74	16.80
SE	0.71	0.58	2.13	1.91	0.59	1.21	1.77	5.09	2.33	1.15	23.23	27.48	1.17	1.69	1.14
CV (%)	21.87	1.51	9.29	7.18	16.84	2.29	3.05	25.77	9.46	15.73	26.69	26.17	9.90	35.64	6.80

†SE = standard error; CV = coefficient of variation; NBR, number of branches; CWV, canopy width at maturity (cm); CWM, canopy width at maturity (cm); DF, Days to 50% flowering; DFPM, Days to first pod maturity; DM, Days to maturity; YLD, seed yield ($t\ ha^{-1}$); HSW, hundred seed weight (g); PLHTM, plant height at maturity (cm); PLHTF, plant height at flowering (cm); PEDHT, peduncle height (cm); PDPL, number of pods per plant; PODWT, pod weight ($t\ ha^{-1}$); PODL, pod length (cm); SDPD, number of seeds per pod.

Table 6. The difference between parents and hybrids of cowpea

Traits	Mean Square (df = 1)	Error	CV (%)	Means		Percentage increase (%)
				Hybrids	Parents	
YLD	19.56**	2.44	48.1	3.50	2.23	56.95
DF	42.56**	5.46	6.1	38.18	40.07	-4.72
PLHTf	1.47NS	44.60	29.1	22.85	23.20	-1.51
PLHTm	7.05NS	58.38	28.7	26.43	27.20	-2.83
NBr	19.25**	1.45	34.6	3.73	2.47	51.01
DFPM	87.48**	9.07	5.7	52.23	54.93	-4.92
DM	205.01**	19.3	7.6	57.1	61.20	-6.70
PDPL	771.20**	83.3	46.2	21.4	13.3	60.90
PEDHT	48.0NS	37.7	24.9	25.07	23.07	8.67
SDPD	21.33**	2.30	20.7	7.07	8.40	-15.83
CWv	34,390.00**	1997.0	51.4	97.7	44.2	121.04
CWm	53,467.00**	2895.0	51.2	118.3	51.6	129.26
PODL	0.01NS	2.72	13.9	11.83	11.87	-0.34
PODWT	4.44NS	5.73	50.5	4.86	4.25	14.35
HWS	0.75NS	12.85	21.3	16.85	16.60	1.51

* P ≤ 0.05; ** P ≤ 0.01

^{††}NBR, number of branches; CWV, canopy width at Vegetation (cm); CWM, canopy width at maturity (cm); DF, Days to 50% flowering; DFPM, Days to first pod maturity; DM, Days to maturity; YLD, seed yield (t ha⁻¹); HSW, hundred seed weight (g); PLHTM, plant height at maturity (cm); PLHTf, plant height at flowering (cm); PEDHT, peduncle height (cm); PDPL, number of pods per plant; PODWT, pod weight (t ha⁻¹); PODL; pod length (cm); SDPD, number of seeds per pod.

the hybrids performed significantly poorer than the parents for DFF, DFM, DM and SDPD with penalties of -4.72, -4.92, -6.70, and -15.83 %, respectively.

3.3. Comparison between top three and bottom three genotypes for grain yield and other traits

A similar one degree of freedom contrast to compare the means of the top three highest yielding genotypes (HIGH genotypes) and the bottom three lowest yielding genotypes (LOW genotypes) shows that the HIGH genotypes significantly outperformed the LOW genotypes in all traits studied with advantages of: 651.22% in YLD, 278.83% in PDPL, 161.28% in PODWT, 114.20% in CWV and 106.59% in PEDHT (Table 6). It is not surprising that, all the three HIGH yielding genotypes were hybrids thus IT86D-610 × PADI-TUYA, SONGOTRA × PADI-TUYA and IT86D-610 × SARC 57-2 with yield advantages of 94.8, 90.8, and 82.5%, respectively compared to the grand mean (3.25 t ha⁻¹). Two hybrids (SANZI × SARC 57-2 and PADI-TUYA × SANZI) and one parental line (SANZI) made up the low yielding genotypes. The highest yielding hybrid IT86D-610 × PADI-TUYA (6.33 t ha⁻¹) out yielded its better parent (IT86D-610) and mid parent value by 3.2, 3.6 t ha⁻¹ with yield advantages of 102.2 and 130.3%, respectively. Similarly, SONGOTRA × PADI-TUYA and IT86D-610 × SARC 57-2 were superior to their better parents SONGOTRA and IT86D-610 by 3.8 and 2.8 t ha⁻¹ with yield increase of 155.1 and 89.5%, respectively. They again proved better than their mid parent values by 3.8 and 3.2 t ha⁻¹ representing yield advantages of 158.3 and 119.6% respectively (Table 7).

3.4. Phenotypic and genotypic correlations for grain yield and other agronomic traits of 25 cowpea genotypes

The phenotypic and genotypic correlations coefficients between grain yield and its components are presented in Table 8. Grain yield had moderate positive phenotypic correlations with PLHTM, PODL and CWV. Phenotypic correlation between YLD and PODWT, HSW, CWM and PEDHT was strongly positive ($r_p \geq 0.60$). However, no phenotypic correlation was recorded between YLD and DF. Moderately positive correlation existed between PLHTf and SDPD. It was interesting to note that,

Table 7. The difference between the highest and lowest yielding cowpea genotypes

Traits	Mean Square (df = 1)	Error	CV (%)	Means		Percentage increase (%)
				High	Low	
YLD	128.00**	0.36	17.2	6.16	0.82	651.22
DF	22.22*	4.30	5.6	38.22	36.00	6.17
PLHTf	600.89**	16.48	18.1	28.22	16.67	69.29
PLHTm	813.39**	25.44	20.1	31.80	18.3	73.77
NBr	12.50**	0.7857	23.8	4.56	2.89	57.79
DFPM	37.56*	7.913	5.5	52.67	49.78	5.81
DM	133.39**	11.91	6.2	58.56	53.11	10.26
PDPL	2473.39**	16.34	19.9	32.00	8.56	32.56
PEDHT	1200.50**	17.14	17.6	31.67	15.33	106.59
SDPD	32.00*	32.00	30.4	8.00	5.33	50.09
CWv	27,927.00**	1151.00	31.3	147.8	69.0	114.20
CWm	31,584.00**	1352.00	29.2	167.8	84.0	99.76
PODL	46.72**	1.06	8.9	13.11	9.89	32.56
PODWT	103.20**	4.19	38.2	7.76	2.97	161.28
HSW	156.06**	9.20	19.4	18.56	12.67	46.49

* P ≤ 0.05; ** P ≤ 0.01;

††NBR, number of branches; CWV, canopy width at Vegetation (cm); CWM, canopy width at maturity (cm); DF, Days to 50% flowering; DFPM, Days to first pod maturity; DM, Days to maturity; YLD, seed yield (t ha⁻¹); HSW, hundred seed weight (g); PLHTM, plant height at maturity (cm); PLHTF, plant height at flowering (cm); PEDHT, peduncle height (cm); PDPL, number of pods per plant; PODWT, pod weight (t ha⁻¹); PODL; pod length (cm); SDPD, number of seeds per pod.

nearly perfect phenotypic correlation was observed between CWV and PODL. On the other hand, genotypic correlation was positive and significant between DM and all the traits examined in the present study except for PLHTF, PDPL and DM which were positive but not significant. The highest form of genotypic correlation ($r_G = 0.85$) was observed between YLD and PEDHT. A perfect genotypic correlation was observed between CWV and PODL. The second highest genotypic correlation of 97% was between NBR and PLHTF and PDPL and DFPM. Strong positive correlations were also observed between DM and DFF, HSW and PDPL. Between the traits, moderately positive r_G was observed between PODWT and PLHTM, whereas moderate to strongly negative r_G were observed between CWV and HSW, CWM and YLD and PODWT and PDPL. DFF had weak negative r_p with NBR and PODL and weak positive r_p with HSW and PLHTF. DM also had weak negative r_p with NBR and a weak positive r_p with CWV, PODWT and HSW.

4. Discussion

The results emanating from the present study showed extensive genetic variability for seed yield and the other traits among the parents and crosses of cowpea genotypes studied. This variability can be explored for the development of new high yielding varieties. The probability of selecting superior genotypes is immensely dependent on the existing genetic diversity in the genotypes, which is also a function of the influence of the additive variance (Ramalho et al., 1993). Significant genetic variation among cowpea crosses and parents for seed yield and other agronomic traits have also been reported in earlier studies by Dias et al. (2016), Ayo-Vaughan et al. (2013) and Pandey and Singh (2010).

The presence of significant GCA and SCA mean squares for traits such as YLD, PDPL, SDPD, HSW, DFF, DM, NBR, CWV, CWM, PLHTF and PLHTM indicates that both additive and non-additive genetic effects were important in determining these traits as averred by Griffing (1956) and there is the probability of obtaining new varieties or hybrids (Silva et al., 2004). Similar results were reported in

Table 8. Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients

Traits	YLD	DF	PLHTF	PLHTM	NBR	DFPM	DMA	PDPL	PEDHT	SDPD	CWV	CWM	PODL	POD_WT	HSW
YLD		N/A	0.14ns	0.45*	0.23ns	0.33ns	0.13	0.76**	0.80**	0.64**	0.52*	0.65**	0.58**	0.77**	0.76**
DF	N/A	1	0.22ns	0.22ns	-0.08ns	-0.09ns	0.82**	0.75**	0.00ns	0.53**	0.19ns	-0.09ns	-0.10ns	0.24ns	0.03nd
PLHTF	0.08ns		1		-0.19ns	-0.16ns	0.44**	0.53**	0.20 ns	0.57**	0.20ns	0.30ns	0.27ns	0.38*	0.30ns
PLHTM	0.46*	0.21ns		1	-0.16ns	-0.13ns	0.45**	0.52**	0.21 ns	0.60**	0.24ns	0.28ns	0.25ns	0.42*	0.26ns
NBR	0.26ns	-0.15ns	-0.21ns	-0.22ns	1		-0.24	-0.14 ns	0.37ns	0.26	0.12ns	0.19ns	0.15ns	0.24ns	0.23ns
DFPM	0.36*	-0.18ns	-0.17ns	-0.19ns		1		0.91**	-0.17ns	0.63**	0.03ns	-0.15ns	-0.16ns	0.19ns	-0.02ns
DMA	0.08ns	0.90**	0.42*	0.52**	-0.30ns		1		-0.09	0.68**	0.12ns	-0.08ns	-0.11ns	0.27ns	0.02ns
PDPL	0.80**	0.83**	0.52**	0.59**	-0.19ns	0.97**		1		0.36	0.39*	0.59**	0.57**	0.66**	0.79**
PEDHT	0.86**	-0.04ns	0.20ns	0.18ns	0.30ns	-0.18ns	-0.12ns		1		0.28ns	0.12ns	0.05ns	0.58**	0.44*
SDPD	0.67**	0.49**	0.58**	0.60**	0.25ns	0.61**	0.67**	0.37*		1		0.11ns	0.06ns	0.47*	0.41*
CWV	0.52**	0.36*	0.21ns	0.32*	0.06ns	0.24ns	0.31*	0.40*	0.31ns		1		0.99**	0.46*	0.57**
CWM	0.68**	-0.18ns	0.29*	0.21ns	0.21ns	-0.21ns	-0.15ns	0.60**	0.11ns	-0.02ns		1		0.38*	0.55**
PODL	0.62**	-0.19 ns	0.26ns	0.17ns	0.18ns	-0.22ns	-0.19ns	0.58**	0.03ns	-0.06ns	1.00**		1		0.55**
PODWT	0.79**	0.42*	0.40*	0.55**	0.07ns	0.41*	0.45*	0.70**	0.63**	0.56**	0.35*	0.27ns		1	
HSW	0.85**	0.02	0.33*	0.26ns	0.11ns	-0.01ns	-0.03ns	0.92**	0.46*	0.48**	0.62**	0.59**	0.69**		1

*, ** Significant F-test at probability levels of 0.05 and 0.01, respectively; ns- not significant; N/A = not available

†NBR, number of branches; CWV, canopy width at Vegetation; CWM, canopy width at maturity; DF, Days to 50% flowering; DFPM, Days to first pod maturity; DM, Days to maturity; YLD, seed yield; HSW, hundred seed weight; PLHTM, plant height at maturity; PLHTF, plant height at flowering; PEDHT, peduncle height; PEDL, number of pods per plant; PODWT, pod weight; PODL; pod length; SDPD, number of seeds per pod

cowpea by Raut et al. (2017) for DFF, NBR, YLD and HSW; Ayo-Vaughan et al. (2013) for YLD, PDPL and HSW; and Pandey and Singh (2010) for PLHT, SDPD and YLD.

The predominance of SCA effects over GCA effects for YLD, NBR, CWV, CWM, DFF, PLHTM, PDPL, PODWT and SDPD suggests that non-additive gene action is more important in controlling the inheritance of the traits. These findings are in agreement with Raut et al. (2017) for YLD, NBR, PLHT, DFF and SDPD; and Singh et al. (2006) for YLD, SDPD, and PDL in cowpea. Contrary to results from the present study for the predominance of SCA over GCA, significant GCA effects over SCA were observed by Ayo-Vaughan et al. (2013) for PDPL, SDPD and YLD in cowpea. However, the differences in the two results could be attributed to the differences in the genetic materials used and also the research conditions (environment) under which the studies were conducted. SCA represents the predominance of non-additive gene action which occur between the hybridizing parents and it is a major component that may be utilized in heterosis breeding. The significance of SCA effect emphasises the existence of genetic diversity among parents tested and demonstrates the impact of dominance and/or epistatic effect which signify the non-fixable components of the genetic variation related to heterosis (Pandey & Singh, 2010). Singh et al. (2006) postulated that non-additive gene action can be exploited by multiple crosses followed by intermating among desirable segregants. Selection should therefore be deferred till later generations when these impacts are fixed in the homozygous lines (Bicer & Sakar, 2008; Ertiro et al., 2013). The preponderant role of SCA effects than GCA could be ascribed to repulsion phase linkage and linkage disequilibrium (Sokol & Baker, 1977). Furthermore, higher SCA than GCA can be elucidated by the usage of closely related parents (Azad et al., 2014; Neele et al., 1991), negative relations between genes (Sokol & Baker, 1977), preceding selection that narrowed the genetic base of the genotypes evaluated (Azad et al., 2014; Plaisted et al., 1962) and directional selection (Killick & Malcolmson, 1973). In the present study, some of genotypes used have been selected primarily for high yield which could have constricted the genetic base. Also, most of the hybrids studied have common pedigrees, for instance, the common parent “PADI-TUYA”, which could have contributed to the narrow genetic base.

The preponderance of GCA effects over SCA effects for traits such as DFPM, DM, HSW, PLHTF, PEDHT and PODL indicates that additive genetic effects are more important than non-additive effects in the inheritance of these traits. These results are in agreement with earlier findings by Patij and Navale (2006) for PLHT and HSW; Raut et al. (2017) for DM and Pandey and Singh (2010) for PODL. Contrarily, higher SCA variances were found by Patij and Navale (2006) for NBR and PODL and by Raut et al. (2017) for PODL, HSW and PDPL. The prevalence of GCA variances over SCA variances suggests that early generation testing of genotypes would be efficient and promising hybrids can be identified and selected based on their prediction from GCA effects (Amegbor et al., 2017; Fasahat, Rajabi, Rad, & Derere, 2016) since the additive effects of genes is fixable through direct selection (Ayo-Vaughan et al., 2013). High GCA values signify that the parental average is superior. This also designates a strong evidence of desirable gene flow from parents to progeny at high intensity and denotes information regarding the concentration of predominantly additive genes (Franco et al., 2001). Accordingly, the significant positive and high GCA effects observed for YLD and other traits by PADI-TUYA and IT86D-610 imply that these parents possess favourable alleles for yield and other traits and would transmit high yield to their offsprings. PADI-TUYA in particular seems to be the most desirable genotype for the genetic improvement of most of the traits. It is therefore suggested that intermating among PADI-TUYA and IT86D-610 would produce superior progenies for seed yield. The non-significance of GCA effects for PADI-TUYA for PDPL and PODWT shows that it had little contribution to additive gene action of PDPL and PODWT exhibited by the crosses. Other parents found to be good general combiners for DFF and DFPM (SARC 57-2), CWM (SANZI) and DFF, DFPM, DM, HSW and PEDHT (SONGOTRA) could easily be inherited by the offsprings.

The negative significant GCA estimates recorded by SANZI for nearly all the traits including YLD; and by IT86D-610 for CWM, CWV and DF; and by PADI-TUYA for NBR suggests that these genotypes have low gene frequencies for the traits (Orawu et al., 2013) thereby making them undesirable for the genetic improvement of these traits (Ayo-Vaughan et al., 2013; Daniel et al., 2006). The variable GCA

estimates observed in the parents for nearly all the traits (except PDWT, PDPL and PLHTF) points to the existence of positive and negative (dominant and recessive) alleles among the parents leading to different levels of expression of the traits, a further confirmation of the genetic variation among the parents for the traits.

The high SCA effects and per se performance for seed yield displayed by IT86D-610 × PADI-TUYA, SONGOTRA × PADI-TUYA and IT86D-610 × SARC 57-2 crosses further confirms the preponderance of non-additive gene action governing the inheritance of this character. The high SCA effects of SONGOTRA × PADI-TUYA and IT86D-610 × SARC 57-2 arising from parents with low × high and high × low GCA values, respectively, for yield and other traits might be due to complementation of high and low combining loci (Raut et al., 2017). Parents of these crosses can be used for biparental mating or reciprocal recurrent selection for developing superior varieties with high yield (Azad et al., 2014). IT86D-610 × PADI-TUYA cross with high SCA effects for seed yield and other traits from parents with high × high GCA effects could be exploited by pedigree breeding method to get transgressive segregants (Azad et al., 2014). The existence of high SCA effects in high × high GCA group such as IT86D-610 × PADI-TUYA might be as a result of the cumulative effect of high combining loci and no mutual annulment of gene effects between high general combining loci (Raut et al., 2017).

All the crosses possessing significant SCA effects for the traits studied involved parents with high × high, high × low or low × low combining ability. According to Patij and Navale (2006), such result indicates the presence of allelic as well as non-allelic interaction in the expression of these characters. Similar results of high SCA values for cowpea crosses have been reported in earlier studies by Ayo-Vaughan et al. (2013) for PDPL and HSW; Dias et al. (2016) for YLD and SDPD; Pandy and Singh (2010) for PLHT and DFF and by Patil and Navale (2006) for NBR and DM.

The fact that the difference between the hybrids and the parents was significantly positive for all traits, except DFF, DFPM, DM and SDPD shows that, the hybrids were superior to the parents in all traits but were earlier in flowering and maturity and had fewer seeds per pod than the parents. The significance of the mean square for parents and hybrids coupled with the vast difference in parental and hybrid means for YLD, NBR, PDPL, CWV and CWM but not for PLHTF, PLHTM, PODL, PODWT, PEDHT and HSW suggests the presence of heterosis and its absence respectively. The low mean performance of the hybrids compared to the parents for DFF, DFMA, DM and SDPD suggests negative heterosis for these traits. It appears that PDPL, PODWT, CWV and PEDHT are good selection criteria to identify high yielding cowpea genotypes based on the results of the comparison of the three highest and three lowest yielding genotypes. Crosses IT86D-610 × PADI-TUYA, SONGOTRA × PADI-TUYA and IT86D-610 × SARC 57-2 with yield advantages of 94.8, 90.8, and 82.5%, respectively compared to the grand mean suggests these are promising combinations that could be advanced for further evaluations.

Generally, genotypic correlation coefficients were higher than its corresponding phenotypic correlation coefficients. This implied that the characters studied were mainly under genetic control corroborating the results of Adetiloye et al. (2017). The small difference between the phenotypic and genotypic correlation coefficients in some cases suggests that the environment had some influence on the correlated characters. The significant positive genotypic correlations between YLD, and PEDHT, CWV, CWM, PODL, SDPD, PDPL, PLHTM, HSW and PODWT suggest that these characters contributed positively towards yield and should be considered when selecting for high grain yield in cowpea. Similar results were reported by Adetiloye et al. (2017) for pods per plant, pod length and seeds per pod; Aliyu and Makinde (2016) for hundred seed weight; and Baghizadeh et al. (2010) for canopy width. The significant genetic and phenotypic correlation observed for hundred seed weight and number of seeds per pod suggests that bigger seed size and many seeds per pod can be achieved contrary to the findings of Adetiloye et al. (2017), that increasing the number of seeds resulted in smaller-sized seeds.

5. Conclusion

This study elucidated the inheritance of grain yield and its related traits in cowpea using a diallel mating design. Both additive and non-additive (dominance and or epistasis) genetic actions were found to condition the inheritance of the characters studied. Non-additive genetic effects however proved to be more important than additive genetic effects for YLD, NBR, CWV, CWM, DFF, PLHTM, PDPL, PODWT and SDPD. PADI-TUYA and IT86D-610 were observed to be good general combiners for grain yield and some other traits. Therefore, this could be exploited as donor parents since they possess favourable alleles for grain yield and other traits directly associated with yield thereby transmitting high yield to their offsprings. IT86D-610 × PADI-TUYA, SONGOTRA × PADI-TUYA and IT86D-610 × SARC 57-2 were identified as superior and promising cross combinations having high per se performance, significant positive SCA effects coupled with high heterosis over better parent for seed yield and other traits. It is therefore recommended that, these genotypes should be included in the cowpea improvement program in that, the likelihood of obtaining transgressive segregants from segregating generations of these crosses is high and should therefore be exploited. Also, the superior crosses identified in this study should be further tested on a wide range of environments and consequently released to farmers to up-scale cowpea production in Ghana. Selection criteria to improve the seed yield of cowpea should focus on plants with long peduncles, bearing many big size seeds along with numerous pods per plant and high canopy width as these traits have high genetic correlation with seed yield.

Acknowledgements

The authors are grateful to the Management of CSIR-Savanna Agricultural Research Institute for their support. Special thanks and appreciations to Dr. S. K. Nutsugah (Director, CSIR-SARI) and the cowpea improvement programme for technical assistance.

Competing Interest

The authors declare no competing interests.

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Citation information

Cite this article as: Gene action and combining ability studies for grain yield and its related traits in cowpea (*Vigna unguiculata*), Emmanuel Yaw Owusu, Isaac Kodzo Amegbor, Kwabena Darkwa, Richard Oteng-Frimpong & Emmanuel Kofi Sie, *Cogent Food & Agriculture* (2018), 4: 1519973.

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