Asian Journal of Research in Crop Science

Volume 8, Issue 1, Page 25-42, 2023; Article no.AJRCS.95377
ISSN: 2581-7167

Preliminary Studies on Cowpea (*Vigna unguiculata*) Offers Opportunity for Selection in the Guinea and Sudan Savanna Agro Ecologies of Ghana

Sanatu Mustapha Alidu [a*]

[a] *Department of Crop Science, Faculty of Agriculture, Food and Consumer Sciences, University for Development Studies, P. O. Box TL1882, Nyankpala, Tamale, Ghana.*

Author's contribution

The sole author designed, analysed, interpreted and prepared the manuscript.

Article Information

DOI: 10.9734/AJRCS/2023/v8i1155

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/95377

Original Research Article

Received: 25/10/2022
Accepted: 28/12/2022
Published: 16/01/2023

ABSTRACT

Genotype by environmental interaction is important for breeding improved cowpea genotypes. The study was designed to identify promising inbred lines with high yield potential, stable mean yield with specific adaptation to a particular environment or environments. The study was conducted at three locations namely Nyankpala, Tumu, and Damongo. Twenty-two inbred lines plus 2 contrasting parents used to generate inbred lines were the test genotypes. Randomized complete block design with 4 replications was used. Seeds were planted at each location but were later thinned to one plant per hill. Each plot contained 5 rows of 10 plants per row with plant spacing of 60 cm between rows and 20 cm within rows with the number of entries being 24 plots giving the total plots as 96 plots for each location. Data collected were days to first flowering, 50% flowering, number of pods per plant, number of seeds per pod and hundred seed weight and grain yield. Data were subjected to analysis of variance using Gen Stat statistical package 12th edition. Combined analysis of variance across locations for grain yield were determine. Results showed significant genotypic

**Corresponding author: E-mail: msanatu@uds.edu.gh;*

differences among inbred lines for studied traits. significant genotype by environment interaction was observed for days to 50% flowering, ranging between 42 and 45 days. Number of pods per plant, number of seeds per pod and biomass also showed variable responses across locations. Phenotypic correlation analysis for days to flowering and maturity did not have any influence on yield, as genotypes 116, 189, 131 flowered within 43 and 45 days with corresponding yields of 1.89,1.82 and 1.7 tonnes per hectare. Yield variability showed the possibility for selecting location specific adapted lines as well as across all three locations.

Keywords: Cowpea; correlation analysis; genotype by environment interaction; recombinant inbred lines.

1. INTRODUCTION

Genotype by environmental interaction (GEI) is an important factor affecting the breeding and stability of improved and elite genotypes developed through plant breeding programmes in both the developed and developing countries including Ghana [1]. Genotype by environment interaction can be defined as the differential response of varying genotypes under change(s) in the environment [2]. The ability, or inability, of organisms to adapt to these changes at the speed necessary, determines the continuation, extinction, or evolution of species. A plant cannot migrate when challenged by fluctuations in environmental conditions, which means that it has to cope with environmental heterogeneity by adapting to the new or fluctuating environment [3]. It can do so via changing the phenotypic expression, a phenomenon called 'phenotypic plasticity', Plasticity often involves altering gene expression and plant physiology in response to environmental cues [4-7]. Although the importance of the differential effect of the environment on different plant genotypes has been known for a long time and has been considered in crop-breeding programmes, it is generally viewed as a challenging issue. Therefore, variety trials in a breeding program are usually conducted in several environments, to minimize the risk of discarding genotypes that potentially perform well in some, but not in all, environments (da Silva et al., 2016; Oliveira et al., 2017; Sabaghnia et al., 2012; Swaray, 2015)Ref)??

The study was designed to assess the genotype by environment interaction and stability of cowpea inbred lines in the Guinea, Sudan and transition ecologies of Ghana. Specifically, the study was designed to identify promising inbred lines with high yield potential, and then identify inbred lines with stable mean yield performance either with specific adaptation to a particular environment or across the three environments that will subsequently be recommended to farmers in the Guinea and Sudan Savanna ecologies of Ghana.

2. MATERIALS AND METHODS

The trial was conducted at three locations in the Guinea, Sudan and transitional zones of Northern Ghana. The three sites were Nyankpala, Tumu, and Damongo. Twenty-two inbred lines plus the two contrasting parents that were used to generate the inbred lines were the test genotypes. During the line development phase, the inbred lines were categorized into three maturity groups based on days to flowering as early maturing (37-42 days), medium maturing (43-48 days) and late maturing (48 days and above). The parental lines were advanced breeding cowpea lines obtained from the International Institute of Tropical Agriculture (IITA) Kano, Nigeria. The two parents were IT93K-503-1, a drought tolerant and medium maturing line and IT97K-279-3, which was the susceptible line but early maturing line (Fig. 1). Inbred lines were screened in wooden boxes in a screen house at the Savanna Agricultural Research Institute for drought tolerance using shoot related traits for seedling drought tolerance measurements. Potentially seedling tolerant lines were subsequently selected and screened under field conditions at Golinga and Libga locations for 2016 and 2017 during the dry season and populations selected were evaluated in the main season at three locations for preliminary stability study for yield in the production agro ecologies.

2.1 Geographical Location and Description of Study Sites

2.1.1 Nyankpala location

The study was carried out at the University for Development Studies experimental site in Nyankpala. Nyankpala is located in the Northern

Guinea Savanna Zone with a mean annual rainfall of about 1100 mm. It is located on latitude 9°, 25' N and longitude 0°, 58' W with an altitude of 183m above sea level. The temperature distribution is fairly uniform with a mean annual surrounding temperature of 28.3°C and annual relative humidity of 54%. The relative humidity varies greatly falling during the dry season and rising during the rainy season.

2.1.2 Damongo location

The study area for the transition Zone was conducted at the Savanna Agricultural out station in Damongo. Damongo has a Mean Annual Rainfall of 1200mm. It is located on Latitude N 09^0 01', Longitude W 01^0 49', (Altitude 189.1); with mean temperature of 29^0 c. The relative humidity was 78%.

2.1.3 Tumu location

The third multi location trial was conducted at the Savanna Agricultural out station in Tumu in the upper West region, representing the Sudan Savanna. Tumu is located on Latitude N 10^0 53' Longitude W 01^0 59'. The annual rainfall was 1100 mm. The average temperature was 32% with relative humidity of 49%.

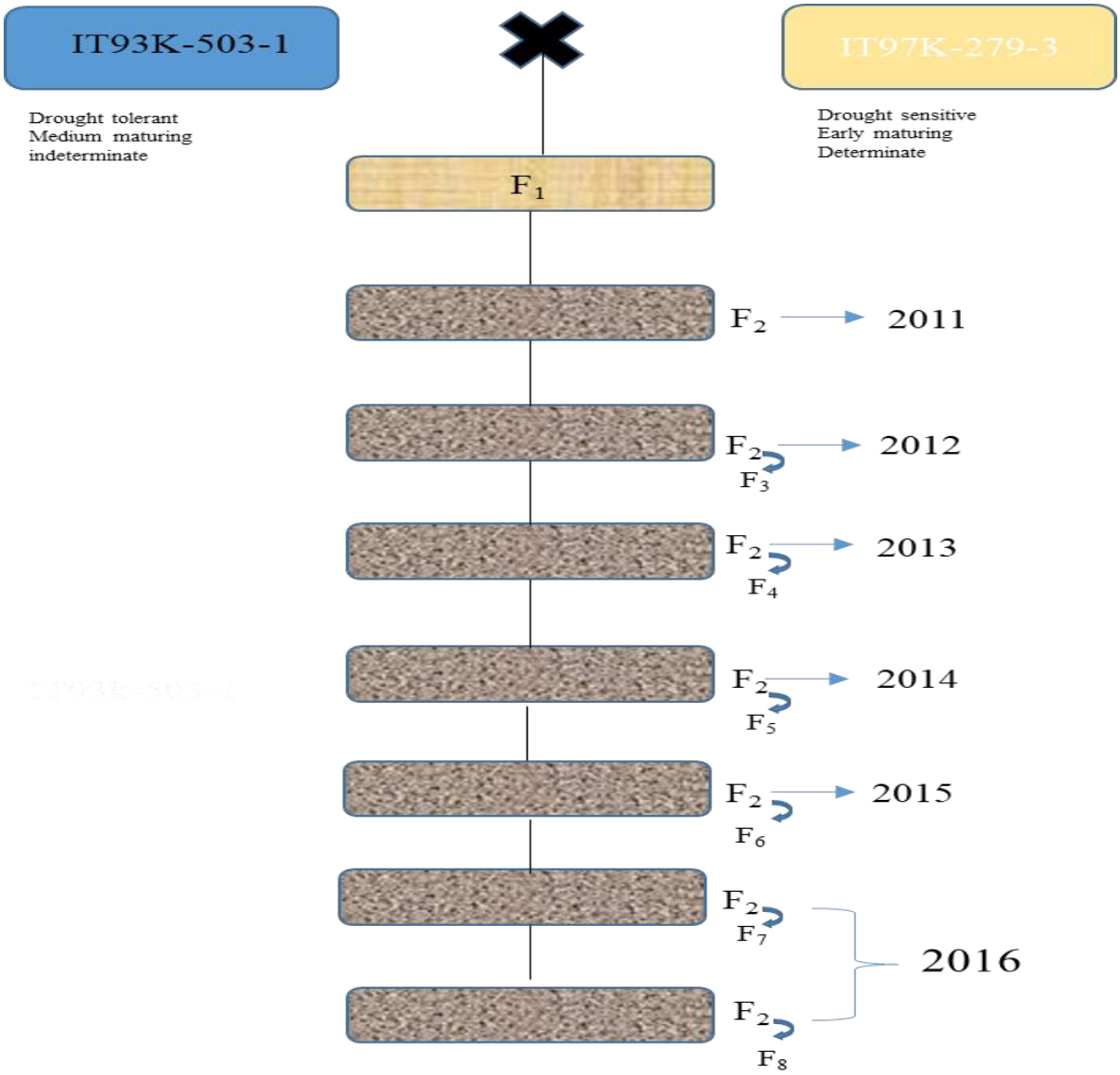

Fig. 1. Schematic diagram of the line development and evaluation

2.1.4 Experimental design

The experimental design used at each test location was a randomized complete block design with four replications. The seeds were planted according to the conditions for each location but were latter thinned to one plant per hill. Plot size was 3 m long; each plot contained 5 rows of 10 plants per row; with plant spacing of 60 cm between rows and 20 cm within rows with the number of entries being 24. Thus, each experimental unit consisted of 50 plants per plot, and each block contained 24 plots giving the total plots as 96 plots for the whole experiment for each location.

The fields were weeded twice during the growing period of the crop. Plants were sprayed twice with lambda cyhalothrin (product K- Optimal) at the rate of 20 g active ingredient per hectare, first at three weeks after planting, at the beginning of floral bud initiation, and during flowering to control insect pests.

As canopy become closed at flowering, the dosage was increased to 80 mills per litre. This was done regularly to prevent insect-pests and diseases.

2.2 Data Collection

2.2.1 Agronomic data

Data were recorded on plot bases for all three locations. Days from planting to first flowering for each plot was recorded, the date to 50% flowering data was recorded when half of the plants per plot produced flowers. Based on this information, the days to 50% flowering were estimated. At harvest, number of pods per plant, number of seeds per pod and hundred seed weight were taken as average of five randomly selected plants within a plot excluding the border plants. The weight of hundred seeds (g) for each treatment was determined by the use of an electronic balance. Data on grain yield was recorded on plot bases using three middle rows of 10 plants (30 plants per plot) in grams extrapolated to t/ha and t/ha:

Grain yield (t/ha) was given as $\frac{\text{grain weight x per plot}}{\text{plot area harvested}} \text{x } 10000$

Biomass yield per plot was estimated by a random sample of five plants uprooted carefully. They were put in labelled envelopes and sun-dried and weighed.

2.2.2 Weather data

The temperature, relative humidity, rainfall and solar radiation at the experimental locations were obtained from the meteorological department of the Savanna Agricultural Research Institute and the meteorological division of the Ministry of food and agriculture office in northern Ghana.

2.2.3 Soil sampling

Soil samples were taken before and after land preparation diagonally to cover all sections across trial field before planting from a depth of 0-20cm and bulked together. The samples for 2016 trial were analysed by the Chemistry Department of CSIR-Savanna Agricultural Research Institute, Tamale.

2.3 Data Analysis

The data for each location were subjected to Analysis of Variance (ANOVA) using GenStat statistical package 12th edition. Combined analysis of variance across locations for grain yield and yield components were also carried out to determine the interactive effects of genotypes by environment. The additive main effect and multiplicative interaction (AMMI) and the genotype, and genotype by environment interaction were concurrently determined using the Breeding management software (BMS) and GenStat [8].

3. RESULTS

3.1 Mean Squares from Analysis of Variance for Yield and Yield Components of Twenty-two (22) Cowpea Inbred Lines and their Parents

Results from the analysis of variance for each location and combined analysis across locations for the main season evaluation of inbred lines and the two contrasting parents are presented in Tables 1, 2, and 3. There were significant ($p < 0.01$) mean squares for all the traits measured at Nyankpala and Tumu locations. For Damongo locations, significant mean squares were observed for all traits except pods per plant (18 and 32) and seeds per pod (10 and 13) respectively. (Tables 1, 2 and 3). Combined

analysis of variance across the three locations showed significant genotypic differences ($p < 0.001$) among inbred lines for Days to 50% flowering, pods per plant, seeds per pod, grain yield and biomass but there were no significant differences for harvest index and hundred seed weight. Also, significant ($p < 0.001$) differences were observed across all the locations for all the traits studied. However, significant genotype by environment interaction was observed for days to 50% flowering, number of pods per plant, number of seeds per pod and biomass.

Table 1. Single site analysis of variance for Nyankpala location

Source of variation	Df	DFF	PPP	SPP	HSW	GY	Biomass	HI
Genotype	23	36.962**	62.99**	4.745*	7.767**	0.6694**	8.0893**	333.45**
Rep	3	2.236	243.86	4.514	2.9073	0.4791	4.211	95.4
Error	69	2.707	25.24	2.086	0.8118	0.2142	0.6656	40.68
CV		3.6	18.8	12.14	5.3	21.3	28.1	14

**P<0.05, P<0.001*

Table 2. Single site analysis of variance for damago location

Source of variation	Df	DFF	PPP	SPP	HSW	GY	Biomass	HI
Genotype	23	16.3691**	20.63ns	2.65ns	9.381**	2.4459**	25.743**	1494.14**
Rep	3	1.3715ns	12.73ns	0.903ns	3.709ns	0.1921ns	0.687ns	2.95
Error	69	0.7556	31.54	2.12	1.978	0.2427	2.143	81.04
CV		2.2	24.4	12.5	7.4	28.2	31.8	27.5

**P<0.05, P<0.001 DFF=days to 50% flowering, HSW= hundred seed weight, PPP=pods per plant, SPP=seeds per pod, t=tonnes, HI= harvest index*

Table 3. Single site analysis of variance for tumu location

Source of variation	df	DFF	PPP	SPP	HSW	GY	Biomass	HI
Genotype	23	62.637**	58.13**	5.456**	5.043*	0.23623**	1.3476**	479**
Rep	3	8.094	12.82	8.038	0.949	0.01168	0.1902	47.2ns
Error	69	2.884	15.66	2.321	2.205	0.03505	0.2964	124.1
CV		3.6	27	14	8.2	29.6	36.7	35.1

**P<0.05, P<0.001 DFF=days to 50% flowering, HSW= hundred seed weight, PPP=pods per plant, SPP=seeds per pod, t=tonnes, HI= harvest index*

Table 4. Analysis of variance across the three environments Combined ANOVA table for AMMO model for measured traits

Source	df	SS	MS	F	F_prob.
Total	287	234.8	0.818		
Treatments	71	198.8	2.8	17.07	< 0.001
Genotypes	23	22.29	0.969	5.91	< 0.001
Environments	2	121.67	60.834	267.52	< 0.001
Block	9	2.05	0.227	1.39	0.196
G x E	46	54.84	1.192	7.27	< 0.001
IPCA 1	24	49.18	2.049	12.49	< 0.001
IPCA 2	22	5.66	0.257	1.57	0.056
Residuals	0	0			
Error	207	33.95	0.164		

**P < 0.05, P < 0.001; DFF=days to 50% flowering, HSW= hundred seed weight, PPP=pods per plant, SPP=seeds per pod, t=tonnes, HI= harvest index*

A further combined analysis of variance was computed for all the three environments (Table 4) using the AMMI model. The results indicate highly significant differences ($P < 0.0001$) among the genotypes, environments as well as the genotype by environments interactions, which is an important entity in a combined analysis of variance across locations (Table 4). The environmental coefficient of variation (CV) in general, indicated good experimental precision for all the evaluated traits since the magnitude of the traits were less than 15% except for the grain yield which of course is highly variable across all the locations.

3.2 Environmental Mean Performance and Variation of Twenty-two Inbred Lines and Parental Checks of the Studied Traits Across Locations for 2016

Comparison of the three environmental locations for their mean performance of the yield and yield components indicates variations among the three locations for each location (Tables 5, 6, and 7) and a combined mean performance (Table 8) also revealed further reactions and variances for all the three locations respectively.

For Nyankpala location (Table 5), inbred line 75 had the highest mean biomass of 6.062kg whereas inbred line 28 had the lowest mean biomass of 1.28kg. The parental checks IT 97K-279-3 and IT93K-503-1 had mean biomass yields of 2.29t/ha and 6.021 t/ha respectively. The means Days to 50% flowering also ranged between 54 days for inbred line 55 and 42 days for inbred line 38. The parental checks IT97K-279-3 and IT93K-503-1 had mean days of 45 and 52 days to 50% flowering. The highest mean for hundred seed weight was observed for inbred line 396, which was 19.71g whereas the lowest mean was observed in inbred line 189 with mean weight of 15.52g. The parental checks (IT93K-503-1 and IT97K-279-3) had means weights of 2.23g and 16.93g respectively. The mean number of pods per plant was in the range of 18 and 35 for inbred line 142 and 55 respectively. The mean seeds per pod as well also ranged between 10 and 14 for inbred line 142 and 408 respectively. The parental checks (IT97K-279-3 and IT93K-503-1) had mean seeds of 10 and 12 respectively. The mean grain yield also ranged between 1.62t/ha and 3.12t/ha the parental checks (IT97K-279-3 and IT93K-503-1) and mean yields of 2.29 and 2.55t/ha respectively. The harvest index also ranged between 28.81 and 61.39 for inbred line 75 and 28 respectively (Table 5).

Damongo location also had different patterns of variability for each trait measured. Biomass mean yields ranged between 0.97 and 10.61 (Table 6). The parental checks (IT97K-279-3 and IT93K-503-1) had 3.95kg and 6.62kg respectively. Days to 50% flowering also ranged between 36 and 44 for inbred lines 57 and 116 respectively. The parental checks had 40 and 43 days mean days to 50% for IT97K-279-3 and IT93K-503-1 respectively. The mean range for hundred seed weight were between 15.13g and 22.05g for inbred lines 55 and 396. The parental checks weighed 18.8g and 20g for IT97K-279-3 and IT93K-503-1 respectively. The pods per plant were ranged between 19 and 27 for inbred line 55 and 255. The parental checks had mean pods of 21 and 28 for IT97K-279-3 and IT93K-503-1 respectively. The mean seeds per pod also ranged between 11 and 13 for inbred lines 396 and 131 the parental checks had mean seeds of 9 and 12 for IT97K-279-3 and IT93K-503-1 respectively. The mean grain yield also ranged between 0.31 and 2.84 for inbred line 55 and 116 respectively. The parental checks had 1.15 and 1.49t/ha. Harvest index also ranged between 4.05 and 74.24 for inbred lines 131 and 116. The parental checks had 15.05 and 27.05 respectively (Table 6).

Tumu location (Table 7) had different genotypic response for all the yield traits measured. The mean biomass ranged between 0.79 and 2.68. The parental checks (IT93K-503-1 and IT97K-279-3) also had mean biomass of 1.19 and 1.69 respectively. The mean days to 50% flowering also ranged between 41 and 58 for inbred line 142 and 57. The parental checks had 47 and 57 days for IT97K-279-3 and IT93K-503-1 respectively. The mean range for hundred seed weight also ranged between 15.23g and 20.29g for inbred line 189 and 398 respectively. The mean pods per plant ranged between 7 and 23 for inbred lines 57 and 325. The parental checks IT97K-503-1 and IT97K-279-3 had mean pods of 18 and 20 respectively. The mean seeds per pod also ranged between 8 and 13 seeds for inbred lines 57 and 325. The parental had 11 and 12 seeds respectively. The mean grain yield also ranged between 0.09 and 1.04t/ha. The parental checks for that location were in the range of 0.55 and 0.78 tonnes for IT97K-279-3 1 and IT93K-503-respectively. Inbred line 325 had the highest mean harvest index of 47.68; whereas inbred line 57 had the mean lowest harvest index of 9.07. The parental checks had 43.75 and 26.42 for IT93K-503-1 and IT97K-279-3 respectively (Table 7).

Table 5. Means for Nyankpala location for the main season evaluation for 2016

Families	Biomass((t/ha))	DFF	HSWg	PPP	SPP	Yield (t/ha)	HI(%)
F 116	2.16	43.25	16.82	24.5	10.75	1.917	46.95
F 142	1.325	42.75	17.79	17.75	10.0	1.902	59.14
F 186	2.687	48.25	15.66	25.5	12.75	2.508	48.69
F 189	1.792	42.5	15.52	21.25	12.0	1.619	48.47
F 20	2.104	48.0	16.27	30.25	11.5	2.025	49.1
F 223	4.083	47.5	16.86	27.5	13.0	2.229	34.83
F 230	1.937	44.5	16.78	32.25	11.25	1.715	47.64
F 255	1.729	43.5	15.6	28.25	12.0	1.703	49.7
F 28	1.208	42.5	16.57	25.5	11.5	1.945	61.39
F 325	3.458	48.5	17.01	24.5	12.75	2.544	42.63
F 353	1.954	45.5	18.11	23.5	11.25	1.846	48.54
F 38	2.146	42.0	18.92	26.25	11.0	2.529	55.24
F 396	1.708	42.5	19.71	26.0	10.25	1.818	54.58
F 398	1.854	45.25	16.26	30.0	11.25	2.083	52.54
F 406	1.937	45.0	15.75	29.5	11.25	1.909	51.0
F 408	3.917	47.75	16.63	22.75	13.5	1.747	31.14
F 55	3.271	54.0	15.62	34.75	12.75	3.115	49.72
F 57	5.042	45.75	16.81	22.75	13.25	2.25	31.23
F 75	6.062	42.75	16.05	23.0	11.75	2.333	28.81
F 78	3.021	44.75	17.02	28.25	12.5	2.456	45.33
F 84	3.104	44.75	17.51	31.5	10.5	2.06	39.88
F131	4.852	45.25	18.35	27.25	12.75	3.099	39.94
Standards							
IT93K-503-1	6.021	52	21.23	32	11.75	2.552	49.16
IT97K-279-3	2.229	45	16.93	26.25	9.25	2.294	29.62
SED	0.5769	1.163	0.6371	3.552	1.021	0.3273	4.51
LSD	1.1508	2.321	1.2710	7.087	2.038	0.6529	8.997

DFF=days to 50% flowering, HSW= hundred seed weight, PPP=pods per plant, SPP=seeds per pod, t=tonnes, HI= harvest index

Table 6. Means for various trials at Damongo location for the main season evaluation for 2016

Families	Biomass(t)	DFF	HSWg	PPP	SPP	Yield t/ha	HI(%)
F 116	0.969	36.75	18.8	26.5	12	2.848	74.24
F 142	1.517	40.75	20.59	22.75	11	2.373	60.95
F 186	4.661	41.25	17.66	21.5	12.25	1.193	21.6
F 189	2.966	40.75	19.31	21.25	12.75	1.383	31.87
F 20	6.022	39.75	18.37	23	11.5	1.665	21.58
F 223	6.002	39.25	16.64	21.25	11.5	0.38	6.0
F 230	2.589	42	20.09	25.25	10.5	2.498	48.82
F 255	3.292	38.25	17.96	27	11.5	2.558	45.12
F 28	1.443	37.5	18.21	23	12	1.678	53.35
F 325	7.879	39.25	18.3	22	12.5	1.515	16.03
F 353	2.412	39.25	19.58	24.25	12	2.632	53.0
F 38	2.441	38.25	20.57	20.75	11.75	1.25	40.1
F 396	3.403	40.25	22.05	25.5	10.5	2.822	46.74
F 398	2.153	38.25	20.82	22.75	11.75	2.243	51.19
F 406	3.218	43.75	20	24.75	11.75	2.54	44.26
F 408	10.061	42	16.71	20.75	12.5	0.603	5.79
F 55	7.775	43.25	15.13	18.5	10.75	0.317	4.05
F 57	5.992	44.75	19.97	20.75	12.25	0.803	12.24
F 75	5.548	40.5	18.65	21.75	10.75	1.85	25.57
F 78	9.136	38.75	18.36	24.5	11.25	1.423	14.24
F 84	3.736	41.25	18.77	23.25	11.5	2.652	41.97

Families	Biomass(t)	DFF	HSWg	PPP	SPP	Yield t/ha	HI(%)
F131	6.806	41	19.96	23.25	13.25	2.145	24.64
Standards							
IT93K-503-1	6.621	42.75	20	27.75	12.25	1.49	27.06
IT97K-279-3	3.958	39.75	18.77	21.25	9.75	1.115	15.05
SED	1.035	0.6146	0.995	3.971	1.03	0.3483	6.366
LSD	2.065	1.2262	1.984	7.922	2.054	0.6949	12.699

DFF=days to 50% flowering, HSW= hundred seed weight, PPP=pods per plant, SPP=seeds per pod, t=tonnes, HI= harvest index

Table 7. Means for Tumu location for the main season evaluation for 2016

Family	Biomass((t/ha)	DFF	HSWg	PPP	SPP	Yield (t/ha)	HI(%)
F 116	1.905	44.75	16.79	13.75	11.5	0.6944	28.25
F 131	0.873	47.25	19.04	14.25	10.25	0.434	35.88
F 142	2.688	41.75	18.42	19.75	12	0.9201	25.61
F 186	0.996	49.75	15.23	14.25	9.75	0.7738	45.33
F 189	0.922	43.5	18.55	13.5	12.25	0.5382	36.33
F 20	1.112	47.25	17.93	17.25	10.00	0.8681	45.77
F 223	1.647	48.25	17.02	9.5	9.00	0.3125	18.22
F 230	1.758	44.75	18.21	16	12.5	0.816	32.51
F 255	2.323	44.5	18.44	17.25	12.25	0.8681	28.06
F 28	0.91	44	18.05	22.5	12.75	0.8214	47.68
F 325	0.811	48.25	18.26	12.25	10.00	0.3646	32.14
F 353	1.241	45.25	17.86	13.00	10.75	0.7691	40.27
F 38	1.739	43.25	19.26	16.00	11.25	0.6076	27.19
F 396	1.924	43.25	20.29	17.75	11.75	1.0417	36.41
F 398	2.557	46	17.78	13.25	10.25	0.4687	16.37
F 406	1.051	45.25	18.33	18.75	11.5	0.8319	44.07
F 408	0.793	46.5	18.41	8.5.00	10.5	0.3007	27.23
F 55	1.032	58.25	17.57	7.25	8.25	0.0928	9.07
F 57	1.868	46.75	17.1	10.5	9.5	0.2951	14.11
F 75	1.493	42.5	18.73	10.5	10.5	0.5382	26.61
F 78	2.212	46.5	19.31	13.75	10.5	0.6701	25.74
F 84	0.959	44.5	18.03	14.25	12	0.8333	47.55
Standards							
IT93K-503-1	1.119	57	19.82	19.75	11.75	0.7873	43.75
IT97K-279-3	1.69	47.75	16.11	17.75	10.5	0.5556	26.42
SED	0.3849	1.201	1.05	2.799	1.077	0.1324	7.88
LSD	0.7679	2.395	2.095	5.583	2.149	0.2641	15.71

DFF=days to 50% flowering, HSW= hundred seed weight, PPP=pods per plant, SPP=seeds per pod, t=tonnes, HI= harvest index

Combined mean yield estimates, environmental means scores as well as variances across all the three locations is indicated in Table 9. The total mean yields across the three locations ranged between 0.88 and 1.89 for inbred lines 408 and 396 respectively. The parental checks IT97K-279-3 and IT93K-503-1 had mean yields of 1.32 and 1.609t/ha respectively. The environmental variance for the three locations were 0.08, 0.33 and 0.77 for Tumu, Nyankpala and Damongo respectively (Table 8).

3.3 Mean Performance of Inbred Lines Across the Three Locations in the Guinea and Sudan Savanna Ecologies for 2016 Main Season

The mean days to 50% flowering and mean yield performance of the twenty-two inbred lines with the two parental checks used to generate the inbred lines were computed for all the three locations. There was variation in terms of mean yield performance across all the three locations

for the inbred lines used for the study (Table 8). For environment one (Damongo location), the highest and lowest mean yields in t/ha were 0.32 and 2.85 for inbred line 55 and 116 respectively (Table 8). The parental in that location had mean yields of 1.1 t/ha and 1.48 t/ha for IT97K-279-3 and IT93K-503-1 respectively. The mean range of yield in tonnes for environment two (Nyankpala) were 1.70 and 3.12 for inbred line 255 and 55 respectively, with the parental checks having mean yields of 2.29 and 2.55 respectively (Table 8). The mean yields for Tumu location also ranged between 0.09 and 1.04 tonnes for inbred lines 55 and 396 respectively, the parental lines had mean yields of 0.56 t/ha and 0.79 respectively.

Superiority of the best four inbred line for each location were ranked (Table 11) to determine whether there were specific adaptations for each environment. Finally, an overall ranking of inbred lines with comparison to their parental checks and their relationship to days to 50% flowering was carried out to ascertain whether days to flowering had any influence on yield and related traits (Table 12). As a consequence of the last ranking with days to flowering, Inbred lines with family numbers 84, 406, 396, 353, 255, 230, 142, 131, and 116 performed better than both parents used in the study with their yields ranging between 1.71 to 1.89 t/ha (Table 13). The second rank of inbred lines in terms of mean yields that performed better than the second parent (IT97K-279-3) were inbred lines with family numbers 186, 20, 28, 325, 38, 398, 75 and 78 with their mean yields ranging between 1.46 and 1.60 t/ha (Table 12). Finally, the last cohort of inbred lines were those whose mean performance were below the second parent; these were inbred lines 189, 223, 408, 55, and 57 with their mean yields ranging between 0.88 and 1.18 t/ha.

Table 8. Genotype and Environmental mean performance of 22 inbred lines and the parental checks at Nyankpala, Damongo and Tumu locations using the AMMI model

RILs	E1-Yield (t/ha)	E2-Yield (t/ha)	E3-Yield (t/ha)	Mean	IPCAg[1]	IPCAg[2]
F 116	2.85	1.92	0.69	1.82	-0.52	-0.24
F 131	2.15	3.10	0.43	1.89	0.18	-0.66
F 142	2.38	1.90	0.92	1.73	-0.34	0.10
F 186	1.19	2.51	0.77	1.49	0.34	0.17
F 189	1.38	1.62	0.54	1.18	-0.07	0.28
F 20	1.66	2.03	0.87	1.52	-0.02	0.27
F 223	0.38	2.23	0.31	0.97	0.54	0.22
F 230	2.50	1.72	0.82	1.68	-0.46	0.06
F 255	2.56	1.70	0.87	1.71	-0.48	0.08
F 28	1.68	1.95	0.82	1.48	-0.05	0.26
F 325	1.51	2.54	0.36	1.47	0.22	-0.27
F 353	2.63	1.85	0.77	1.75	-0.46	-0.08
F 38	1.25	2.53	0.61	1.46	0.32	0.01
F 396	2.82	1.82	1.04	1.89	-0.54	0.07
F 398	2.24	2.08	0.47	1.60	-0.23	-0.26
F 406	2.54	1.91	0.83	1.76	-0.40	-0.02
F 408	0.60	1.75	0.30	0.88	0.28	0.32
F 55	0.32	3.12	0.09	1.18	0.89	-0.28
F 57	0.80	2.25	0.30	1.12	0.39	0.05
F 75	1.85	2.33	0.54	1.57	0.02	-0.17
F 78	1.42	2.46	0.67	1.52	0.23	0.03
F 84	2.65	2.06	0.83	1.85	-0.39	-0.12
Standards						
IT93K-503-1	1.49	2.55	0.79	1.61	0.24	0.06
IT97K-279-3	1.12	2.29	0.56	1.32	0.29	0.12

E1= Damongo, E2= Nyankpala, E3= Tumu; IPCA = Interaction principal component axis

Table 9. Environmental mean scores across all the three locations

Environment	NE	Em	IPCAe[1]	IPCAe[2]
Damongo	1	1.749	-1.3526	-0.4151
Nyankpala	2	2.175	1.29356	-0.4747
Tumu	3	0.633	0.05907	0.88988

IPCA = Interaction principal component axis

Table 10. Variances observed across the three environments

Location	No. Observed	Mean	Variance
Damongo	96	1.749	0.7751
Nyankpala	96	2.175	0.3328
Tumu	96	0.633	0.083
Margin	288	1.519	0.8181

Table 11. Best four inbred lines for yield for each location across three environments

Table of first four AMMI selections per environment							
Number	**Environment**	**Mean**	**Score**	**1**	**2**	**3**	**4**
2	Nyankpala	2.175	1.2936	F 55	F 131	IT93K-503-1	F 325
3	Tumu	0.633	0.0591	F 396	F 142	F 255	F 20
1	Damongo	1.749	-1.3526	F 116	F 396	F 84	F 353

Table 12. Comparison of mean days to 50% flowering and yield performance of inbred lines across the three locations in the Guinea and Sudan Savanna Ecologies for 2016 Main Season

Inbred line	DFF	Yield
F 116	**42**	**1.82**
F 131	**45**	**1.89**
F 142	**42**	**1.73**
F 186	46	1.49
F 189	42	1.18
F 20	45	1.52
F 223	45	0.97
F 230	**44**	**1.68**
F 255	**42**	**1.71**
F 28	41	1.48
F 325	45	1.47
F 353	**43**	**1.75**
F 38	41	1.46
F 396	**42**	**1.89**
F 398	43	1.60
F 406	**45**	**1.76**
F 408	45	0.88
F 55	52	1.17
F 57	46	1.12
F 75	42	1.57
F 78	43	1.52
F 84	**44**	**1.85**
IT93K-503-1	51	1.61
IT97K-279-3	44	1.32
Mean	44	1.52
SE	0.48	0.10
CV	9.27	55.07

3.4 Correlation Analysis for Yield and Yield Components for 22 Inbred Lines and the Two Parental Checks for Each Location and Across All the Locations

Correlation analysis for most of the yield related traits were strongly associated for each location and a further correlation was done for all the three locations (Tables 13, 14, 15 and 16). The mean heritability's for each trait were also estimated and results presented in Table 18. Genotypic and phenotypic correlations were significant for most of the traits across all the three locations. A combined correlation for all the three locations indicates significant but negative correlations for days to 50% flowering, with the other traits studied (Table 16).

Grain yield correlated positively (r = 0.57) with harvest index, but negatively (r = -0.58) with biomass. Also, the number of pods per plant correlated positively (r = 0.67) with grain yield, biomass (r = 0.20) and harvest index (r = 0.4).

Table 13. Genotypic below (diagonal) and phenotypic (above diagonal correlation analysis of yield and yield components of 22 inbred lines at Nyankpala location for 2016 Multi-location

Traits	DFF	PPP	Seeds_pod	HSW	Yieldt_ha	Bimoass	HI
DFF	1	0.3524	0.463*	-0.2799	0.467*	0.1535	-0.1582
Pods_plant	0.560**	1	-0.1382	0.0383	0.314	0.0627	-0.0261
Seeds_pod	0.625***	-0.2192	1	-0.596**	0.2579	0.2387	-0.3159
HSW	-0.2909	0.0242	-0.746***	1	0.1796	0.255	-0.128
Yieldt_ha	0.630***	0.2747	0.3945	0.2458	1	0.535**	-0.2319
Biomass	0.1868	0.0885	0.3292	0.2892	0.632***	1	-0.912***
HI	-0.1675	-0.0939	-0.437*	-0.15	-0.422*	-0.945***	1

Significant P < 0.05; p < 0.001; DFF=days to 50% flowering, HSW= hundred seed weight, PPP=pods per plant, SPP=seeds per pod, t=tonnes, HI= harvest index

Table 14. Correlation analysis of yield and yield components of 22 inbred lines at Damongo location for 2016 Multi-location genotypic (below diagonal) phenotypic (above diagonal)

Traits	DFF	Pods_plant	Seeds_pod	HSW	Yieldt_ha	Biomass	HI
DFF	1	-0.3217	0.0752	-0.085	-0.2174	0.2935	-0.3503
Pods_plant	NA	1	-0.434*	0.468*	0.696***	-0.3735	0.514**
Seeds_pod	0.024	NA	1	-0.129	-0.1871	0.2252	-0.198
HSW	-0.069	NA	-0.1977	1	0.656***	-0.586***	0.653***
Yieldt_ha	-0.338	NA	-0.528**	0.758***	1	-0.610***	0.835***
Biomass	0.395	NA	0.557**	-0.689***	-0.705***	1	-0.895***
HI	-0.490*	NA	-0.477*	0.682***	0.865***	-0.924***	1

Table 15. Correlation analysis of yield and yield components of 22 inbred lines at Tumu location for 2016 Multi-location evaluation genotypic (below diagonal) phenotypic (above diagonal)

Traits	DFF	Pods_plant	Seeds_pod	HSW	Yieldt_ha	Biomass	HI
DFF	1	-0.3171	-0.651***	-0.533***	-0.525**	-0.238	-0.329
Pods_plant	-0.3703	1	0.7269	0.2354	0.808***	0.1634	0.605***
Seeds_pod	-0.868***	0.948***	1	0.450*	0.731***	0.1213	0.545**
HSW	-0.664***	0.423*	0.698***	1	0.2732	0.1048	0.1238
Yieldt_ha	-0.562***	0.903***	0.862***	0.3234	1	0.2191	0.694***
Biomass	-0.2699	0.2274	0.1665	0.0774	0.2905	1	-0.510**
HI	-0.3838	0.718***	0.714***	0.2456	0.720***	-0.441***	1

Table 16. Combined correlations for the traits across all three environments

	DFF	PPP	SPP	HSW	GY	Biomass	HI
DFF	1						
PPP	-0.2022*	1					
SPP	-0.1235*	0.2641*	1				
HSW	-0.3382*	-0.0475	-0.0863	1			
GY	-0.2185*	0.6683*	0.2582*	0.0615	1		
Biomass	-0.2707*	0.1957*	0.1442*	0.018	0.1337*	1	
HI	-0.0899	0.3541*	0.1312*	0.0239	0.5752*	-0.5837*	1

Significant P< 0.05; p<0.001

Table 17. Genotypic (below diagonal) and phenotypic (above diagonal) correlations across the three locations

Traits	DFF	Pods_plant	Seeds_pod	HSW	Yieldt_ha	Biomass	HI
DFF	1	-0.162	-0.159	-0.549**	-0.429*	0.467*	-0.569**
Pods_plant	-0.316	1	-0.316	0.386	0.614***	-0.395	0.542**
Seeds_pod	NA	NA	1	-0.299	-0.208	-0.065	0.063
HSW	-0.726***	0.706	NA	1	0.559**	-0.212	0.38
Yieldt_ha	NA	NA	NA	NA	1	-0.448*	0.707***
Biomass	0.999***	-0.999***	NA	-0.103	NA	1	-0.902***
HI	-0.967***	0.894***	NA	0.382	NA	-0.999***	1

Table 18. Heritability estimates for the various traits studied across the three locations

Traits	Heritability
DFF	0.95
PPP	0.73
SPP	0.57
HSW	0.57
GY	0.85
Biomass	0.78
HI	0.75

3.5 GGE Biplot and Stability Analysis of Twenty-two Cowpea Inbred Lines with their Parental Checks Across the Three Environments for 2016 Main Cropping Season

The GGE biplot analysis using GenStat software, provides a graphical presentation of results for the twenty-two inbred lines and their parental checks (Fig. 2, Fig. 3 and Fig. 4). The GGE biplot of the grain yield of twenty-two inbred lines and the two parental checks revealed that PC1 explained 82.25% of the total variation whereas PC2 explained 14.97% thus both PC 1 and PC2 explained in total 97.22% of the variation in the grain yield performance of the inbred lines and the parental checks across all the three environments (Fig. 2). PC1 explained most of the variation among inbred lines in all the environments, however, the Damongo location which is the main location responsible for the genotype by environment interaction because it had the longest vector compared to the other two locations (Fig. 2). Also, the inbred lines with the longest vectors in their respective directions from the origin of the biplot are the most responsive and best cultivars across the three environments [9-12]; therefore, inbred lines 131, 398, 84, 406, 353, 116, 255, 142, and 396, were the best inbred lines (Fig. 2 and Fig. 3). The most stable inbred lines are the ones closer to the origin and thus their mean yields would rank the same in all the three environments. Inbred lines in that category are 75, 28, 20, 189, 325, 78 and the parental genotypes (Fig. 3). Fig. 4 is a comparison of all the genotypes with the ideal cultivar. The ideal inbred line in this case, is represented by the small circle with an arrow pointing to it, it is defined as having the highest yield in all the environments; thus, inbred line 131 is the highest and the ideal genotype across all the three locations; while 55 is the poorest in terms of yield as seen in Fig. 4. Again, Fig. 2 GGE biplot displayed two groups of environments; one mega environment which consist of Damongo and Tumu locations. Inbred lines in these two -grouped environments have genotypes that performed the same and are the best performing inbred lines for those two locations. The inbred lines that fell in that mega environment are 116, 396, 398, 142, 406, 353 and 84 (Fig. 2). Fig. 5 and Fig. 6 are GGE biplots for days to 50% flowering. Inbred

lines differed in their days to flowering in response to environmental cues; therefore, inbred lines found in the mega environment in Fig. 6 had similar mean days to flowering for the two locations (Nyankpala and Tumu 2016).

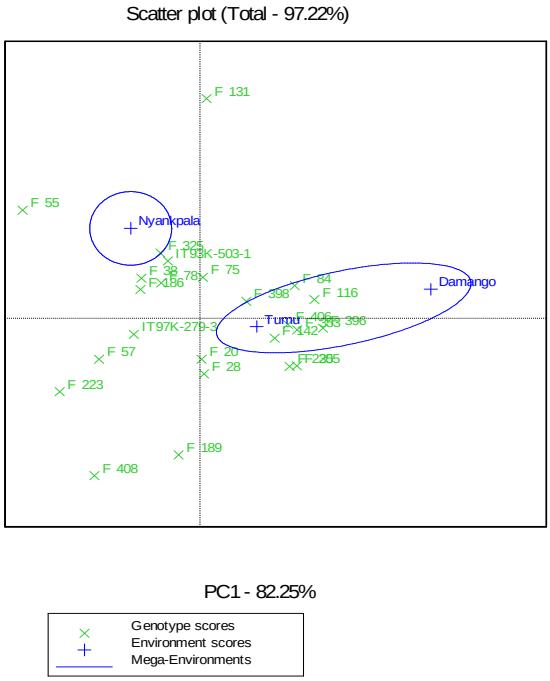

Fig. 2. The" which-won-where" GGE biplot-based on cowpea grain yield for three environments (Nyankpala, Damongo and Tumu) locations in the Guinea and Sudan Savanna Ecologies of Ghana

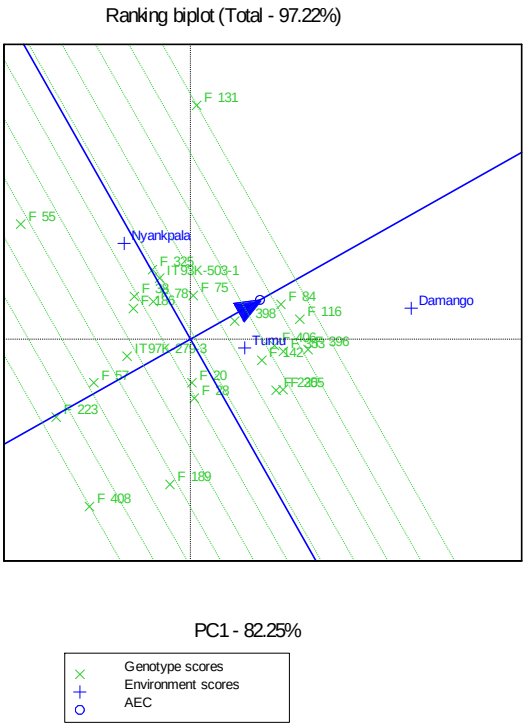

Fig. 3. GGE biplot view of mean grain yield performance and stability of cowpea inbred lines across the three environments in the Guinea and Sudan Savanna ecologies of Northern Ghana

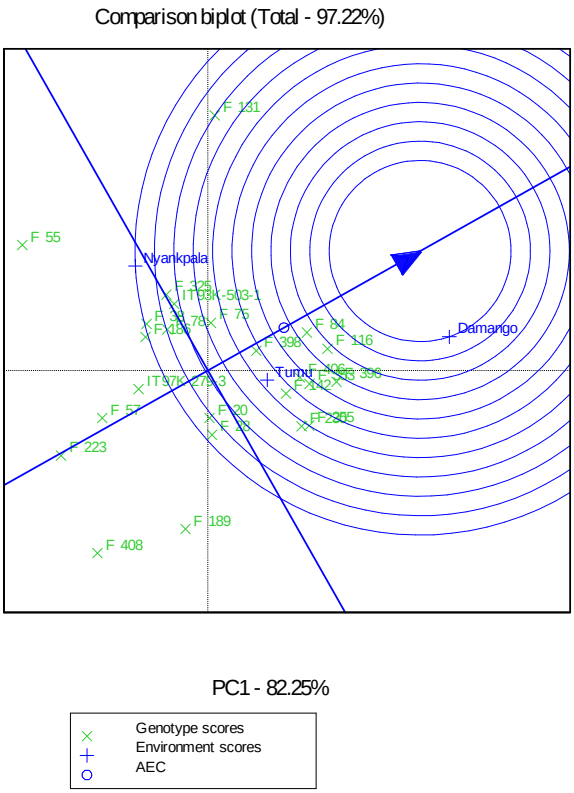

Fig. 4. GGE biplot, based on genotype-focused scaling of comparing the inbred lines with the ideal genotype across all the three environments (Nyankpala, Damongo and Tumu)

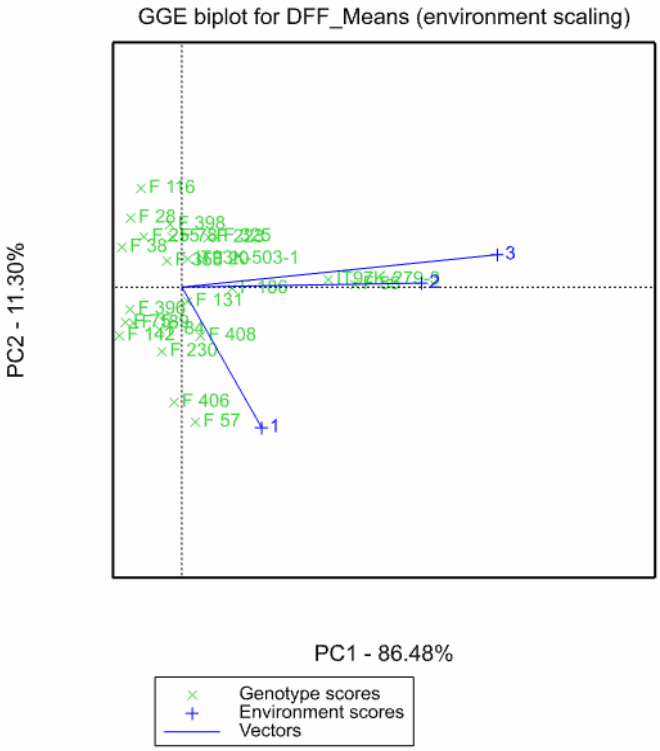

Fig. 5. GGE biplot, comparing the inbred lines for days to 50% flowering across all the three environments (Nyankpala, Damongo and Tumu)

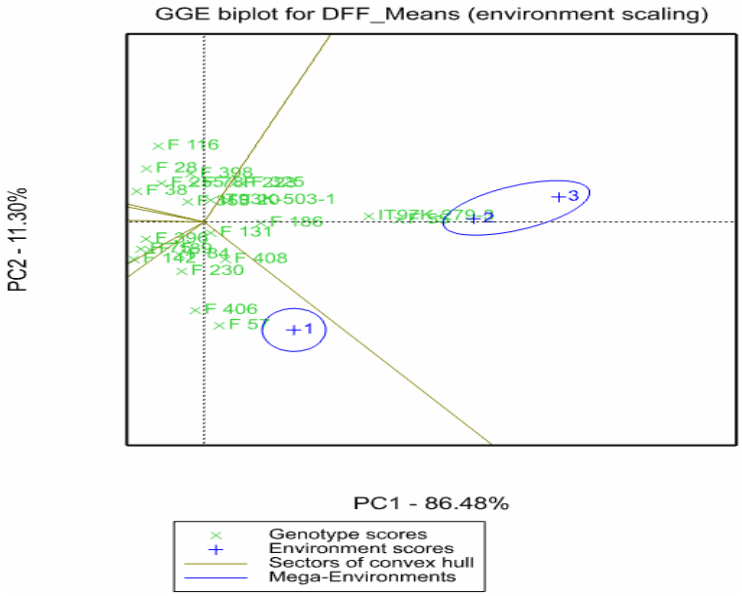

Fig. 6. GGE biplot, grouping within environments of inbred lines for days to 50% flowering across all the three environments (Nyankpala, Damongo and Tumu 2016 year???)

4. DISCUSSION

Analysis of variance for yield and yield components for each location as well as analysis of variance for all the three environments revealed significant differences for all the traits studied. The combined analysis of variance showed significant differences among genotypes and environments for grain yield indicating the presence of variability in genotypes and the diversity of growing conditions and locations. This has been reported by Punto and Lantican [13] who in their study on the genotype by environment interaction on yield of Mung bean; indicated that certain varieties were superior in yield at only specific growing environments compared to others. Across the entire environments, there were significant associations between grain yield and number of pods per plant. This result corroborates a study by Addo-Quaye *et al.*, [14] on trial set up to test the performance of three cowpea varieties in the two agro ecological zones of the central region of Ghana. In their study, they concluded that there were highly significant varietal differences in seed weight across locations. This also further agreed with the findings of Masenya [15] and Okafor [16]. Masenya [15] found weight per 100 seeds revealed that 51 and 32 breeding lines had weights higher than Glenda in the early and medium maturity trials, respectively. Okafor [16] found significant differences in 100 seed weight among nine cowpea varieties tested in Nigeria. Therefore, this was an indication that seed weight as well as grain yield were influenced by both genetic and environmental factors. However, lower yields were observed for some inbred lines compared to other locations. This could be as a result of environmental factors across the three locations. Sangakkara [17] also observed that planting cowpea in the wet season produced the highest grain yields. In multi environment trials researchers try to find genotypes that clearly indicate the largest responses to particular locations while minimizing their seasonal variations at those locations [18,19]. In this study, inbred lines were grouped into mega environments as two clusters. Those inbred lines found between the two environments (mega environment) were the inbred lines whose mean performances were the same for the two locations. However, there were some inbred lines that were rather specific only to Nyankpala environment alone. It was observed that for all the traits studied, the number of pods per plant (PPP), seeds per pod and pod yield were the ones that showed the highest phenotypic correlation with grain yield (GY), as reported by [20].

This relationship study has to confirmed that traits such as the pods per plant, seeds per pod and grain yield are good selection indices for high yielding inbred lines. The GGE biplot [21,9,11] analysis and the AMMI analysis [22] provide an effective methodology of visualizing the “which-won-where” patterns of a multi-location environment trial data set. In this study

inbred lines multi-location data were subjected to the biplot analysis using GenStat and the Breeding Management Software. Various graphical representation of the genotypic potential of the 22 inbred lines with their parental checks were obtained from the output. The biplot displayed by AMMI [22] gave three main graphical representation of the variability that existed in the population. The principal character of this graphical representation is the grouping of genotypes into principal components one and two (PC1 and PC2). Each component explained the portion of variability of mean yields that existed in the population. It generated means and interactions, which indicated both the mean yields and interaction scores of the genotypes and the environments in a single plot. An ideal genotype is located at the centre of a concentric circle. In this study, inbred line 84 satisfied this criterion. The ideal genotype projection on the average tester coordinate Y- axis is zero. It has the longest vector of all the genotypes [23,18,24]. In this study, inbred line 131 best fits this criterion. The grouping of genotypes into mega environments [25,26] and [27] based on the graphical display, groups together inbred lines that have similar mean yield performance for those locations. In this study, inbred lines with family numbers 84, 116, 396, 406, 142, 398 and 255 satisfy that requirement. Finally, the ultimate aim of any genotype by environment evaluation is the mean performance and stability of genotypes across the studied environments [28,10,29]. However, the stable genotypes across all the environments are those inbred lines that are close to the ideal genotype (Fig. 6). These inbred lines are 84, 116, 396, 406, 142, 398 and 255. Apparently, they performed well in two environments with similar mean yields. But then the most stable inbred lines were those very close to the origin also known as the vertex cultivars. They will rank the same in all the environments and are less responsive in their respective directions [30,31,11,32].

5. CONCLUSION AND RECOMMENDATIONS

Analysis of variance for each location as well as combined analysis of variance across all the locations revealed that there were significant differences among genotypes and their environments for grain yield and yield components indicating the presence of variability in the inbred lines as well as diversity of growing conditions and locations. The genotype by environment interaction was highly significant reflecting the differential response of the inbred lines in various environments. Phenotypic correlation analysis for days to flowering and maturity did not have any influence on yield as reflected in the selection of potential stable and high yielding inbred lines. This is in contrast to earlier studies reporting that cowpea genotypes with longer cycles are more productive. The substantial variability of the inbred lines is an indication of the potential for identifying drought tolerant and high yielding inbred lines across all the locations in the Guinea and Sudan Savanna ecologies based on mean performance and stability. Potentially stable as well as high yielding inbred lines across all the environments were 84, 116, 142, 398, 406, 396, 353, and 255. Inbred line 131 had the highest mean yield for Nyankpala location (environment two), whereas inbred line 189 was the highest yielding at Tumu location (environment one). These would be further evaluated and released to farmers in the Guinea and Sudan Savanna ecologies.

COMPETING INTERESTS

Author has declared that no competing interests exist.

REFERENCES

1. Sabaghnia N, Karimizadeh R, Mohammadi M. Genotype by environment interaction and stability analysis for grain yield of lentil genotypes. Žemdirbyst. 2012a;99:305-12.
2. Mather K, Caligari PDS. Genotype and environment interactions. I. Regression of interaction on overall effect of the environment. Heredity. 1974;33(1):43-59. DOI: 10.1038/hdy.1974.63
3. El-Soda M, Boer MP, Bagheri H, Hanhart CJ, Koornneef M, Aarts MG. Genotype–environment interactions affecting preflowering physiological and morphological traits of Brassica rapa grown in two watering regimes. J Exp Bot. 2014;65(2):697-708. DOI: 10.1093/jxb/ert434, PMID 24474811.
4. Nicotra AB, Segal DL, Hoyle GL, Schrey AW, Verhoeven KJ, Richards CL. Adaptive plasticity and epigenetic variation in response to warming in an Alpine plant. Ecol Evol. 2015;5(3):634-47. DOI: 10.1002/ece3.1329, PMID 25691987.
5. Juenger TE. Natural variation and genetic constraints on drought tolerance. Curr Opin Plant Biol. 2013;16(3):274-81.

DOI: 10.1016/j.pbi.2013.02.001, PMID 23462639.

6. Assmann SM. Natural variation in abiotic stress and climate change responses in Arabidopsis: Implications for twenty-first-century agriculture. Int J Plant Sci. 2012; 174(1):3-26.
7. Van Kleunen M, Fischer M. Constraints on the evolution of adaptive phenotypic plasticity in plants. New Phytol. 2005; 166(1):49-60.
   DOI: 10.1111/j.1469-8137.2004.01296.x, PMID 15760350.
8. Genstat R. Genstat for Windows. Release 11.1. Oxford, UK: VSN International Ltd; 2008.
9. Yan W, Kang MS, Ma B, Woods S, Cornelius PL. GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci. 2007a;47(2):643-53.
   DOI: 10.2135/cropsci2006.06.0374
10. Yan W, Hunt LA. Interpretation of genotype× environment interaction for winter wheat yield in Ontario. Crop Sci. 2001a;41(1):19-25.
    DOI: 10.2135/cropsci2001.41119x
11. Yan W, Kang MS. GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC press; 2002.
12. Yang R-C, Crossa J, Cornelius PL, Burgueño J. Biplot analysis of genotype× environment interaction: proceed with caution. Crop Sci. 2009;49(5):1564-76.
    DOI: 10.2135/cropsci2008.11.0665
13. Punto N, Lantican R. Genotype× environment interaction for yield in field legumes: II. Mungbean [Vigna radiata (L.) Wilczek]. Philipp J Crop Sci. 1982; 7(3):137-40.
14. Addo-Quaye A, Darkwa A, Ocloo G. Yield and productivity of component crops in a maize-soybean intercropping system as affected by time of planting and spatial arrangement. ARPN. J Agric Biol Sci. 2011;6(9):50-7.
15. Masenya TA. Evaluation of introduced cowpea breeding lines in South Africa; 2016.
    Available:http://ulspace.ul.ac.za/handle/10386/1638 [thesis]
16. Okafor L. Adapting improved Cowpea cultivars to the Nigeria and Arid zone. Tropical grain legume bulletin. 1986;33:20.
17. Sangakkara UR. Growth and yields of cowpea (*Vigna unguiculata* (L.) Walp) as influenced by seed characters, soil moisture and season of planting. J Agron Crop Sci. 1998;180(3):137-42.
    DOI: 10.1111/j.1439-037X.1998.tb00383.x
18. Sabaghnia N, Karimizadeh R, Mohammadi M. Grouping genotypes and test environments by some cluster methods regarding genotype × environment interaction in multi-environment trials. Genetika. 2012c;44(3):457-73.
    DOI: 10.2298/GENSR1203457S
19. Sabaghnia N, Karimizadeh R, Mohammadi M. The use of corrected and uncorrected nonparametric stability measurements in durum wheat multi-environmental trials. Span J Agric Res. 2012d;10(3):722-30.
    DOI: 10.5424/sjar/2012103-384-11
20. Teixeira FF, Gomide RL, Albuquerque PEPd, Andrade CLTd, Leite CEP, Parentoni SN, et al. Evaluation of maize core collection for drought tolerance. Crop Breed Appl Biotechnol. 2010;10(4):312-20.
    DOI: 10.1590/S1984-70332010000400005
21. Yan W. GGEbiplot—A Windows application for graphical analysis of multienvironment trial data and other types of two-way data. Agron J. 2001; 93(5):1111-8.
    DOI: 10.2134/agronj2001.9351111x
22. Zobel RW, Wright MJ, Gauch HG. Statistical analysis of a yield trial. Agron J. 1988;80(3):388-93.
    DOI:10.2134/agronj1988.00021962008000030002x
23. Sabaghnia N, Sabaghpour S, Dehghani H. The use of an AMMI model and its parameters to analyse yield stability in multi-environment trials. J Agric Sci. 2008;146(5):571-81.
    DOI: 10.1017/S0021859608007831
24. Sabaghnia N, Karimizadeh R, Mohammadi M. Genotype by environment interaction and stability analysis for grain yield of lentil genotypes. Žemdirbyst. 2012b;99:305-12.
25. Gauch HG, Zobel RW. Identifying mega-environments and targeting genotypes. Crop Sci. 1997;37(2):311-26.
    DOI:10.2135/cropsci1997.0011183X003700020002x
26. Yan W, Hunt L. Genotype by environment interaction and crop yield. Plant Breed Rev. 1998;16:135-78.
27. Yan W, Hunt LA. Interpretation of genotype× environment interaction for winter wheat yield in Ontario. Crop Sci. 2001b;41(1):19-25.
    DOI: 10.2135/cropsci2001.41119x

28. Yan W, Kang MS, Ma B, Woods S, Cornelius PL. GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci. 2007b;47(2):643-53.
DOI: 10.2135/cropsci2006.06.0374
29. Yan W, Tinker NA. Biplot analysis of multi-environment trial data: principles and applications. Can J Plant Sci. 2006; 86(3):623-45.
DOI: 10.4141/P05-169
30. Becker HC. Correlations among some statistical measures of phenotypic stability. Euphytica. 1981;30(3):835-40.
DOI: 10.1007/BF00038812
31. Becker HC, Leon J. Stability analysis in plant breeding. Plant Breed. 1988; 101(1):1-23.
DOI: 10.1111/j.1439-0523.1988.tb00261.x
32. Purchase JL, Hatting H, Van Deventer CS. Genotype× environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. S Afr J Plant Soil. 2000; 17(3):101-7.
DOI: 10.1080/02571862.2000.10634878

Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle5.com/review-history/95377