

Regular Article

Genetic variability and heritability of yield and related characters in cowpea (*Vigna unguiculata* L. Walp.)

Diriba Shanko¹, Mebeasselassie Andargie^{1*}, Habtamu Zelleke²

¹Biology Department, ²Plant Sciences Department, College of Agriculture and Environmental Sciences (CAES), Haramaya University (HU), P.O. Box: 138, Dire Dawa, Ethiopia

*Corresponding author email : mehel@yahoo.com

Cowpea (*Vigna unguiculata* (L.) Walp.) is a grain legume commonly grown and consumed in many parts of the tropics and subtropics. The general grain yield of cowpea especially in marginal areas is still low and no single variety can be suitable for all growing conditions. Exploiting genetic variability to identify high yielding genotype is one of the strategies used to overcome the complex nature of cowpea breeding. Forty-nine cowpea accessions were tested in 7 x 7 triple lattice design at Haramaya University, Dire Dawa Tony farm with three replications in 2010/11. Analysis of variance revealed significant differences among the forty nine accessions for all the characters studied. High phenotypic and genotypic coefficient of variation, heritability in broad sense and genetic advance estimated for the characters viz., yield per plant, number of pods per plant, and 100-seed weight indicated the scope of improvement of these characters through selection.

Key Words: Cowpea, genetic advance, genotypes, heritability

Cowpea (*Vigna unguiculata* L. Walp.), whose global annual production stands at 7.6 million tones, is one of the most important food grain legumes in the tropics including Africa, which accounts for 64 percent of the world production (Timko *et al.*, 2008). The major cowpea producing countries in Africa are Nigeria, Niger, Mali, Senegal, Burkina Faso and Ghana with modest amounts emanating from the east African countries of Uganda, Mozambique, Tanzania, and to some extent, Ethiopia (Timko *et al.*, 2008).

Cowpea is one of the most important food leguminous crop plant of great socio-economic, cultural, nutritional importance and a valuable component of the traditional cropping systems in the semi-arid tropics

covering Asia, Africa and Central America (Langyintuo *et al.*, 2003). It is cultivated around the world primarily for seed, but also as a vegetable (for leafy greens, green pods, fresh shelled green peas, and shelled dried peas), as cover crop and for fodder (Andargie *et al.*, 2011).

It also has many beneficial horticultural characteristics that are usually non-food associated. It plays a vital role in many farming systems. It has the ability to fix atmospheric nitrogen through its root nodules, and grows well in poor soils with more than 85% sand and with less than 0.2% organic matter and low levels of phosphorus (Singh, 2003). In most African countries, cowpea is either grown alone or intercropped

with various cereal crops such as leaf vegetables, maize, millet, sorghum, beans, pigeon peas, bananas and others (Bittenbender *et al.*, 1984; Singh *et al.*, 1997). Since, it is shade tolerant and compatible as an intercrop with cereal crops helps to prevent build up of diseases incidence, insect pests and weeds. Its variability of uses, nutritive content and storage qualities have made cowpeas an integral part of the farming system in the West African area (Eaglesham *et al.*, 1992).

In spite of the significance of cowpea as a food crop to millions of people on the continent, grain yields today remain low averaging 0.3 tones/ha due to several biotic and abiotic factors. In the humid tropics, seed yield of cowpea is low due to unfavorable environmental conditions such as high rainfall, high disease incidence, reduced sunshine hour, poor soil fertility level etc. (Singh *et al.*, 2005). Furthermore, the general grain yield of cowpea especially in marginal areas is still low and no single variety can be suitable for all growing conditions; whereby varietal requirements in terms of plant type, seed type, maturity and use pattern are highly diverse from region to region and these makes cowpea breeding programs more complex than any other crops (Singh *et al.*, 1997). So the choice of cowpea specific genotypes adaptable to this unfavorable environmental condition is determined by careful breeding program (Singh *et al.*, 2005).

The objective of any breeding program is to develop desirable genotypes with high yield potential. Selection is an integral part of breeding program by which genotypes with high productivity in a given environment are selected. So, selection for high yield is made difficult by the complex nature of this trait. Yield per unit area is the end product of components of several yield contributing characters. But the study of the genetic parameters controlling the expression of yield and its components are essential in

determining the effect of such genetic parameters in enhancing the seed yield of cowpea (Katiyar *et al.*, 1977).

One of the important strategies plant scientists adopted to overcome the problem of getting a better yield is to exploit genetic variability of the available germplasm to identify high yielding genotypes that may give a reasonable yield on different soil and environmental conditions (Kaur *et al.*, 2007).

Therefore, this research attempted to investigate the genetic variability of cowpea (*Vigna unguiculata* L. Walp.) genotypes which grow in the different parts of Ethiopia in relation to yield and yield related agronomic traits. The reason for selecting cowpea is that no sufficient work has been done for understanding and describing the nature and extent of genotypic and phenotypic variation, heritability, expected genetic advance, as well as correlation and association between yield and yield components of cowpea in Ethiopia.

Materials and Methods

The material for the study comprised of 49 accessions that are collected from different areas and localities. The accessions were raised in a field experiment in a 7x7 triple lattice-design with three replications in the Haramaya University's research station located in Dire Dawa Ethiopia, in 2010/2011. Plot size was 2m x 2m with spacing between rows was 50cm, between plants within the row was 25cm and also spacing between block was 2m within plot was 0.5m. There were 4 rows in each plot, which accommodates 8 seeds per row. All other cultural practices were done as required.

Data on plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant, and pod length were collected from five randomly selected plants from each plot and the average value was considered per plant basis. Whereas data on

days to 50% flowering, days to 95% maturity, 100- seed weight, grain yield in kg/ha were recorded on plot basis. The data were subjected to analysis of variance. The genetic parameters viz., phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated according to the methods suggested by Burton *et al.* (1953). The heritability in broad sense and genetic advance as percentage of mean were estimated employing the methods suggested by Allard (1960) and Johanson *et al.* (1955) respectively.

Results and Discussion

The analysis of variance (Table 1) revealed significant differences among the accessions for the eleven characters studied indicating the presence of adequate variability which can be exploited through selection. The existence of high variability for different characters among cowpea varieties had been earlier reported by Ramachandran *et al.* (1982), Hazra *et al.* (1993); Resmi (1998);

Omoigui *et al.* (2005); Lesly (2005); Xu *et al.* (2009); and Idahosa *et al.* (2010).

The genetic parameters viz., genotypic and phenotypic coefficients of variation, heritability in broad sense and genetic advance along with mean and range of different characters are presented in Table 2. The wide range especially for number of secondary branch per plant, plant height, number of pods per plant, seed yield per plant, 100-seed weight and seed yield per hectare indicated the diversity among the cowpea accessions and also suggest that the possibility of improving these traits through selection. According to Deshmukh *et al.* (1986) PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be medium. High GCV and PCV values for pod yield and number of pods per plant were earlier reported by several workers (Trehan *et al.*, 1970; Resmi, 1998).

Table 1. Analysis of variance of 11 quantitative characters in 49 Cowpea accessions

Source of variation	Df	Mean squares										
		NPB	NSB	PH	DF	DM	NPPP	PL	NSPP	YPP	HSW	SYLD
Replication	2	40.83	1313.4 6	675.6	99.24	63.39	183.9	3.91	1.64	727.67	0.27	178195
Block within replication (adj.)	18	0.94	26.13	422.43	9.6	13.09	27.47	1.39	3.12	50.14	1.63	162294
Treatment (unadj.)	48	5.05**	44.92**	1047.44**	100.58**	176.76**	66.86**	17.69**	8.35**	80.44**	23.99**	662707**
Intra block error	78	1.54	20.02	310.28	12.46	18.3	25.06	1.3	1.41	27.08	1.34	188818
RCB error	96	1.43	21.16	331.28	11.92	17.33	25.51	1.31	1.73	31.4	1.39	183845
Total	146	3.16	46.68	571.45	42.26	70.37	41.27	6.73	3.91	57.06	8.81	363163
CV%		10.39	19.65	21.05	8.02	5.76	23.87	7.58	9.72	22.58	9.52	21.29
LSD at (1%)		2.666	9.602	37.795	7.575	9.182	10.742	2.448	2.789	11.693	2.485	932.4
LSD at (5%)		2.014	7.252	28.547	5.721	6.93	8.113	1.84	2.103	8.817	1.877	704.26

**Significant at 1% probability level. NPB= Number of primary branch, NSB= Number of secondary branch, PH= Plant height, DF= Days to 50% flowering, DM= Days to 95% maturity, NPPP= Number of pod per plant, PL= Pod length, NSPP= Number of seed per pod, YPP= Seed yield per plant, HSW= 100-seed weight, SYLD= Seed yield per ha.

Table 2. Genetic variability parameters of cowpea genotypes

	Range	Mean	SE	σ^2_p	σ^2_g	σ^2_e	PCV (%)	GCV (%)	H (%)	GA	GAM (%)
NPB	9.73-13.3	11.53	0.18	2.63	1.2	1.43	13.58	9.17	45.62	1.52	12.76
NSB	16.6-24.91	19.85	0.55	29.08	7.92	21.16	23.75	12.36	27.23	3.02	13.29
PH	70.96-91.03	84.64	2.66	570	238.72	331.28	28.53	18.46	41.88	19.99	23.89
DF	43-54	46.52	0.82	41.47	29.55	11.92	14.63	12.35	71.25	9.45	21.47
DM	72.67-83	76.96	1.09	70.47	53.14	17.33	11.29	9.8	75.4	13.04	17.54
NPPP	15.4-23.5	19.54	0.67	39.27	13.78	25.51	29.88	17.7	35.09	4.52	21.6
PL	11.95-19.08	15.02	0.34	6.77	5.46	1.31	17.3	15.53	80.64	4.32	28.7
NSPP	9.64-14.95	12.35	0.22	3.93	2.2	1.73	16.23	12.14	55.97	2.28	18.72
YPP	16.23-22.05	19.83	0.74	47.74	16.34	31.4	29.98	17.54	34.25	4.87	21.14
HSW	7.06-16.56	12.24	0.44	8.92	7.53	1.39	24.20	22.23	84.41	5.19	42.05
SYLD	1082.61-3046.3	2042.31	67.14	34346	15962	183845	28.71	19.57	46.47	561.06	27.48

NPB= Number of primary branch, NSB= Number of secondary branch, PH= Plant height (cm), DF= Days to 50% flowering, DM=Days to 95% maturity, NPPP= Number of pod per plant. PL= Pod length (cm), NSPP= Number of seed per pod, YPP= Seed yield per plant (g), HSW= 100-seed weight (g), SYLD = Seed yield (kg/ha), phenotypic (σ^2_p), genotypic (σ^2_g) and environmental (σ^2_e) components of variances, phenotypic (PCV) and genotypic (GCV) coefficient of variability, broad sense heritability (H), expected genetic advance (GA) and genetic advance as percent of the mean (GA%).

The high PCV values for number of pods per plant and seed yield were in harmony with the previous report by several authors (Trehan *et al.*, 1970; Arora, 1991). The difference between PVC and GCV values was high for plant height, number of secondary branches per plant, number of pods per plant, seed yield per plant and seed yield per hectare; indicating the influence of environment on these characters. Since, the difference was low for days to 50% flowering, days to maturity, number of seeds per pod, number of primary branch, pod length and 100 seed weight, suggesting minimal influence of environment on the expression of the characters. Similar results were reported by Yucel *et al.* (2006) for days to flowering and plant height.

Heritability estimates were generally high for all the characters studied. The values were especially high for 100 seed weight, pod length, days to maturity, and days to 50 % flowering. High heritability value for 100-seed weight, for vegetable pod yield and pod weight reported by Resmi (1998) and Thiyagarajana (1989) supports the present

findings. Further, similar to the present results, high heritability for number of pods per plant and pod length was reported by (Vardhan and Savithramma, 1998; Sreekumar *et al.* (1996) and Idahosa *et al.* (2010) respectively. According to Singh (2001) if heritability of a character is very high, say 70% or more, selection for such traits could be fairly easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relatively small contribution of the environment to the phenotype. There was also a relatively high genetic advance for plant height, days to maturity and days to flowering. Gupta and Lodhi (1979) also reported that plant height had a high estimate of genetic advance. Johnson *et al.* (1955) suggested that high heritability combined with high genetic advance is indicative of additive gene action and selection based on these parameters would be more reliable.

In view of the high estimates of genotypic coefficient of variation, heritability and genetic advance recorded for days to 50 % maturity, seed yield and plant height in the

present study, it is concluded that worthwhile improvement in these characters can be achieved through selection.

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