

Genetic variability and heritability of some selected of cowpea (*Vigna unguiculata* (L) Walp) lines

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Abstract

The success of most crop improvement programs largely depends upon the genetic variability and the heritability of desirable traits. The magnitude and type of genetic variability help the breeder to determine the selection criteria and breeding schemes to be used for improvement purposes. Two different but related experiments, one in 2011 rainy season (August to November) and the second in 2012 dry season (February to May) were carried out at ICRISAT-Kano, Nigeria screen house to estimate the genetic variability and heritability of some traits in selected cowpea lines. Results of the study showed that there were considerable variations among the lines for duration of vegetative and reproductive phase and for yield characters (seed/pod, number of pod/plant, weight of pod/plant, and 100 seed weight). Broad sense heritability estimate (h^2) was 83% for 100 seed weight, 53% for Number of seed per pod, 48% for days to first flower and 46% for number of root nodules. This information showed that there is sufficient genetic variability to justify selection for improvement in the cowpea. This result will be of immense practical uses for plant breeders to choose parent of interest to meet different breeding objectives.

Introduction

Cowpea (*Vigna unguiculata* (L) Walp) is the most important food legume in the dry savannas of West Africa where it is an important source of vegetable protein in the daily diets of the rural and urban masses as well as nutritious fodder for ruminant livestock in (Ajeigbe *et al.*, 2008). However, due to a number of biotic and abiotic constraints, the grain and fodder yields of cowpea are low in the varying cropping systems of subsistence farmers in the dry savannas of West Africa. The International Institute of Tropical Agriculture (IITA) and several National Research Institutes in West Africa are therefore continuously developing improved lines of cowpea to alleviate these constraints. The development of superior crop lines depends mainly on the genetic diversity available for the crop (Baudoin and Marechal 1985). Diversity within wild as well as cultivated forms of cowpea is high and therefore cowpea offers itself for genetic manipulation and breeding. Lines can be prostrate, semi erect, erect or climbing and pods are coiled, round, crescent or linear (Ng and Marechal 1985).

Development of cultivars with early maturity, acceptable grain quality, resistance to some important diseases and pest has significantly increased the yield and cultivated area of cowpea (Ehlers and Hall, 1996). Grain yield is a complex trait; it is influenced by many other important yield contributing characters controlled by polygenes and environmental factors. Any breeding program aiming at increasing yields consider association between yield and its attributes through estimation of genotypic and phenotypic correlation, which help a great deal in formulating selection indices to aid in crop improvement programs. An understanding of the variability existing in a crop is necessary to formulate and accelerate breeding program (Johnson *et al*, 1955). The overall effect of plant breeding on genetic diversity has been a long standing concern in the evolutionary biology of crops plants. Heritability measures the fraction of phenotypic variability that can be attributed to genetic variation. It is an important concept in quantitative genetics, particularly in selective breeding. A study was undertaken to evaluate the genetic variability and heritability of different characters in selected improved cowpea lines available in IITA. The ability to fix atmospheric nitrogen makes legumes excellent components within the various farming systems because they provide residual nitrogen and reduce the needs for mineral nitrogen fertilizers by associated non-legumes. Intensification of low-input agricultural production has led to a rapid increase in soil degradation and nutrient depletion in many parts of sub-Saharan Africa, constituting serious threats to food production and food security

Materials and Methods

Two different but related trials were conducted in two different seasons: 2011 rainy (August-November) and 2012 dry season (February-May) in a screen house of International Crop Research Institute for the Semi-Arid Tropics (ICRISAT) Kano, Nigeria. The location is on latitude 11° 58, 844'N and longitude 8° 33, 499' E in the Sudan savanna zone of Nigeria. Forty seven (47) lines were used for the rainy season trial while ninety four (94)

lines including all the 47 lines were used in the dry season trial. Cowpeas were planted in pot (20×64×54 cm) arranged in Completely Randomize Design (CRD) with three (3) replications. The pots were filled with top soil, mixed with manure in the ratio of 10:1, and fill to 5 cm to the tip. Pots were arranged on the screen house table and labeled before planting. Six (6) seeds were planted in each pot, and thinned to 4 plants per pot at 2 weeks after planting. Destructive samplings were conducted at 20 days after planting by cutting to 2 plants per pot leaving the remaining 2 plants\pot until maturity. The mean data of rainfall, sunshine, minimum and maximum temperature for the experimental period were collected from Institute of Agricultural Research (IAR) Kano station (Table1). The following data were recorded on 2 plants\pot: days to first seed germination, plant height at flowering (cm), number of leaves at flowering, plant biomass at 20 days after planting (g), number of branches at podding, days to 50% flowering, days to 90% maturity, number of pods per pot, number of seed per pod, number of root nodules, weight of pod (g), weight of biomass (g) and 100 seed weight (g).

Table 1. Mean monthly minimum and maximum temperature, sunshine and rainfall from August 2011 to May 2012.

Month	Minimum Temp (°c)	Maximum Temp (°c)	Sunshine(h)	Rainfall (mm)
August	21.58	30.71	7.12	8.95
September	22.23	33.20	8.68	5.46
October	21.90	35.87	8.81	0.37
November	16.43	34.20	10.39	-
December	14.77	29.84	8.39	-
January	14.19	30.65	9.30	-
February	19.24	35.93	8.46	-
March	20.52	36.77	8.05	-
April	26.17	41.33	7.72	-
May	26.10	39.42	7.60	Trace

STATISTICAL ANALYSIS

The data collected were subjected to analysis of variance (ANOVA) using Genstat discovery statistic software.

Estimation of Genetic parameters

In order to assess and quantify the genotypic variability among the lines for the characters under study, the following parameters were estimated as given below.

Estimation of variance components

Phenotypic and genotypic variances were estimated using following formula,

$$\text{Genotypic variance} = \frac{\text{MS (variety)} - \text{MS (error)}}{\text{Number of replications (r)}}$$

$$\text{Phenotypic variance} = \text{Genotypic variance} + \text{MS error}$$

Heritability (h^2): Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance as suggested by Hanson *et al.* (1956) and expressed as percentage.

$$\text{Heritability (} h^2 \text{)} = \frac{\text{Genetic variance}}{\text{Phenotypic variance}} \times 100$$

Results

The results of the statistical analysis of 2011 rainy season data are shown in Table 2. Significant differences were observed among the cowpea lines for all the variable measured. Large variability was observed for days to 50% flowering, days to 90% maturity and number of root nodules in descending order. The least variation was observed for plant weight at 20 days and pod weight for the rainy season, the genotypic variance for 100 seed weight were greater than the error variances. Wide ranges of difference for genotypic coefficient of variation were observed for the characters studied. Biomass weight and number of pod per pot had lower broad sense heritability (5.20 and

7.76% respectively) compared to other characters while number of root nodules (45.82%) and days to first germination had the highest broad sense heritability.

Table 2. Mean and variability parameters for twelve characters in cowpea genotypes during 2011 rainy season

S/N	Character	Grand Mean	MS Error	Genotypic variance	Phenotypic variance	Heritability (H ²)%
1	Plant height at flower initiation	26.03	4.08	3.2667	17.3467	18.83
2	Plant biomass at 20 days(g)	11.83	0.0130	0.0032	0.0162	19.87
3	Days to 50% flowering	4.937	22.53	16.2633	38.7933	41.92
4	Days to 90% maturity	76.54	43.04	18.8433	61.8833	30.45
5	Days to first germination	45.03	0.6491	0.3508	0.9999	35.08
6	Number of branches at podding	14.77	5.02	2.3183	7.3383	31.59
7	Number of leaves at flow	19.88	21.27	2.59	23.86	10.86
8	Number of Root nodules	49.4	681.3	576.2	1257.5	45.82
9	Number of pods per pot	4.99	7.02	0.5903	7.6103	7.76
10	Number of seeds per pod	6.33	5.252	1.4087	6.6607	21.15
11	Weight of biomass (g)	7.1	3.909	0.2143	4.1233	5.20
12	Weight of pod (g)	1.293	0.2245	0.0602	0.2847	21.15

Results of the analysis of the dry season data are shown in Table 3. Large variability were also observed for plant weight at 20 days, plant height and leaves petiole length, while least variability were observed for standard petal length and breadth. High heritability was also estimated for 100 seed weight (66.4%), number of root nodules (53.4%) and plant height (47.7%), while weight of pod and weight of biomass showed least heritability of 5.2 and 6.0% respectively. In similar trend to the Rainy season, heritability estimated for 100 seed weight and numbers of root nodules were also found to be high.

Discussions

Generally, large genotypic variation may be caused by small means square relative to large error terms, or vice versa. In this study, proportion of total variation attributable to the error variance was relatively small. The moderate-to-large genetic variance and heritability obtained in the present study suggest that substantial residual genetic variability is still available to ensure good progress from further selection for the desired characters, which in turn will lead to increase in grain yield.

High heritability estimates (h^2) was obtained for 100-seed weight, number of root nodules, plant height and days to 50% flowering in the two experiments. This suggests that selection for these characters would be effective for further improvement. The results of the present study corroborate those of Idahosa *et al* (2010); Omoigui *et al.* (2005); Xu *et al.*, (2009); and Lesly (2005). While Kohli *et al* (1971) and Omoigui *et al* (2005) reported low heritability in weight of biomass and number of pod which was also obtained in the present studies.

The low genetic coefficient of variation and heritability obtained for grain yield is not particularly surprising since yield is a product of many complex characters. Therefore, direct selection for grain yield improvement may not be possible, but through indirect selection of other secondary traits may be feasible. However, the low genetic coefficient of variation and heritability obtained for pods per pot and biomass weight per pot are at variance with those of Ogunbodede and Fatula (1985) who reported high broad sense heritability for these traits. Within the range of materials used in this study, there exist substantial genetic coefficient of variation and heritability in the characters studied to warrant selection in the genotypes for further improvement. The level of genetic variability observed for different characters would be useful for breeding lines of cowpea for high yield. The high heritability estimates obtained for days to first flower, number of root nodules, number of seed per pod, and 100-seed weight, suggests that these characters are highly heritable and therefore the traits can be easily transferred from parent to offspring. The high to moderate heritability for root nodules can be used where the management of Biological Nitrogen Fixation (BNF) would help improved yields of cowpeas in tropical farming system.

Conclusion

The present studies have shown that enough variability and genetic heritability exist in the studied characters among cowpea lines in the IITA germplasm for breeders to exploit for further improvement of released cowpea varieties. Major constraints to increased cowpea productivities include diseases, insect pests and parasitic weeds attack. There

is therefore the need for genetic researches to be conducted on cowpea for variability and heritability for these constraints.

Table 3. Mean and variability parameters for twenty characters in cowpea genotypes during 2012 dry season

S/N	Character	Mean	MS Error	Genotypic variance	Phenotypic variance	Heritability (H ²)%
1	Plant height at flower initiation	21.24	109.5	100.03	209.53	47.7
2	Plant weight at 20 days(g)	0.811	180.2	117.77	297.97	39.5
3	Days to 50% flowering	60.05	1.648	0.298	1.946	15.3
4	Days to 90% maturity	88.71	0.4607	0.1143	0.5750	19.9
5	Days to initial germination	7.344	3.436	1.1903	4.6263	25.7
6	Internodes length	1.442	2.479	0.5117	2.9907	17.1
7	Leaf stalk length	6.47	1.057	0.7583	1.8153	41.8
8	Leaflet	2.719	2.477	1.31	3.787	34.6
9	Leaves petiole length	3.818	23.54	11.57	35.11	33.0
10	Leaves petiole breadth	7.244	4.559	2.24	6.799	33.0
11	Number of branches at pd	12.52	11.07	2.2767	13.3467	17.1
12	Number of leaves at flow	18.93	3.766	0.3137	4.0797	7.7
13	Number of root nodules	42.2	4.625	5.2907	9.9157	53.4
14	Number of pods/pot	2.66	8.575	5.6493	14.2243	39.7
15	Number of seeds/pod	5.67	17.87	5.0067	22.8767	21.9
16	Standard petal breadth	1.491	0.1623	0.0541	0.2164	25.0
17	Standard petal length	1.657	0.0844	0.0275	0.1119	24.6
18	Weight of biomass(g)	7.92	26.92	1.7033	28.623	6.0
19	Weight of pod(g)	2.87	6.38	0.3157	6.0643	5.2
20	100 seed weight(g)	17.29	6.452	12.7643	19.2163	66.4

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