Electronic Journal of Plant Breeding, 5(1): 58-62 (Mar 2014)
ISSN 0975-928X

Research Article

Variability for dry fodder yield and component traits in cowpea [*Vigna unguiculata* (L.) Walp]

Olayiwola M.O. [1] **and P.A.S. Soremi** [2]

[1] Department of Plant Breeding and Seed Technology, Federal University of Agriculture, Abeokuta P.M.B. 2240, Abeokuta, Ogun State, Nigeria

[2] Department of Plant Physiology and Crop production, Federal University of Agriculture, Abeokuta P.M.B. 2240, Abeokuta, Ogun State, Nigeria

Email: ollyrichie@gmail.com

(Received: 17 Feb 2014; Accepted: 23 Mar 2014)

Abstract

Eleven cowpea genotypes were evaluated and significant genotypic effects for most of the traits studied. Number of pods/plants, pod, seed and dry fodder yields were high for phenotypic and genotypic coefficients of variation. High heritability values were recorded for number of pods/plant, 100 seed weight and dry fodder yield. Genetic advance was high for seed, pod and dry fodder yield indicating that the traits could be improved through selection. All traits had high genetic advance as per cent of mean except days to 50% flowering and number of seeds/pods. Dry fodder yield alone had combined high genetic advance and heritability values indicating that this trait has high selection value and considered important in cowpea improvement. IT99K-494-6 and IT98k-573-2-1 that were high for seed and pod yield; and dry fodder yield respectively, may be considered for further improvement.

Keywords: Cowpea, genetic advance, heritability, selection, variability

Introduction

Plant breeding aims at improving the performance of crop plants to meet the growing demand of the world for food and other purposes. The magnitude and knowledge of level of genetic control of variability are vital to the success of any breeding programme. High level of variability is a pre-requisite for selection and therefore determines the potentials of developing new and superior varieties. However, the response or gain from selection is mainly dependent on the knowledge of gene action controlling the traits of interest. A detailed understanding of gene effects underlying a trait is reliably obtained from the genetic analysis of such trait and its components. Heritability, the genetic or heritable portion of observed variation, and genetic advance, the gain from selection, are important pointers to the gene actions controlling all traits in any crop (Thirupathi *et al*., 2012 and Mehta *et al*., 2006). This information guides the breeder appropriately on the breeding method(s) to be adopted in the improvement programme of crops including cowpea.

Cowpea, a leguminous grain and member of the family Fabaceae, is highly important in human diet and livestock feed due to its high protein content. Every part of the cowpea crop is useful as they contain high amount of nutrients and fibre. The young leaves, immature pods and seeds, and the mature dried seeds are palatable to humans. In animal husbandry, the stems, leaves, and vines, whether fresh or dried serve as livestock feed (Ajeigbe et al., 2008). Africa's total production was put at 5.2 million tons, 52% of which is used for food, 13% as animal feed, 10% for seeds, 9% for other uses, while 16% is wasted (IITA, 2007). Nigeria is the largest cowpea producer, accounting for 61% and 58% of the total Africa and world production respectively. This notwithstanding, Nigeria remains the highest consumer and importer of the crop (Lowenberg-DeBoer and Ibro, 2008). This abundantly implies that the local demand for cowpea is far higher than what is available. Though breeding efforts had led to the development of improved cowpea types in the past, the growing need of the populace makes continuity of such efforts pertinent. Therefore, it is important that research aimed at enhancing the development of high performing cowpea varieties be encouraged. The study provides information on the extent and control of genetic variability among cowpea genotypes for further use in the improvement of cowpea yield.

Material and methods

The study was conducted at the Teaching and Research Farm of the Federal University of Agriculture, Abeokuta (FUNAAB) in Nigeria during the late seasons of 2011 and 2012. Abeokuta, a transition between rainforest and derived savannah agro-ecology is on latitude $7^o38'$N and longitude $3^o88'$E with a mean annual rainfall of 1200mm. Eleven cowpea genotypes; IT04K-332-1, IT04K-333-2, IT06K-134, IT06K-242-3, IT07K-303-1, IT98K-573-1-1, IT98K-573-2-1, IT99K-1060, IT99K-494-6, IT99K-529-2 and IFE BROWN were sourced from Grain Legume

Improvement Programme (GLIP) of International Institute of Tropical Agriculture (IITA), Ibadan. The genotypes were laid out in a randomised complete blocked design, replicated three times. In each year (2011 and 2012), the field was cleared, ploughed and harrowed. Two seeds were sown and thinned to one at ten days after sowing (DAS) on a plot size of 2.25 x 3 m at spacing of 0.75 x 0.25m. Lambda-cyhalothrin was applied at the rate of 80 ml/15 litre of water at two weeks interval to check insect pest infestation and weeds were controlled manually as needed.

In each year data were collected on yield and yield components on 12 inner competitive plants. These included days to 50% flowering, dry fodder weight, evaluated by harvesting above ground biomass and drying them to constant weight in an oven at a temperature of 80^0C, 100 seed weight, number of pods/plant, number of seeds/pod, pod yield and seed yield were evaluated after harvest maturity. Data collected were subjected to Analysis of Variance (ANOVA) and means were separated using Duncan Multiple Range Test (DMRT) of SAS 2002. The genotypic and phenotypic variances were calculated following Singh and Choudhary (1985). Phenotypic and genotypic coefficients of variation were calculated according to Burton (1952). Broad-sense heritability and expected genetic advance, assuming a selection intensity of 5% were estimated according to the formulae of Allard (1960) and Miller *et al.* (1958).

Results and discussion

The combined (2011 and 2012) analysis of variance revealed high significant differences among the cowpea genotypes for all traits evaluated except number of seeds/pod (Table 1). These significant mean squares due to genotype, high phenotypic and genotypic variances, as well as phenotypic and genotypic coefficients of variation for most of the characters indicate the presence of substantial variability among the cowpea genotypes and therefore provides basis for genetic improvement (Omoigui *et al*., 2006 and Thirupathi *et al*., 2012). However, the magnitude of differences between phenotypic and genotypic variances, and coefficients of variation varied for all traits. High magnitude of difference among phenotypic and genotypic values implies greater environmental influence. Number of seeds/pod, number of pods/plant, 100 seed weight and dry fodder yield all had low magnitude of differences between phenotypic and genotypic values for variances and coefficients of variation in this study.

The mean performances of the cowpea genotypes (Table 2) showed that Days to 50% flowering ranged from 48.33 days for IT99K-529-2 to 55.67 days for IT07K-303-1. Number of seeds/pods ranged from 9.33 for IT99K-1060 to 12.50 for IT04K-332-1. Number of pods/plant ranged from 10.00 for IT98K-573-1-1 to 18.67 for IFE BROWN. 100 seed weight ranged from 14.79g for IT99K-494-6 and IT04K-332-1 to 21.56g for IT07K-303-1. Pod yield ranged from 384.60g for IT07K-303-1 to 1033.90 for IT99K-494-6g. Seed yield ranged from 260.10g for IT06K-134 to 807.30g for IT99K-494-6. The highest seed and pod yields were recorded on IT99K-494-6 indicating that the genotype is high yielding and could be candidate for further improvement. Dry fodder yield ranged from 85.65g for IT06K-134 to 228.53g for IT98K-573-2-1. IT98K-573-2-1 with the highest dry fodder yield has high improvement potential for the trait and could be useful in breeding programme aimed at increasing fodder yield. A cross between IT99K-494-6 and IT98K-573-2-1 may be useful in the development of a dual purpose cowpea genotype.

The phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were ranked as low (< 10%), moderate (10-20%) and high (>20%) according to Sivasubramanian and Menon (1973). Characters with high GCV have more improvement potential than those with moderate, and those with moderate are superior to those that were low (Gandhi *et al*., 2001; Thirupathi *et al*., 2012). Estimates of PCV were higher than GCV for all traits. High PCV values were recorded on number of pods/plant (24.39), pod yield (54.98), dry fodder yield (26.77) and seed yield (60.76). Number of seeds/pod (11.35) and 100 seed weight (14.39) had moderate values while days to 50% flowering (5.00) had low value. Number of pods/plant (23.63), pod yield (34.73), seed yield (38.82) and dry fodder yield were high for GCV and therefore could be targeted in cowpea improvement. 100 seed weight (12.22) was moderate while days to 50% flowering (3.43) and number of seeds/pod (4.16) were low (Table 3). The higher PCV than corresponding GCV for all traits implies that the variability observed were not solely under genotypic influence but with some levels of environmental influence justifying the need to explore more genetic parameters to ascertain the trait(s) to be considered as important.

Heritability values were rated as low (<30.00%), moderate (30-60%) and high (>60.00%) following Johnson *et al.* (1955). Heritability was high for number of pods/plant (94%), 100 seed weight (72%) and dry fodder yield(91%) indicating that the variability for these traits are under genetic control and therefore heritable. Heritability was moderate for days to 50% flowering (47%), pod yield (39%) and seed yield (41.1%); and low for number of seeds/pod (13%) (Table 3) indicating moderate genetic control and implies that direct selection for these traits may not be very successful. This observation contradicts the findings of Ogunbodede and Fatula (1985) who reported high heritability and Inuwa *et al.* (2012) who reported low heritability for pod yield. Heritability in broad sense (total genetic variance) is a composite of fixable (additive) and non-fixable (dominance and epistatic) variances, and therefore should not be solely used in determining the genetic potentials of a trait. Johnson *et al*. (1955) advanced that the simultaneous consideration of estimates of heritability and genetic advance in predicting the value of selection is more valuable than heritability used singly.

Genetic advance represents the advancement in the mean of selected population over the base population. It could also be expressed as percentage of mean and referred to as genetic advance as per cent of mean (GAM). Characters with high genetic advance would respond favourably to selection as it implies preponderance of additive gene effect. The estimates of genetic advance and genetic advance as per cent of mean were categorized as high (>20), low (<10) and moderate (10-20). Genetic advance was high for pod (258.31), seed (203.18) and dry fodder yields (71.89) while it was low for other traits. Genetic advance as per cent of mean was high for all characters except days to 50% flowering(4.86) and number of seeds/pod (3.14) that were low (Table 4). The high genetic advance and GAM for seed, pod and dry fodder yield indicate that these traits may have high additive genetic variance and under additive gene effects. Manggoel *et al*. (2012) reported high additive gene effects for pod and grain yield in cowpea. Only days to flowering and number of seeds/pod were low for GAM indicating that the characters may possess low selection value.

The high genetic variability observed among these cowpea genotypes confirms that large potentials for improvement still exist within cowpea germplasm despite efforts made in the past to explore the variability in cowpea. Since demand for the crop is ever growing there is need to increase breeding efforts. Partitioning variability into heritable and non-heritable components gives appropriate guide to cowpea breeders in efforts to improve the crop. Number of pods/plant, 100 seed weight and dry fodder yield all had high heritability values; whereas pod, seed and dry fodder yields had high genetic advance and GAM. It is generally accepted that a combination of heritability and genetic advance gives more accuracy in predicting the selection value for a trait. In this study only dry fodder yield combined high heritability with high genetic advance which indicates high additive genetic variance for the trait. Dry fodder yield could therefore be considered as important in cowpea improvement programme. In such a programme IT99K-494-6 and IT98k-573-2-1, with high seed and pod yield and dry fodder yield respectively, would serve as good parent stock.

Acknowledgement

The authors are grateful to the Grain Legume Improvement Programme (GLIP) of International Institute of Tropical Agriculture (IITA), Ibadan for providing the plant materials.

References

Ajeigbe, H.A.,Ihedioha, D., and Chikoye, D. 2008. Variations in Physicochemical Properties of Seed of Selected Improved Cowpea Lines. *African J. Biotech.*, **7** (20): 3639-3644.

Allard R.W. 1960. Principles of plant breeding. New York; John Wiley and Sons Inc. 485 pp

Burton G.W. 1952. Quantitative inheritance in grasses. *Proceed. of the 6th International Congress,* **1**: 277-283

Gandhi, H.T., Yadav, M.D. and Naval, P.A. 2001. Studies on variability in okra (*Abelmoschus esculentus* (L.) Moench). *J. Maharashtra Agric. Univer.,* **26**(2): 146-148.

IITA ,2007. Cowpea. A publication of the International Institute of Tropical Agriculture (2007).

Inuwa A.H., Ajeigbe, H.A., Muhammed, S.G. and Mustapha, Y. 2012. Genetic variability and heritability of some selected of cowpea (*Vigna unguiculata* (L) Walp) lines. *ICRISAT Bulletin.* Oar.icrisat.org/6516

Johnson, H.W., Robinson, H. and Comstock, R.F. 1955. Estimates of Genetic and Environmental Variability in Soybean. *Agron. J.,* **47**: 314 – 318.

Lowenberg-DeBoer J. and Ibro, G. 2008. The Potential Effect of Economic Growth and Technological Innovation on Women's Role in the Cowpea Value Chain in Kano State, Nigeria. USAID/NIGERIA: A study of the cowpea value chain in Kano state, Nigeria, from a pro-poor and gender perspective. Greater Access to Trade Expansion (Gate) Project under the Women In development IQC. CONTRACT NO. GEW-I-00-02-00018-00, Task Order No. 02. 2008.

Manggoel, W, Uguru, M. I. , Ndam, O. N. and Dasbak, M. A. 2012. Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpea [*Vigna unguiculata* (L.) Walp] accessions. *J.Plant Breed. Crop Sci.*,**4**(5): 80-86.

Mehta, D.R., Dhaduk, L.K. and Patel, K.D. 2006. Genetic variability, correlation and path analysis studies in okra (*Abelmoschus esculentus* (L.) Moench). *Agric. Sci. Digest,* **261**: 15- 18.

Miller, P.A., Williams, J.C., Robinson, H.F. and Comstock, R.E. 1958. Estimates of genetic and environmental variances and covariances in inland cotton and their implications in selection. *Agron. J.,* **50**: 126-131.

Ogunbodede, B.A, and Fatula, T. 1985. A Note on the Heritability of Pod Length and Number of Seeds per Pod in Cowpea (*Vigna unguculata* (L.) (Walp) Traits. East Africa. *Agric.Forest. J.,* **50**: 89-100

Omoigui L.O., Ishiyaku, M.F., Kamara, A.Y. , Alabi, S.O., Mohammed, S.G. 2006. Genetic variability and heritability studies of some reproductive traits in cowpea (*Vigna unguiculata* (L.) Walp.). *African J. Biotech.,* **5** (13): 1191-1195.

SAS Institute Inc. 2002. SAS Institute Inc., Cary, NC.

Singh R. K. and Chaudhary, S. D.1985. Biometrical methods in Quantitative Genetic Analysis. Kalyan Publishers, New Delhi, pp.205-214.

Sivasubramanian, S. and Menon, M. 1973. Heterosis and inbreeding depression in rice. *Madras Agric. J.,* **60**: 1139.

Thirupathi Reddy, M., Hari Babu, K., Ganesh, M. , Chandrasekhar Reddy, K. , Begum, H., Purushothama Reddy, B. and Narshimulu, G. 2012. Genetic variability analysis for the selection of elite genotypes based on pod yield and quality from the germplasm of okra (*Abelmoschus esculentus*) L. Moench. *J. Agric. Technol.,***8**(2): 639-655

Table 1 Combined Analysis of variance of yield and related traits evaluated on cowpea genotypes across two years

Trait	Mean sum of squares				
	Replications	Variety	Year	Variety*Year	Error
Days to 50% flowering	0.33	25.26***	329.08***	7.01	3.98
Number of seeds/pod	0.2	2.45	55.46**	3.42*	1.27
Number of pods/plant	0.78	54.57***	574.32***	40.85***	0.59
100 seed weight	3.88	32.51***	13.86**	15.64**	1.96
pod yield	48643.62	295753.5***	244543.1**	157601.0*	59339.37
seed yield	80249.93	177546.7***	127969.6***	70165.0	34554
dry fodder yield	139.12	8168.44***	42304.0*	14516.0	133.23

*** significant at P≤0.001. values in parenthesis represent degree of freedom.

Table 2 Mean performance of cowpea genotypes evaluated for yield and related traits across two years.

Genotypes	**Days to 50% flowering**	**Number of Seeds/pod**	**Number of Pods/plant**	**100 seed weight(g)**	**Pod yield(g)**	**Seed yield(g)**	**Dry fodder yield(g)**
IT04K-332-1	53.00ab	12.50a	18.33a	14.79c	588.1bc	451.70bc	141.41e
IT04K-333-2	54.33ab	11.17a	15.67cd	18.05b	675.1bc	497.40bc	156.24cd
IT06K-134	53.17ab	11.00a	18.33a	16.92b	436.3c	260.10c	85.65g
IT06K-242-3	52.33bc	12.33a	14.00e	17.45b	875.3ab	644.20ab	193.37a
IT07K-303-1	55.67a	11.50a	16.00c	21.56a	384.60c	259.60c	145.35de
IT98K-573-1-1	52.33bc	11.00a	10.00g	20.11a	864.90ab	589.80ab	125.42f
IT98K-573-2-1	53.50ab	11.17a	14.83de	20.74a	866.40ab	616.00ab	228.53a
IT99K-1060	54.00ab	9.33a	17.33b	16.54bc	790.10ab	546.30b	161.44c
IT99K-494-6	50.00cd	12.00a	15.83c	14.79c	1033.90a	807.30a	137.24ef
IT99K-529-2	48.33d	12.33a	11.00f	20.74a	1030.10a	694.00ab	160.10cd
IFE BROWN	54.33ab	11.67a	18.67a	17.29b	711.2a-c	477.00bc	170.89c

Means with similar alphabets along same column are not significantly different from one another using DMRT at P≤0.05.

Table 3 Genetic parameters for yield and related traits evaluated on cowpea genotypes across two years.

Traits	Variance		Coefficient of variation		Heritability (%)	Genetic advance (GA)	GA as % of Mean
	Phenotypic	Genotypic	Phenotypic	Genotypic			
Days to 50% flowering	7.52	3.55	5.00	3.43	47.0	2.66	4.86
Number of seeds/pod	1.47	0.19	11.35	4.16	13.0	0.34	3.14
Number of pods/plant	9.58	8.99	24.39	23.63	94.0	5.99	47.17
100 seed weight	7.05	5.09	14.39	12.22	72.0	3.95	21.39
pod yield	98741.73	39402.36	54.98	34.73	39.0	258.31	45.19
seed yield	58386.12	23832.00	60.76	38.82	41.1	203.18	51.09
dry fodder yield	1472.43	1339.20	26.77	25.53	91.0	71.89	50.16