__Original Research Article__

ASSESSING THE GENETIC VARIABILITY OF AGRO-MORPHOLOGICAL TRAITS RELATED TO FODDER PRODUCTION IN COWPEA (*Vigna unguiculata L. walp*)

ABSTRACT

The existence of genetic variety within a population is a fundamental requirement for promoting the effectiveness of any breeding operation. The study was carried out at Dr. RPCAU's research farm in Pusa Samastipur, Bihar, during the kharif season of 2019-20. The objective was to assess the genetic variability among 23 cowpea genotypes (22 genotypes from various locations in the country and 1 check genotype). The study employed a randomised block design, consisting of three replications and a total of fifteen characters were recorded during the study. The analysis of variance (ANOVA) revealed statistically significant mean sum of squares (MSS) values attributed to genotype for all recorded variables, suggesting the existence of a substantial amount of diversity across the cowpea genotypes utilised in the study. In general, the recorded values for the phenotypic Coefficient of Variation were found to be higher than those for the Genotypic Coefficient of Variation. The study observed high heritability estimates and high genetic advance for various traits, including plant height, number of leaves per plant, stem thickness, leaf-to-stem ratio, dry matter percentage, leaf fresh weight per plant, dry weight of stem per plant, seed yield per plant, and dry matter yield per plant. These findings suggest that the influence of the environment on these phenotypes is minimal. One of the key conclusions drawn from the study is that the direct selection of these traits can be employed to enhance these characters.

Keywords: *Fodder cowpea, Heritability, Genetic Advance, GCV, PCV*

INTRODUCTION

Cowpea (*Vigna unguiculata L. walp*$2n=2x=22$)also called as lobia, black eyed pea or southern pea is a self-pollinated,annually grown *kharif*crop of pea family ‘Fabaceae’ (Chaudhary *et al.,* 2021). It is considered to have its native in western Africa (Vavilov, 1939) however; in 1976 Steele advocated Ethiopia and Africa as Primary and Secondary centers for diversity respectively. Wild cowpea exists mainly in Africa (Steele 1976), But Now a days the growing areas of cowpea is extended from the tropical areas ranging from Asia, Central and South America to sub-Saharan Africa (Singh *et al*., 2003). It also extends to southern states of USA and to the Northeast Brazil, India, Mediterranean region &Middle East, (Lazaridi*et al*., 2017). Cowpea is one of the important members of pulse family which is used as a protein source for human as well as livestock. The crop being herbaceous in nature is grown usually for vegetable purpose, and as fresh cut forage including for hay and silage (Roy *et al*., 2016). Owing to a high protein content the crop is also named as“Poor Man’s Meat” while it is also called as ‘Hungry season crop’ because it can be grown in wider climatic conditions and temperature especially during summer season when pastures are usually dry. Being a legume, this crop is distinguished for its inbuilt capabilities like tolerance to shade, drought, protein content and quick growth causing a rapid ground cover (Agbicodo*et al*., 2009). Its Short duration and multi-cut nature makes it suitable to be used as fodder crop amenable to farmers. The input requirement of this crop is very low due to the presence of nodules in the root which helps in fixation of atmospheric Nitrogen. It grows well in poor soils with more than 85% sand and with less than 0.2% organic matter and low levels of phosphorus (Singh*et al*., 2003; Shanko *et al.,* 2014).

India being agriculture-based economy, the livestock sector plays decisive role in the economy and livelihood in rural areas. Also, the livestock sector of India is highest in the world (Banik *et al.,* 2021)possessing 11.6% of the total livestock population of the world. With the increasing global market and demands for animal products, there lies a great opportunity for India to expand its share in global market. The productivity of livestock depends directly on the quality and quantity of feed & fodder given as food to them. The lacuna between the availability and demand of fodder needs to be bridged. Stubbles and straws from cereal crops such as rice wheat barley etc. are generally fed to the ruminants but their protein content is zero along with low energy content due to the lignified cell walls present in them (Banik *et al.,*2021). Besides, the higher silica content in them creates the problem of digestion in the ruminants. So, the leguminous crops can be a better option for increasing the quality of feed for livestock (Singh *et al*., 2003; Pitman, 2011).

The objective of any breeding program is to develop desirable genotypes with high yield potential and presence of genetic variability in a crop is a prerequisite before the formulation of any crop breeding scheme (Allard, 1960). Fodder yield in cowpea is a complex character as it is the end product of several components which contribute towards the yield. Besides, it is also affected bythe genetic potential of the genotype andprevailingenvironmental factors. The study of the genetic parameters and its contributing components controlling the expression of yield are essential fora better understanding of forage yield in cowpea. The best way toget a better yield is to exploit the genetic variability ofavailable germplasm in order to identify high yielding genotypes which may give a reasonable yield on different soil and environmental conditions (Kaur et al., 2007).Besides being a grain legume cowpea also has a significant potential as forage crop but, there are limited studies on cowpea so far to investigate about its forage quality and yield. Therefore, this research was conducted to find out the genetic variability present in the genotype collected from various places across the country also to characterize and classify the extent of genetic variability present in these germplasms.

MATERIALS AND METHODS

Experimental Materials.To conduct the experiment a total of 23 genotypes of cowpea (22 + 1 check) was obtained from various sources throughout the country. The complete list of the genotypes along with the source is listed in the table 1.

Experimental Site. The research wasplanned and conducted at Pusa Research Farm of Dr. Rajendra Prasad Central Agricultural University located in Pusa, Samastipur, Bihar during *kharif*-2019. While the lab work done in the research laboratory of department of Genetics and Plant Breeding, Dr.RPCAU, Pusa. The experimental plot had sandy loam soil type with fairly uniform topography and normal fertility status having a pH range of 5to 6. The field was well drained with good irrigation water facility.

Data collection and Statistical Analysis. All the 23 cowpea genotypes were planted in three replications using Randomized Block Design Layout. The spacing was 60 cm X 30 cm, other agronomic and cultural crop practices were done as per the specifications for a satisfactory crop growth. Five better competitive plants were chosen randomly for recording the observations for a total of fifteen agro-morphological traits *viz*. Number of Days to 50% flowering (DFF), Plant height (PH) (cm), No. of leaves/ plant(NLPP), Leaf length(LL) (cm), Leaf width (LW)(cm), Stem thickness(ST) (cm), Leaf-stem ratio(LSR), Dry matter %(DM), Leaf fresh weight/ plant (LFWPP), Dry weight of stem/ plant (DWSPP) (kg/plant), Production efficiency (PE) (q/ha/day), Relative water content (RWC), Seed yield/ plant(SYPP) (gm), Dry matter yield (DMY) (kg/plant), Green fodder yield /plant (GFY) (kg/plant)in each replication and their averages were used afterwards for further statistical analysis. The Analysis of variance (ANOVA) was performed and illustrated using Panse and Sukhatme (1967), the coefficient of variation *i.e.* Genotypic coefficient of Variation (GCV) and Phenotypic coefficient of Variation (PCV) was estimated using the formulae given by Burton *et al.,* 1952. The Heritability in broad sense (h^2_{bs}) was calculated using Burton &De Vane (1953). Genetic Advance as percent of Mean (GAM) Was calculated using the formulae of Johnson *et al.*, 1955.

Table 1. List of genotypes used in the study along with their procurement sources:

S.No	Genotype Name	Source
1	FD- 2038	TNAU
2	FD -2259	TNAU
3	FD -2027	TNAU
4	FD -2265	TNAU
5	FD -2261	TNAU
6	FD -2275	TNAU
7	FD -2240	TNAU
8	FD -2244	TNAU
9	FD -2246	TNAU
10	FD -2257	TNAU
11	MFC- 16-4	ZRS, Mandya
12	C-217	IGFRI, RRS Dharwad.
13	EC -9135B	IIVR
14	GP-58	GBPUA&T
15	PL-1	GBPUA&T
16	GP-56	GBPUA&T
17	EC- 19736	IIVR
18	RL-2	Local Collection
19	RL-5	Local Collection
20	UPC-628	BAU, Ranchi
21	HFC-16-1	HAU, Hissar
22	PFC-12	PAU, Ludhiana
23	UPC- 5286 (CHECK)	National Check.

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA) wasperformed tosplit the total variance present in the genotypes into its components; *viz.* genotypic and environmental variances. The data of ANOVA is presented in table 2. ANOVA showed significant differences amongst all the 23 genotypes evaluated for all the 15 morphological character. The Mean Sum of Square (MSS) for the replications were non-significant for all the 15 traits while MSS due to treatments/genotypes recorded highly significant values which pointed towards the presence of sufficient genetic variability into the selected population.Such type of results for traits *viz.* plant height, seed yield/plant, days to 50% flowering, green fodder yield, dry matter yield, leaf length and leaf width has also been reported previously byAnamika-nath and Tajane (2014), Singh and Omvir (2014), Khan *et al.* (2015), Havaraddi& Deshpandey (2018) and Praveena *et al.* (2019). Coefficient of variation can beclassified as Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV) and Environmental Coefficient of Variation (ECV).The values and the differences among these tell us about the extent of involvement of environment in governing any character. In general, higher value of PCV than GCV and ECV was recorded in the experimental result (Table 3), indicating the decisive role of environment in governing a phenotype. High GCV & PCV values respectively were perceivedfor traits; Number of leaves/plant (28.83,29.55), Stem thickness (29.30,31.16), Leaf: Stem ratio (26.39,27.0), Dry matter % (22.81,24.56), Leaf fresh weight/plant (23.52,24.0), Dry weight of stem/plant (20.81,22.0) and Seed yield/ plant (28.10,31.54) pointing towards the presence of great amount of variability in the mentioned traits as compared to other traits. Similar findings have also been reported previously by Patel*et al.* (2016), Lal *et al.* (2007) & Khan *et al.* (2015). A moderate value of GCV & PCV was recorded for the traits, Days to 50% flowering (10.15,11.10), Plant height (10.62,11.47), Leaf width (12.80,17.0) and Dry matter yield/ plant (15.02,18.19). Medium PCV and Low GCV values wereobtained for Leaf length (9.96,13.08) as well as Production efficiency (10.20,11.05). A high PCV with moderate GCV value was perceived for Green fodder yield/ plant (16.4, 22.53). The above findings are in parallelism with the results obtained by Anamika-nath and Tajane (2014).A low PCV and GCV value was recorded for Relative water (7.56,9.29) content which is a clear indicative of the fact that selection in case of this trait can be misleading and ineffective.The variability present in the population can be subjected to find out the heritability (heritable portion of the variation present in a germplasm) and genetic advance which can be further utilized to find out the genetic advance as % of mean (GAM) / Genetic gain. GAM is the true measure of selection for any trait in a breeding programme. According to Johanson *et al.,* 1995 heritability estimates accompanied with genetic advance values were more informative than heritability estimates considered alone for predicting the worth of response to selection. Since heritability and genetic advance are two complementary concepts therefore heritability estimates along with genetic advance is used to predict the genetic advance owing to selection. In the present experiment, high heritability (%) alongside high GAM was observed respectively for the traits *viz.* Plant height (85.8,20.27), Number of leaf/plant (95.2,57.96), Stem thickness (88.4,56.76), Leaf: Stem ratio (95.8,53.22), Dry matter % (86.3,43.65), Leaf fresh weight/ plant (96.7,47.64), Dry weight of stem/ plant (89.5,40.55), Seed yield/ plant (79.3,51.53) and Dry matter yield/ plant (68.2,25.56). High heritability in these traits indicates that there is less influence of environment in governing these respective characters. High heritability estimates with high genetic advance gives us an idea of preponderance of additive gene effects in governing these traits and the selection can lead to improvement in these characters in the desired direction. Similar findings have been reported previously by Narayankutty*et al.* (2003), Singh *et al.* (2010), Khan *et al.* (2015) and Nyugen *et al.* (2019). High heritability along with moderate genetic advance as % of mean was perceived for Production efficiency (82.1,18.69) Relative water content (66.4,12.69), and Green fodder yield**/** plant (89.1,11.10) suggesting that direct selection for these traits can be misleading. While, moderate heritability estimates coupled with moderate genetic advance as percent of mean values were recorded for Leaf length (58.0,15.63) and Leaf width (57.0,19.91) suggests that the phenotypes cannot be considered as true representative of the genotypes. Similar findings have been obtained by Omvir and Singh (2014) and Vishwanatha and Yogesh (2017). The detailed estimates of the heritability and genetic advance is presented in table 3.

Table 2. Analysis of variance representing mean sum of squares (MSS) for different characters of cowpea

S. No	Characters under study	Replications (df=2)	Treatment (df= 22)	Error (df= 44)
1	Days to 50% Flowering	8.06	116.567**	6.830
2	Plant height (cm)	4.77	676.141**	35.45
3	Number of leaves per plant	13.04	469.060**	7.740
4	Leaf length (cm)	1.0695	3.047**	0.591

5	Leaf width (cm)	0.3833	2.896**	0.582
6	Stem thickness (cm)	0.008	0.130*	0.005
7	Leaf: stem ratio	0.001	0.119*	0.001
8	Dry matter %	23.740	158.41**	7.979
9	Leaf fresh weight per plant (gm)	19.55	2505.341**	28.34
10	Dry weight of stem per plant (kg/plant)	0.00026	0.0007**	0.00028
11	Production efficiency (q/ha/day)	0.0309	0.2633**	0.0178
12	Relative water content (%)	17.906	140.965**	20.378
13	Seed yield per plant (gm)	140.33	117.154**	9.382
14	Dry matter yield /plant (kg/plant)	0.000010	0.000884**	7.43
15	Green fodder yield/ plant (kg/plant)	0.000319	0.002130**	0.000083

Table3. Mean Range &Estimates of different variability parameters in cowpea genotypes

Characters	Mean	Range	PCV (%)	GCV (%)	Heritability (h^2) (%)	Genetic Advance	GAM
DFF	59.53	50.33-70.66	11.10	10.15	84.3	11.44	19.21
PH	137.53	122.12-173.63	11.47	10.62	85.8	27.88	20.27
NLPP	43.00	24.33-64.66	29.55	28.83	95.2	24.93	57.96
LL	9.07	6.83-10.66	13.08	9.96	58.0	1.42	15.63
LW	6.85	5.26-8.93	17.00	12.80	57.0	1.37	19.91
ST	0.697	0.45-1.06	31.16	29.30	88.4	0.40	56.76
LSR	0.75	0.52-1.17	27.00	26.39	95.8	0.40	53.22
DM %	31.03	20.49-50.30	24.56	22.81	86.3	13.55	43.65
LFWPP	122.15	77.83-177.70	24.00	23.52	96.7	58.20	47.64
DWSPP	0.074	0.039-0.098	22.00	20.81	89.5	0.03	40.55
PE	2.85	2.10-3.44	11.05	10.20	82.1	0.53	18.69
RWC	83.77	73.68-92.81	9.29	7.56	66.4	10.64	12.69
SYPP	21.33	13.33-34.66	31.54	28.10	79.3	10.99	51.53
DMY	0.106	0.076-0.140	18.19	15.02	68.2	0.03	25.56
GFY	0.459	0.428-0.527	22.53	16.4	89.1	0.05	11.10

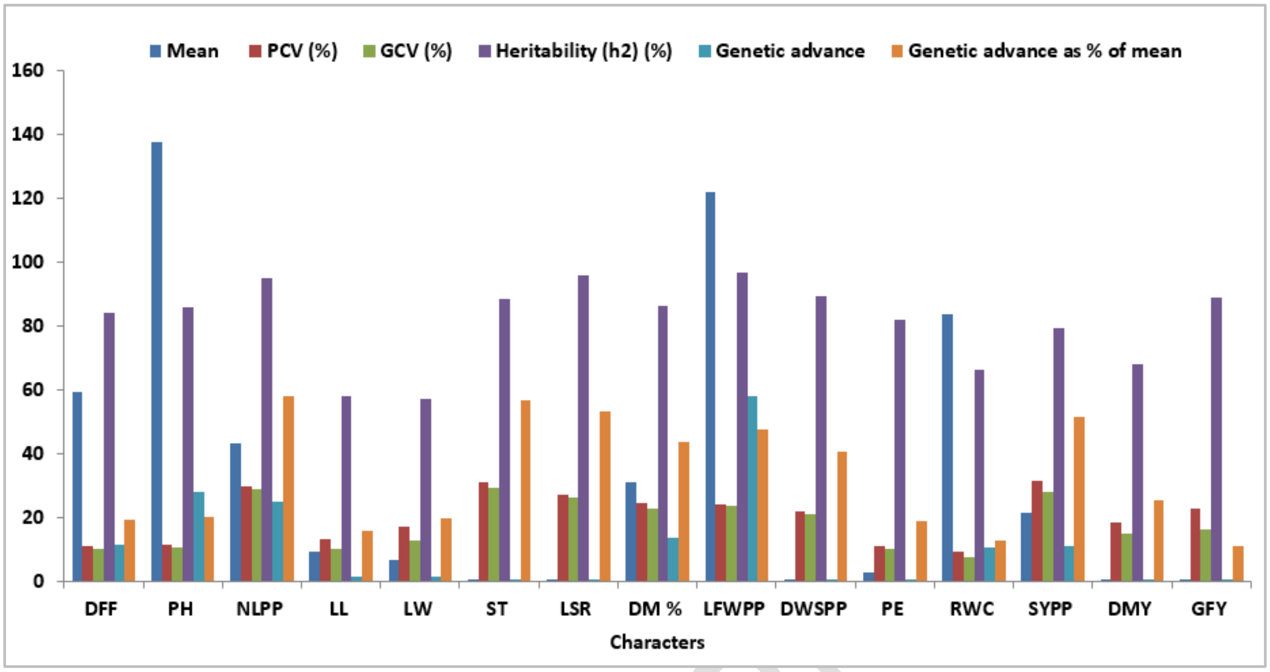

Fig 1: Graphical representation of different variability parameters in Cowpea Genotypes

CONCLUSION

The present investigation concluded that a wide amount of variability exists amongst the genotypes chosen for the study which was evident by the results of ANOVA which reported substantial genotypical variations for all characters under study. In general, the PCV values were recorded superior than the values of GCV which highlights the effect of environment on the morphological appearance of these traits.High heritability estimates obtained in certain characters was indicative of the fact that these traits are having a less influence of environment paving the way for direct selection for early maturing genotypes. It also enlightens the fact that the phenotypes were almost the proper representative of the genotypes for these traits. Since, Heritability estimates alone cannot be used to predict the selection response so it is important to quantify Genetic advance in addition to heritability to find out the selection effectiveness. High heritability estimates when combined with high genetic advance as obtained for the traits *viz.* Plant height, No. of leaf / plant, Stem thickness, Leaf: Stem ratio, Dry matter percent, Leaf fresh wt./ plant, Dry stem wt./ plant, Seed yield / plant and Dry matter yield/plant gives us an idea of preponderance of additive gene effects in governing these traits which are heritable and fixable in nature, and the selection can lead to improvement in these characters in desired direction.

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