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Full Research Article

Genetic Variability and Association Analysis in Intervarietal Segregating Population of Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] for Quantitative Traits

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Abstract

Forty line of intervarital segregating population of clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] along with their parents were analyzed for genetic variability, correlation and path coefficients. Significant differences observed for various traits indicated substantial amount of variability existed among the genotypes for various traits, which indicated further genetic studies. High heritability coupled with high genetic advance was observed for number of branches plant^{-1}, plant height, no. of clusters plant^{-1}, days to flowering and seeds pod^{-1} indicating that selection would be rewarding for these characters. In general genotypic correlation coefficients were higher in magnitude than their phenotypic correlation coefficient, this indicated the association at genotypic level and control of sampling error. Seed yield plant^{-1} was found to be positively and significantly correlated with number of pods plant^{-1}, number of cluster plant^{-1} and number of pods cluster^{-1}. Path analysis revealed that characters such as number of pods cluster^{-1}, number of clusters plant^{-1} and pod length were the major component traits of seed yield and hence these characters should be given priority in selection based on their high heritability coupled with high genetic advance also.

1. Introduction

Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.], commonly known as guar, is a member of leguminaceae (Fabaceae) family and derived its name from a Sanskrit word Gauaahar' which means cow fodder or otherwise fodder of the livestock. The crop is self pollinated, diploid (2n=14), summer annual legume and is an important cash crop of Indian subcontinent. Clusterbean is believed to be originated in Africa but it is grown throughout the Southern Asia since ancient times as a vegetable and fodder crop. It is widely cultivated in countries like India, Pakistan, USA, Morocco, Italy, Germany, Greece, and Spain and is thus considered as a new crop for western agricultural practices. It is a source of high quality galactomannan and protein (Punia et al., 2009), Clusterbean is an upright, bushy, drought hardy, deep rooted crop and assumed to be highly adapted to poor and erratic rains, less care and low input areas (Pabal and Yengokopam, 2013). Being a member of legume family, it has a property to fix atmospheric nitrogen, which improves the soil health and yield of succeeding crops (Elsheikh and Ibrahim, 1999). Clusterbean endosperm is a rich source of high quality galactomannan which is very important industrially (Rai et al., 2012). Guar gum has 5−8 times the thickening power of starch and is used as a viscosity enhancer for both food and non food crops (Sharma and Sharma, 2013). Guar gum is being used in textiles, cosmetics, explosives and oil industries. In food industries, clusterbean gum can be utilized as germ meal in cookies. Moreover, potential of this crop can be further extended by using it in numerous pharmaceutical and industrial additives as per the global market (Bajaj, 2011). The crop also has medicinal properties due to the presence of antioxidants in the plant. It is used for treating diarrhea, irritable bowel syndrome (IBS), obesity, diabetes and reducing cholesterol (Badugu, 2012). Recently, galactomannans have also been used in the production of water proof biocide films (Das et al., 2011). India is the largest supplier of clusterbean seed in the world contributing 80% been done and very little attention has been given for its genetic improvement in the past, in order to enhance the productivity level of clusterbean. Hence, there is a great opportunity for breeders in identifying the genetic make-ups that are superior in yield. To reach this goal, the basic requirements are to have adequate information on the extent of variability, correlation and path coefficient among the different characters. In view of this, the present investigation was carried out with the objective of assessing genetic variability, correlation and path coefficient among the various yield contributing traits.

2. Material and Methods

The present investigation was carried out during *kharif* 2014, in Forage Section, Department of Genetics and Plant Breeding, College of Agriculture, CCS Haryana Agricultural University, Hisar, Haryana, India. The experimental material for the present study comprised of random of 40 F_3 plants of intervarietal cross of clusterbean (HG75×PNB) with the respective two parents. Pusa Nav Bahar is a vegetable type, long size pods, early maturing and highly susceptible to Bacterial Leaf Blight and HG75 is a grain type, medium size pods, lat maturity and moderately resistant to Bacterial Leaf Blight resistant. The experimental materials were grown at research Farm of the Forage section and F_3 generation was obtained from F_2 seed. The materials were planted in a Randomized Block Design replicated thrice having plot size of 2×4 m^2. Data on five randomly selected plants were recorded on days to 50% flowering, days to maturity, plant height (cm), number of branches plant^{-1}, number of clusters plant^{-1}, number of pods cluster^{-1}, number of pods plant^{-1}, pod length (cm), seed pod^{-1}, 100 seed weight (g), seed yield plant^{-1} (g). The data obtained were statistically analyzed with OPSTAT software program. The mean data were subjected to statistical analysis for estimating variability, phenotypic and genotypic coefficient of variation using formula suggested by Cockerham (1963), heritability (h2BS) according to Weber and Moorthy (1952) and genetic advance as per cent of mean was predicted by formula given by Johnson et al. (1955), correlation coefficient was calculated by formula given by Karl Pearson's and path coefficient analysis was predicted by formula given by Dewey (1959).

3. Results and Discussion

The analysis of variance was carried out for 11 characters and the results are presented in Table 1. Variation due to genotypes were highly significant for all the characters except for 100 seed weight and no. of pod cluster^{-1} indicating existence of significant genetic variability among the genotypes used in the present study. The coefficient of variation was low (<20%) for all the characters studied which indicates that the local control of experiment was effectively done. The mean, range, genotypic and phenotypic coefficient of variation, heritability and genetic advance as per cent of mean are presented in Table 2. Wide range of variation was observed for most of the traits like seed yield plant^{-1}, number of branches plant^{-1}, number of pods plant^{-1}, plant height, days to flowering, days to maturity, and number of clusters plant^{-1}. Genotypic and phenotypic coefficient of variation was highest for number of branches plant^{-1} followed by seed yield plant^{-1} and number of clusters plant^{-1}. Lowest genotypic and phenotypic coefficient of variation was recorded for 100 seed weight. Both of these parameters were quite close to each other for different characters. The magnitude of genotypic coefficient of variation was lower than phenotypic coefficient of variation in all the characters. Success of any selection programme mainly depends on the extent and nature of genetic variability present and also on the genetic architecture of yield and the component characters with high heritability as it is likely to give high genetic advance provided the traits are direct components of yield. High genotypic coefficient of variation was observed for number of branches plant^{-1} (25.71%) followed by seed yield plant^{-1} (23.287%), number of clusters plant^{-1} (21.40%) and plant height (18.83%). There was a close correspondence between phenotypic and genotypic coefficient of variation in almost all the characters. This indicated that environment had little effect to impact genetic potential of trait expression in most cases. It was obvious that for this reason the selection of better genotypes could be done based on their phenotype. The studies of Mahla and Kumar (2006), Singh et al. (2010); Chaudhary et al. (2010) indicated presence of enough variability for various traits in clusterbean confirming the results of the present study. However, Saini et al. (2010) suggested that genetic coefficient of variation alone is not sufficient for determination of the amount of heritable variation and hence heritability in conjunction with genetic advance is required to be studied. Chaudhary et al. (2004) also suggested that genetic coefficient of variability together with the heritability estimates would give

Table 1: Analysis of variance for seed yield and its component characters in cluster bean

Source of variation	d.f.	Days to flowering	Plant height (cm)	100-seed weight (g)	Seed yield plant^{-1} (g)	No. of clusters plant^{-1}	No. of pods cluster^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	Pod length (cm)	Days to maturity	No. of branches plant^{-1}
Replications	2	0.66	25.57	0.03	1.19	0.23	0.01	8.47	3.18	0.01	12.05	0.89
Treatments	41	86.61**	1785.26**	0.23	5.56**	9.09**	0.78	46.33**	4.44**	2.95**	329.18**	7.19**
Error	82	4.49	107.33	0.05	0.90	0.56	0.16	6.25	0.73	1.09	18.96	0.60
CV (%)		4.43	8.27	6.79	17.76	9.50	10.87	9.56	10.55	19.17	4.73	13.48

Table 2: Mean, Range, Genotypic co-efficient of variation (GCV), Phenotypic co-efficient of variation (PCV), Heritability and Genetic advance for seed yield and its component characters in cluster bean

Characters	Means	Range	GCV	PCV	Heritability (Broad sense)	Genetic Advance value % means
Days to flowering	47.82	36.00 - 60.23	10.94	11.80	85.92	20.89
Plant height (cm)	125.20	94.80 -166.03	18.36	18.96	93.77	36.63
100 seed weight (g)	3.15	2.27 - 3.57	7.83	10.36	57.02	12.18
Seed yield plant^{-1} (g)	5.35	3.07 - 8.53	23.29	29.29	63.22	38.14
No. of clusters plant^{-1}	7.88	5.53 -13.37	21.40	23.41	83.54	40.29
No. of pods cluster^{-1}	3.67	2.50 - 4.57	12.40	16.49	56.53	19.21
No. of pods plant^{-1}	26.15	19.33 -34.50	13.98	16.93	68.15	23.77
No. of seeds pod^{-1}	8.14	4.47 - 9.33	13.65	17.24	62.73	22.27
Pod length (cm)	5.45	2.80 - 9.33	14.45	24.00	36.21	17.91
Days to maturity	101.99	93.93 -121.63	9.97	10.85	84.49	18.88
No. of branches plant^{-1}	5.76	2.50 - 8.97	25.72	29.04	78.44	46.92

reliable indication of the expected amount of improvement by selection. Correlation coefficients at genotypic and phenotypic levels are presented in Table 3 and 4. In general, the genotypic correlation coefficient was higher in magnitude than their corresponding phenotypic correlation coefficient for most of the character combinations. This indicated the association at genotypic level and control of sampling error. A critical perusal of correlation coefficients revealed that the seed yield plant^{-1} was found to be positively and significantly associated with number of pods plant^{-1}, number of cluster plant^{-1} and number of pods cluster^{-1}. Number of pods plant^{-1} exhibited positive and significant association with number of clusters plant^{-1} and number of pods cluster^{-1}, however negative and significant association was observed with days to flowering, plant height, pod length and days to maturity. Number of clusters plant^{-1} exhibited positive and significant correlation with number of pods cluster^{-1}, number of branches plant^{-1} and no of pods plant^{-1}. However, it showed negative and significant association with days to flowering, days to maturity, plant height and pod length. Number of pods cluster^{-1} exhibited positive and significant association with number of seeds pod^{-1}. However, this trait exhibited negative and significant association with days of flowering and days of maturity. Pod length showed positive and significant association with number of seeds pod^{-1}. However, it had negative and significant association was observed with seed yield plant^{-1} and number of branches plant^{-1}. Plant height had positive and significant association with days to flowering and days to maturity. Number of branches plant^{-1} had positive and significant association with days to flowering and days to maturity, however, this trait expressed negative and significant association with number of pods cluster^{-1}, number of seeds pod^{-1} and pod length. This was in consonance with the findings of Chaudhary et al. (2004); Mahla and Kumar (2006); Sultan et al. (2012) in clusterbean. The interrelationship and path matrices estimated on the basis of values of eleven morphological trait in 4o lines and two parents of clusterbean are presented in table 4. Number of pods cluster^{-1} had positive and high direct effect (0.290). However, it contributed indirectly via 100 seed weight (0.050). The direct effect of pod length (0.257) was positive and high, whereas, indirect effect was high via number of pods plant^{-1} (0.038). The plant height exhibited positive direct effect (0.146), whereas indirect effect was high via no. of pods cluster^{-1} (0.042) and pod length (0.028). Although number of seeds pod^{-1} (-0.239), days to flowering (-0.072), 100 seed weight (-0.311), number of pods plant^{-1} (-0.314) and number of seeds pod^{-1} (-0.239) exhibited negative direct effects, whereas indirect effect was high via pod length (0.099), no. of pods cluster^{-1} (0.063) and number of clusters plant^{-1} (0.050). It is obvious from the gist of results of path-coefficient analysis that number of pods cluster^{-1}, pod length and plant height were the component traits of seed yield as these had high values of direct effects. But all these characters also had large positive indirect effects on seed yield through each other. These results are in conformity with the findings of Singh et al. (2005), Mahla and Kumar (2006) and several workers were also work out same trend of their findings. The multitude of component characters, their positive and negative effects with one another and seed yield along with environmental interactions make the prediction and determination of high yielding genotypes extremely difficult. Hence, the selection should only be based on above mentioned component traits for faster genetic amelioration of yield in clusterbean. In the light of results obtained in the present investigation, it is clear that number of pods plant^{-1}, number of clusters plant^{-1} and number of pods cluster^{-1} are comparatively more important component

Table 3: Genotypic correlation coefficients among seed yield and its component characters

Character	Days to flowering	Plant height (cm)	100 seed weight (g)	Seed yield plant^{-1} (g)	No. of clusters plant^{-1}	No. of pods cluster^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	Pod length (g)	Days to maturity	No. of branches plant^{-1}
Days to flowering	1										
Plant height (cm)	0.700**	1									
100 seed weight (g)	-0.141	-0.240*	1								
Seed yield plant^{-1} (g)	-0.617**	-0.473**	0.125	1							
No. of clusters plant^{-1}	-0.576**	-0.662**	0.064	0.792**	1						
No. of pods cluster^{-1}	-0.827**	-0.385**	0.003	0.719**	0.596**	1					
No. of pods plant^{-1}	-0.670**	-0.566**	-0.049	0.863**	0.927**	0.858**	1				
No. of seeds pod^{-1}	-0.555**	-0.350**	0.081	0.014	0.018	0.822**	0.169	1			
Pod length (cm)	-0.139	-0.049	0.223*	-0.297**	-0.464**	0.184	-0.322**	0.798**	1		
Days to maturity	0.931**	0.821**	-0.249*	-0.626**	-0.671**	-0.812**	-0.691**	-0.539**	-0.130	1	
No. of branches plant^{-1}	0.351**	0.019	-0.057	0.001	0.280**	-0.733**	0.068	-0.518**	-0.577**	0.342**	1

Table 4: Direct and indirect effects of different characters on seed yield in clusterbean

	Days to flowering	Plant height (cm)	100 seed weight (g)	No. of clusters plant^{-1}	No. of pods cluster^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	Pod length (cm)	Days to maturity	No. of branches plant^{-1}	Seed yield plant^{-1} (g)
Days to flowering	-0.072	-0.019	0.046	0.050	0.094	-0.070	0.002	0.026	-0.024	0.007	-0.616
Plant height (cm)	0.009	0.146	-0.014	-0.090	0.042	-0.055	-0.022	0.028	-0.016	0.011	-0.473
100 seed weight (g)	0.010	0.006	-0.311	0.045	-0.046	0.027	-0.024	0.099	0.030	-0.008	0.125
No. of clusters plant^{-1}	-0.009	-0.033	-0.035	0.400	-0.001	0.021	0.022	-0.026	-0.015	-0.002	0.792
No. of pods cluster^{-1}	-0.023	0.021	0.050	-0.001	0.290	-0.064	0.007	-0.019	0.046	-0.010	0.718
No. of pods plant^{-1}	-0.016	0.025	0.027	-0.028	0.059	-0.314	0.047	-0.031	-0.054	0.007	0.863
No. of seeds pod^{-1}	0.001	0.013	-0.032	-0.037	-0.009	0.062	-0.239	0.088	-0.022	-0.004	0.014
Pod length (cm)	-0.007	0.016	-0.120	-0.041	-0.021	0.038	-0.082	0.257	-0.001	-0.020	-0.293
Days to maturity	0.00853	-0.011	-0.044	-0.030	0.063	0.081	0.026	-0.001	0.210	-0.007	-0.6260
No. of branches plant^{-1}	-0.00828	0.024	0.037	-0.017	-0.044	-0.033	0.017	-0.077	-0.023	0.066	0.001

characters for seed yield. The improvement and selection based on these traits would also result in increased seed yield.

4. Conclusion

Significant differences for various traits indicated that ample genotypic variability existed among the F3 progenies. Significant variability was observed for various traits and estimates of genotypic and phenotypic coefficients of variation were quite close to each other. Thus, the present study was a successful attempt in identifying the advanced genotypes based on genetic variability, their *per se* performance and the understanding of complex interrelationship among attributes involved in genetic control of seed yield. Therefore, these results will provide valuable added guidelines in future breeding programmes for improving the seed yield and related traits in cluster bean.

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