

crop mean values. Hence, the ratooning ability has to be assessed in later generations. When heritability was considered, days to flowering and leaf l/b ratio in the open pollinated population showed high heritability. In the self pollinated population, plant height and stem girth showed high heritability in the ratoon crop. It was also observed that in some of the instances, there were negative estimates of heritability which may be attributed to the inadequacy of sample or due to sampling error (Mahmud and Kramer, 1951).

The estimation of intergeneration correlation coefficient in this study showed negative value for

biomass yield, number of nodes and number of leaves. This indicates that there is no relationship between F₂ main crop and its ratoon crop. Hence, the ratooning ability has to be assessed in later generation. Also isolate genotypes with stepped up yield in ratoon over main crop, selection should be postponed to the later generation.

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GENETIC VARIATION AND DIVERSITY IN GREEN GRAM

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ABSTRACT

Genetic variation and diversity studies among 21 genotypes of green gram collected from different sources were carried out for five economic characters. The seed yield and plant height showed moderate genotypic coefficient of variation. High heritability coupled with high genetic advance as percent of mean was noticed for plant height and seed yield. By application of D2 analysis, the twenty one genotypes were grouped into three clusters. The types chosen from the same eco-geographic region were found scattered in different clusters. The clustering together of types from the same eco-geographic region into one cluster was also observed. Maximum inter cluster distance was observed between cluster I and III indicating their divergence in origin.

KEY WORDS: Genetic Variation, Genetic Diversity, Green gram

The seed yield in green gram (*Vigna radiata* (L.) Wilczek), is a complex character which is highly subjected to environmental variations. Information on nature and magnitude of variability present in a population due to genetic and non genetic causes is an important pre-requisite for a systematic breeding programme to improve the yield potential genotypes. An attempt was made in the present investigation to assess the variability, heritability and genetic advance of some

quantitative characters in a set of selected green gram varieties.

MATERIALS AND METHODS

A total of 21 genotypes of green gram of diverse origin was chosen and studied during *kharif* 94 at the National Pulses Research Centre, Vamban, in randomised block design replicated four times. Each type was sown in a single row of

Table 1. Mean variability, heritability and genetic advance of economic characters in green gram

Characters	Mean	Range	GCV	PCV	Heritability	Genetic advance	GA as % of mean
Plant height	33.98	26.3-50.3	14.92	28.48	0.69	7.25	21.35
No. of primary branches	1.61	1.3-2.7	8.42	27.6	0.3	0.08	5.27
No. of secondary branches	4.21	3.3-5.3	6.98	25.26	0.28	0.08	1.92
No. of pods / plant	11.93	8.0-15.7	7.95	29.18	0.27	0.53	4.45
Single plant yield	2.8	1.9-4.4	22.29	31.07	0.72	0.77	27.5

GA : Genetic advance ; GCV : Genotypic coefficient of variation ; PCV : Phenotypic coefficient of variation

Table 2. Clustering pattern of 21 green gram genotypes

Clusters	No. of genotypes	Origin	Genotypes
I	17	Delhi Warangal Lam Akola Bombay Kanpur Vamban	Pusa 9032, PS 16, Pusa 9072, Pusa 9031, Pusa SR 22, WGG 48, WGG 47, WGG 37, WGG 2 LGG 410, LGG 450 TARM 2 TAP 7, TAM 22 PDM 84-146 Vamban-1, VGG 4
II	2	Delhi	Pusa 103, Pusa 118
III	2	Delhi	Pusa 9071

4m length spaced 30 cm apart and 10 cm between plants. Ten plants were randomly selected in each type and observations were recorded on five economic characters. Genotypic and phenotypic co-efficient of variation (Burton, 1952), heritability in broad sense (Lush, 1940) and genetic advance (Johnson *et al.*, 1995) were calculated. The diversity in characters was studied using Mahalanobis D2 statistics as described by Rao (1952).

RESULTS AND DISCUSSION

Mean, range, phenotypic and genotypic co-efficients of variation (PCV and GCV), heritability and genetic advance are presented. Table 1. In general, the PCV, and GCV were low to medium for different characters. High PCV was observed for single plant yield followed by plant height. Similar finding was reported by kahir sagar and Deore (1990) for single plant yield. Heritability estimates, being higher in case of single plant yield and plant height, can be attributed to the fact that these characters are least influenced by environmental effects and there could be greater correspondence between phenotypes and breeding value while selecting individuals (Jonhson *et al.*, 1955). An association existed between high heritability estimates for plant height and single plant yield and high corresponding values of

Table 3. Average intra and intercluster distance between different clusters

Clusters	I	II	III
I	30.58(5.53)	9.26(3.05)	16.45(4.05)
II	-	1.81(1.35)	9.69(3.11)
III	-	-	6.74(2.60)

expected genetic advance as per cent of mean for these traits. This indicates the prevalence of additive gene effects for these characters as suggested by Sagar *et al.*, (1976) in black gram. Hence, pureline selection may prove effective for exploiting these two characters in greengram.

By application of D2 analysis, 21 genotypes were grouped into three different clusters (Table 2). Among the clusters, cluster I grouped with 17 genotypes while cluster II and III with 2 genotypes each. The cluster II consisted types from the same geographical region showing similar architecture among the types of the cluster. Such a parallelism was reported by Shanmugam and Sree Rangasamy (1982) and Natarajan *et al.* (1983) in green gram. Cluster I and III consisted types from different geographical regions, indicating that the geographic diversity through important may not be the only factor genetic divergence. Factors other than geographic divergence might be responsible for the differential grouping of the varieties. The clustering pattern failed to establish the fact that genetic divergence is due to geographic distribution.

Eight types from Delhi were found scattered in three clusters indicating the wider genetic variability in the material chosen from the same region. Among the clusters, the inter cluster distance between I and III was maximum followed by the distance between II and III (Table 3). The types in these clusters may serve as potential source and crossing between the types may results in heterotic expression for yield components. Cluster I had increased mean values for number of primary branches, secondary branches and number of pods (Table 4). Cluster III recorded high mean values for

Table 4. Cluster means for five characters in 21 green gram genotypes

Clusters	Plant height	No. of primary branches	No. of secondary branches	No. of pods per plant	Single plant yield
I	33.56 1.70	4.63	12.76	2.91	
II	37.00 1.50	4.00	9.00	3.40	
III	41.15 1.50	3.85	11.10	3.60	

plant height and single plant yield. Intercrossing the types from these clusters might result in array of variability for exercising effective selection in these traits.

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GENETIC ARCHITECTURE OF METRIC TRAITS IN PEARL MILLET

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ABSTRACT

The P₁, P₂, F₁, F₂, BC₁ and BC₂ generations of five pearl millet crosses were studied for six metric traits. The additive dominance model was adequate for plant height, leaf breadth, earhead length and earhead breadth in one cross each. An epistatic digenic model was assumed for other crosses. Heterosis breeding is suggested for improvement of all traits. Duplicate epistasis plays a relatively greater role than complementary epistasis. Among the interactions, dominance X dominance played a major role. Therefore, reciprocal recurrent selection is suggested for development of a superior variety.

KEY WORDS : Genetic Architecture, Pearl millet, Metric Traits

The efficiency of selection for the improvement of metric traits depends upon the nature and magnitude of gene effects involved in the inheritance of a particular trait. In *Pennisetum glaucum* (L.) R. Br the importance of dominance gene effect has been reported (Virk, 1988) for different yield component traits. An attempt has been made in the present study to estimate gene effects for yield and other traits using a set of six generations derived from five crosses.

MATERIALS AND METHODS

Five cross combinations viz., Pt 3832 X ICMPE 11, Pt 3832 X ICMPE 15, Pt 3832 X 81 B, Pt 3832 X 732B and 81B X 732 B were used for the study. Six generations i.e., P₁, P₂, F₁, F₂, BC₁ and BC₂ of each cross were sown in randomised block design with four replications at the National Pulses Research Centre, Vamban. The spacing was 45 cm between rows and 15 cm within the rows. The total number of population raised in each