

## Genetic variability in Greengram (*Vigna radiata* (L.) wilczek)

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### SUMMARY

The estimates of variability parameters namely PCV and GCV were higher for the traits viz., single plant yield, number of branches per plant, number of pods per plant, number of clusters per plant, plant height and length of branch indicating greater scope of selection within the core for these traits. The traits, dry matter production and number of clusters per branch revealed wide differences between the estimates of PCV and GCV values indicating high influence of environmental factors while the traits, days to initial flowering, days to 50 per cent flowering, days to initial maturity, days to full maturity, hundred seed weight, seed length, seed breadth, length of pod and protein content were found less influenced by the environmental factors as the difference between the estimates of PCV and GCV were narrow. The estimates of heritability in the core collection indicated that the trait days to full maturity, days to initial maturity, days to initial flowering, days to 50 per cent flowering, seed length, seed breadth, plant height, length of branch, hundred seed weight and length of pod were highly heritable. High genetic advance as percentage of mean was observed for the traits, number of clusters per branch, length of branch, single plant yield, number of pods per plant, number of clusters per plant, plant height and number of branches per plant suggesting scope for selection for these traits in the core collection. High genetic advance coupled with high heritability and GCV was observed for length of branch, number of branches per plant, number of clusters per branch, number of clusters per plant, number of pods per plant, single plant yield and plant height indicating the predominance of additive gene action for these traits.

Key words: Greengram, PCV, GCV, Variability, Pathanalysis.

*Vigna radiata* (L.) wilczek, commonly known as green gram or mungbean is the most widely distributed species among the six Asiatic *Vigna* species. The yield level of green gram as like other pulses is well below the optimum level. The average yield of mungbean is very low not only in India (425 kg/ha) but in entire tropical and subtropical Asia. In Tamil Nadu it is cultivated in an area of 1.63 lakhs hectare with a production of 0.78 lakhs tonnes. The varietal breeding program taken up in this crop had resulted only with limited success as far as yield improvement is concerned. The basic reason for limited success had been due to the limited variability prevailed among the parents used for hybridization in most of the studies, this study was taken up keeping the following objective in mind, to assess genetic components and to perform association analysis among yield and yield attributes within the core collection.

### MATERIALS AND METHODS

Seeds of 646 accessions of greengram were collected from the Department of Pulses and utilized for the study. The field experiments were carried out at Department of Pulses, Centre for Plant Breeding and Genetics (CPBG), Tamil Nadu Agricultural University, Coimbatore during 2002-2004 Rabi and Kharif seasons. Each genotype was sown in two single row plot each of four metre length, plants were raised at a spacing of 30 x 10 cm and replicated twice. The package of practices recommended in the crop production guide were followed. Eighteen quantitative traits

viz., plant height (cm), number of branches per plant, length of branch (cm), days to initial flowering, days to 50 per cent flowering, number of clusters per branch, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, seed length (cm), seed breadth (cm), hundred seed weight (g), single plant yield (g), dry matter production (g), protein content (%), days to initial maturity and days to full maturity. The observations were recorded in five randomly selected plants in each of the accession per replication. The data on 18 quantitative traits for 65 accession of core collection were subjected to statistical analysis of variance (Panse and Sukhatme, 1967) The phenotypic, genotypic and environmental variances were calculated by utilizing respective mean sum of squares from the analysis of variance calculated according to (Johnson *et al.*, 1955) The co-efficient of variation was worked out by the formula of Burton (1952). Heritability in the broad sense was calculated according to Lush (1940) and expressed in percentage. The heritability percent was categorized as suggested by Robinson *et al.*, (1949). Genetic advance by Johnson *et al.*, (1955).

### RESULTS AND DISCUSSION

Analysis of variance for 18 traits involving 65 accessions of core collection showed significant differences among the genotypes for all the characters except seed length and seed breadth (Table 1). The maximum phenotypic variance was observed for the character dry

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