Association analysis in greengram (Vigna radiata (L.) wilczek)

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ABSTRACT
The estimates of correlation co-efficient of the traits *viz.,* number of branches per plant, length of branch, number of clusters per branch, number of clusters per plant, number of pods per plant, hundred seed weight and protein content with the seed yield were higher indicating the importance of the traits in the selection for high seed yield.

Key words : Greengram, Straits.

INTRODUCTION

Vigna radiata (L.) *wilczek*, commonly known as green gram or mungbean is the most widely distributed species among the six Asiatic *Vigna* species. It is one of the predominant sources of protein and certain essential amino acids like lysine and tryptophan in vegetarian diets. It possessed certain added features compared to other pulses. It is relatively drought tolerant and well adapted to a range of soil conditions including light soils and can thrive even under limited irrigation, more over, it is suited for crop rotation and crop mixtures. However, this crop is suffering from the yield advantage as realized in case of C4 cereals.

Presently, 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. Yield is complex character which is determined by many traits. To find out the characters which are high influence to the yield, this study was taken up with this objective. To assess genetic components and to perform association analysis among yield and yield attributes

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 Correlation co – efficients were worked. The significance of correlation co- efficients was tested by referring to the table given by Snedecor (1967).

RESULTS AND DISCUSSION

The results of correlation for the 18 characters are presented in the Table.1. The data showed that number of pods per plant (0.56), number of clusters per plant (0.45), number of cluster per branch (0.44), number of branches per plant (0.31), length of branch (0.29), protein content (0.29) and hundred seed weight (0.25) exhibited

Table 1 : Genotypic correlation co efficient of 65 core collection accession for yield and yield components

	PHT	NOB	BRL	DIF	DFF	NCB	NOC	NPP	POL	NSP	SDL	SDB	HSW	DMP	PTC	DIM	DFM	SPY
PHT	1.00	0.44**	0.76**	0.33**	0.29*	0.49**	0.52**	0.44**	0.16	0.34**	-0.16	-0.27	-0.12	-0.02	-0.01	0.26	0.26	0.20
NOB		1.00	0.77**	0.14	0.11	0.74**	0.62**	0.58**	0.02	0.25*	-0.22	-0.41	-0.15	0.10	0.08	0.14	0.10	0.31*
BRL			1.00	0.21	0.16	0.75**	0.64**	0.59**	0.10	0.36**	-0.21	-0.33	-0.15	0.02	0.13	0.17	0.13	0.29*
DIF				1.00	0.96**	0.10	0.11	0.00	-0.19	-0.11	-0.03	-0.14	-0.22	0.00	-0.18	0.98**	0.93**	-0.15
DFF					1.00	0.05	0.07	-0.02	-0.21	-0.08	-0.06	-0.15	-0.22	0.05	-0.21	0.95**	0.98**	-0.18
NCB						1.00	0.90**	0.80**	0.13	0.25*	-0.13	-0.24	-0.03	0.04	0.25*	0.09	0.02	0.44**
NOC							1.00	0.85**	0.16	0.26*	-0.08	-0.21	-0.06	-0.01	0.22	0.11	0.05	0.45**
NPP								1.00	0.19	0.32**	-0.07	-0.18	0.03	-0.04	0.32**	0.00	-0.04	0.56**
POL									1.00	0.35**	0.27*	0.23	0.27*	-0.18	0.17	-0.20	-0.18	0.21
NSP										1.00	-0.13	-0.21	-0.23	-0.15	0.02	-0.14	-0.08	0.13
SDL											1.00	0.75**	0.54**	0.04	0.01	0.01	-0.06	0.00
SDB												1.00	0.56**	0.09	-0.09	-0.11	-0.17	-0.07
HSW													1.00	0.20	0.21	-0.22	-0.23	0.25*
DMP														1.00	-0.07	0.04	0.02	0.02
PTC															1.00	-0.20	-0.18	0.29*
DIM																1.00	0.93**	-0.16
DFM																	1.00	-0.15
SPY																		1.00

* Significant at 5 per cent level　　　　　　** Significant at 1 per cent level

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significant and positive correlation with seed yield. Considering the inter correlation among yield components, the trait plant height exhibited highly significant and positive correlation with branching traits namely length of branch (0.76), number of clusters per plant (0.52), number of cluster per branch (0.49). The traits hundred seed weight revealed highly significant and positive correlation with seed dimension traits namely length of pod (0.27) , seed breadth (0.56) and seed length (0.54).

The ultimate aim of plant breeding is to achieve a higher level of seed yield, which is a complex trait. The intricate nature of seed yield is largely influenced by number of component characters. Hence, information on the strength and direction of association of these component characters with seed yield and also inter association among themselves would be very useful in formulating an effective and viable breeding programme for improvement of seed yield *per se* (Naidu and Rosaiah ,1993).

Genetic correlation analysis using the core collection in this study revealed a strong and positive association of the traits studied. The estimates of correlation co -efficient of the traits, number of branches per plant, length of branch, number of clusters per branch, number of clusters per plant, number of pods per plant, hundred seed weight and protein content with the seed yield were higher indicating the importance of the traits in the selection for high seed yield. Hence these traits should be given due weightage for selection towards the yield improvement in green gram as suggested by Joshi and Kabaria (1973), Malik *et al.* (1982), Raut *et al.* (1988), Vikas *et al.* (1999) and Manivannan (2002).

However, the information about the association between yield and yield attributes alone may not be sufficient. The interrelationship between these component characters themselves may also affect the overall influence of the characters on yield.

In this investigation, the characters showing strong significant and positive correlation with seed yield such as number of branches per plant, length of branch, number of clusters per branch, number of clusters per plant, number of pods per plant and hundred seed weight also showed strong and positive association among themselves, indicating that selection for combination of these traits is likely to improve seed yield. The results reported by various authors, Giriraj and Vijayakumar (1974), Gayen *et al.* (1991), Malik and Singh (1983) and Vikas *et al.* (1999) are in accordance with the present study.

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