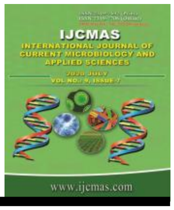
Int.J.Curr.Microbiol.App.Sci (2020) 9(7): 2316-2319

EXCELLENT PUBLISHERS

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 9 Number 7 (2020)**
Journal homepage: http://www.ijcmas.com



Original Research Article https://doi.org/10.20546/ijcmas.2020.907.270

Study of Genetic Diversity for Yield and Yield Contributing Traits in Black Gram (*Vigna mungo* L.)

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ABSTRACT

Keywords

Black gram,
Genetic diversity,
Cluster analysis

Article Info

Accepted:
20 June 2020
Available Online:
10 July 2020

Genetic diversity analysis through cluster were performed in 62 mutant lines of black gram inclusive two checks namely Indira Urd Pratham and KU 96-3. In cluster analysis, the 62 genotypes were grouped into 5 cluster for 13 quantitative yield related characters. In study there were 27 mutant lines in cluster I, 32 in cluster II, 1 in cluster III, 1 in cluster IV and 1 in cluster V. The maximum inter cluster distance were obtained between cluster V and cluster III (69.94), which is followed by cluster V and cluster I (63.86). The inter cluster value varied from a range of 69.94 to 8.74.

Introduction

Black gram (2n =22), originated in India and *Vigna mungo* L. Hepper is the scientific name of black gram. *Vigna mungo* var. *silvestris* is considered as progenitor of black gram which grows wild in India. It is most popular pulse and can be most appropriately referred to as the king of the pulses due to its mouth watering taste and a lot of nutritional qualities. It is also largely used in South Indian culinary preparations. Black gram is one of the key ingredient in South Indian dishes such as *idli* and *dosa*. It is used in preparation of dal makhini and is very popular in Punjabi cuisine. It is used in preparation of dal in Bengal. It is an important ingredient of dal which is usually consumed with bati in Rajasthan. Black gram contain amino acids, vitamins, fat (1.5), carbohydrates (60%) and protein (25-26%). It is rich source of Vitamin A, B$_1$,B$_{3a}$ and it contain small amount of niacin, riboflavin, thiamine and vitamin C in it. It followed soybean in dietary protein content. Dry seed of black gram are good source of phosphorus. Genetic diversity is an essential pre-requisite in selecting parents for hybridization and generating high yielding genotypes in any crop breeding programme. Genetic diversity play a valuable role in plant breeding, because crossing between lines of divergent origin, give more diverse progenies than closely related parents.

Materials and Methods

The experiment was conducted in MULLaRP Experimental Field, Research cum Instructional Farm, Indira Gandhi Krishi Vishwavidalaya, Raipur, Chhattisgarh, India. The experiment was conducted in randomized block design with two replications.

The material was sown on 19th July, 2018. The seed was dibbed at 30 cm distance between row to row and 10 cm distance between plant to plant. Observations were recorded on five randomly selected plants from each treatment in each replication.

The representative bulk sample from each entry in each replication were used for analysis of protein content. Mean value of 5 plants were used for statistical analysis. Observation were recorded for 13 yield related characters such as days to 50 % flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plants, pod length, number of pods per plant, number of seeds per pod, 100-seed weight, biological yield per plant, harvest index, protein content and seed yield per plant, respectively.

Results and Discussion

Genetic diversity analysis was estimated through cluster analysis. All the 62 genotypes were grouped into five clusters as shown in Table 1. The cluster -II had maximum number of mutant lines (32) followed by cluster –I (27), cluster –III (1), cluster- IV (1) and cluster –V (1).

The maximum cluster mean for days to 50% flowering was obtained cluster V (74.00) and minimum in cluster IV (62.50). The cluster mean for days to maturity was higher for cluster I (118.29) whereas, the lowest mean value exhibited in cluster IV (111.00). For plant height, the maximum cluster mean value was exhibited for cluster IV (71.25) and minimum in cluster V (52.30). The highest cluster mean for primary branches per plant was obtained cluster III (7.25) whereas, lowest value was exhibited for cluster V (1.83). The maximum cluster mean recorded for secondary branches per plant was obtained cluster IV (9.35) whereas, the lowest value was exhibited for cluster III (3.75). The highest cluster mean for pods per plant was obtained cluster IV (16.80) and lowest in cluster V (7.80).

Table.1 Characteristics of black gram mutant line in cluster

S. No.	Cluster no.	No. Of mutant line in each cluster	% of line	Prominent trait
1	**I**	27	43.54	Days to 50% flowering, days to maturity.
2	**II**	32	51.61	
3	**III**		1.61	Primary branches per plant, seed per pod, protein content
4	**IV**	1	1.61	Plant height, secondary branches per plant, pod per plant, 100 seed weight, biological yield, seed yield per plant,
5	**V**	1	1.61	Harvest index

Table.2 Cluster means for the characters under study in black gram

Cluster	I	II	III	IV	V
Days to 50% flowering	73.59	69.91	66.5	62.5	74
Days to maturity	118.30	115.14	117	111	118
Plant height	61.95	60.99	65	71.25	52.3
Number of primary branches per plant	3.20	4.34	7.25	6.75	1.83
Number of secondary branches per plant	5.22	7.32	3.75	9.35	3.3
Number of pods per plant	10.46	12.72	14.75	16.8	7.8
Pod length	6.03	6.11	4.80	8.05	6.28
Number of seeds per pod	8.24	8.93	9.5	7.85	8.05
100 seed weight	6.53	6.26	6.2	6.75	6.35
Biological yield	12.11	12.32	13.35	14.5	5.22
Harvest index	35.40	41.62	30.79	48.65	98.02
Protein content	34.96	36.36	38.61	37.6	36.54
Seed yield per plant	3.09	3.14	2.64	4.63	2.07

Table.3 List of top mutant lines on the basis of yield

S.No.	Name of lines	Yield (g /plant)
1	IU450-3	4.57
2	KU500-2	4.42
3	KU450-10	4.17
4	IU450-4	3.95
5	KU96-3	3.88
6	IU400-1	3.35
7	KU400-4	3.4
8	IU450-1	2.95
9	KU400-3	2.89
10	KU500-3	2.87

Table.4 Distances between cluster centroids (intra and inter-cluster D^2 value)

CLUSTER	I	II	III	IV	V
I	**13.772**	8.746	11.739	22.969	63.863
II		**15.352**	13.496	16.343	58.146
III			**0.000**	21.585	69.943
IV				**0.000**	56.716
V					**0.000**

The maximum cluster mean value for pod length was obtained for cluster IV (8.05), whereas the lowest mean exhibited for cluster III (4.81). The maximum cluster mean for seeds per pod was obtained for cluster III (9.50), whereas the minimum value was exhibited for cluster IV (7.85). The highest cluster mean for 100-seed weight was exhibited for cluster IV (6.75) and lowest in cluster III (6.20). The highest cluster mean for biological yield was exhibited for cluster IV (14.51), whereas lowest value was exhibited for cluster V (5.22). The maximum cluster mean value for harvest index was reported in cluster V (98.02) and lowest in cluster III (30.79). The highest cluster mean for protein content was found in cluster III (38.61) and lowest value in cluster I (34.96).

The maximum inter cluster distance were obtained between cluster V and cluster III (69.94) which is followed by cluster V and cluster I (63.86). The minimum inter cluster value observed between cluster II and cluster I (8.74). The inter cluster value varied from a range of 69.94 to 8.74. The finding of the study are in general agreement to the observation of Jayamani and Sathya (2013), Konda *et al* (2009), Krishna *et al* (2002), Shanti *et al* (2006) and Venkatesan *et al* (2003).

In conclusion it is clear from the above results that the cluster mean for various quantitative traits related to yield attributes revealed that different respond differentially for various traits. Cluster IV showed highest mean performance for seed yield per plant (4.63) followed by cluster V (2.07). After the evaluation of mutant lines, it was observed that IU 450-3 was top yielder followed by KU 500-2 (4.42), KU 450-10 (4.17), respectively. These lines can be further utilized in crop improvement programme.

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How to cite this article:

Deeksha Chandrakar, Abhinav Sao and Deepak Gauraha. 2020. Study of Genetic Diversity for Yield and Yield Contributing Traits in Black Gram (*Vigna mungo* L.). *Int.J.Curr.Microbiol.App.Sci.* 9(07): 2316-2319. doi: https://doi.org/10.20546/ijcmas.2020.907.270