Biological Forum – An International Journal **13(3a): 556-561(2021)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Genetic Variation and Extent of Genetic Diversity in Urdbean [*Vigna mungo* (L.) Hepper]

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(Received 20 July 2021, Accepted 24 September, 2021)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Urdbean is the third most important pulse crop in India. But, no significant breakthrough has been achieved for enhancing its productivity primarily due to narrow genetic variability. Therefore, a set of urdbean germplasm comprising 58 urdbean genotypes were characterized for genetic variability. Analysis of variance revealed highly significant differences among the genotypes for ten yield and yield attributing traits indicating the presence of considerable genetic variation in the experimental material. The GCV was lower than PCV for all traits, however, there was narrow difference in PCV and GCV, indicating the effect of environment in lesser frequency. Characters *viz.*, plant height, number of branches/plant, number of clusters/plant, number of pods/plant and seed yield/plant showed high heritability in conjunction with high genetic advance, showing effects of additive gene action and providing ample scope for selection in segregating generations. Further, D^2 statistics grouped the fifty-eight genotypes into eight clusters. Genetic diversity was not in parallelism with the geographical diversity. Highest inter-cluster distance was established between cluster VI and VII ($D^2 = 1765.15$) followed by cluster III and VI, cluster IV and VI, cluster I and VI, cluster II and VII, cluster V and VII and cluster V and VI, respectively. While lowest intra-cluster distance was found between cluster IV and VI ($D^2 = 40.68$). Therefore, selection of parents from diversely related clusters can give rise to better recombinants with increased hybrid vigour.

Keywords: Blackgram, genetic variation, D^2 statistics, genetic diversity.

INTRODUCTION

Pulses occupy a very unique position in Indian agriculture by virtue of the fact that these are highly nutritious and provide a protein-filled diet via food. Pulses are the major source of protein. But, India has experienced progressive decline in per capita availability of pulses from 60.7 g day^{-1} in 1951 to 56.0 g day^{-1} in 2019-20 as against the WHO's recommendation of 80 g day^{-1} (Reddy *et al.*, 2021). Such crops are cultivated particularly in semi-arid to sub-humid low land tropics and sub tropics. In fact, the production of urdbean is mostly confined to Asian countries (Rao *et al.*, 2021a), of which, India is the largest producer of the crop, yielding 3.60 million tons of grains in an area about 5.60 million hectares (Rao *et al.*, 2021b). The crop withstands adverse climatic conditions and improves the soil fertility by fixing atmospheric nitrogen (22.10 kg N/ha) through root nodules (Kachave *et al.*, 2018). As compared to the cereal production globally, urdbean is being produced sporadically in low fertile lands having moisture stress condition which eventually conceal its true yield capacity and acclimatize itself to poor management practices. The expanding population has compelled the need for more supply of plant protein. However, higher value of lysine makes urdbean an excellent complement to rice in terms of balanced human nutrition (Baisakh *et al.*, 2021). Since, there is unavailability of sufficient per capita protein requirements, special attention is needed to exploit its higher genetic potential to compensate for the shortage in pulse production than cereals. Among pulses, urdbean (*Vigna mungo* L. Hepper) is an important short-duration grain legume crop grown throughout the country (Bansal *et al.*, 2019). Though India has topped in contributing highest in pulse production, the average productivity is very low (585kg/ha).

To overcome these constraints underlying low production, many breeding efforts are being practiced to break the yield plateau. Germplasm evaluation is probably one of the most significant step to harness the benefit of natural resources available in providing desirable traits for producing high-yielding and input responsive varieties that are resistant to various abiotic and biotic stresses. Hence, evaluation of germplasm lines under the prevailing environment is vital for the selection of donors with quality traits needed to be improved in future breeding programmes. So, to frame an effective breeding programme in the next generation, the exploitation of existing genetic variability by estimating different genetic parameters like genotypic, phenotypic, and environmental variances, their coefficient of variability, genetic advance, and heritability is quite necessary. It mainly helps to study the inheritance of various developmental-cum-productive traits. The pre-requisite factor in any hybridization programme is thorough analysis and assessment of the existing genetic diversity in the population under investigation to accomplish the ultimate aim of increasing yield. Therefore, keeping in view these facts, the present investigation was carried out to assess genetic variation and extent of genetic diversity in a panel of 58 urdbean test genotypes.

MATERIAL AND METHODS

The present investigation was carried out at EB-II section, Department of Plant Breeding and Genetics, College of Agriculture, OUAT, Bhubaneswar during *Rabi* 2020-21. The materials for the recent study comprised of 58 urdbean genotypes including elite cultivars, released varieties, and selected varieties. The experiment was conducted in Randomized Block Design with two replications. The genotypes were grown at a spacing of 30 × 10 cm in each plot (2.25 m^2). Standard recommended fertilizer dose, intercultural operations, crop management practices, and plant protection measures were followed to ensure proper and healthy crop establishment. Observations were recorded for ten characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of branches/plant, number of clusters /plant, number of pods/plant, pod length(cm), number of seeds/pod, 100-seed weight (g) and seed yield $plant^{-1}$ (g). Data obtained were subjected to statistical analysis for Analysis of Variance following procedure suggested by Panse and Sukhatme (1985), variability (PCV, GCV) by Burton (1952); Sivasubramanian and Madhavamenon (1973), and D^2 analysis as per Mahalanobis (1928).

RESULTS AND DISCUSSION

A. Analysis of Variance (ANOVA)

ANOVA was carried out for 10 yield and yield related traits in 58 urdbean germplasm accessions to test the significant differences among the genotypes under study (Table 1). ANOVA revealed highly significant differences among the genotypes for all the traits indicating the presence of considerable genetic variation in the experimental material. The range of variation in different traits in the present study was wide because of their diverse origin and geographical adaptation. The present study corroborates the previous findings of Panda *et al.*, (2017); Tanveer *et al.*, (2018) showing significant values of mean sum of squares for all the characters studied in urdbean.

Table 1: Analysis of Variance for ten morpho-agronomic traits in a set of 58 urdbean test genotypes.

Sources of Variation	d.f.	Days to 50% flowering	Days to maturity	Plant height	No. of branches /plant	No. of clusters / plant	No. of pods/ plant	Pod length	No. of seeds/ pod	100-seed weight	Seed yield/ plant
Replication	1	4.56	1.043	2.114	0.601	1.315	0.552	0.259	1.406	0.437	1.356
Treatment	57	9.569**	13.245**	89.61**	0.884**	9.497**	133.660**	0.534**	1.309**	0.760**	6.854**
Error	57	1.157	1.306	1.420	0.154	0.779	0.695	0.129	0.367	0.135	0.342
CD at 5%		2.159	2.295	2.392	0.787	1.772	1.674	0.721	1.217	0.738	1.174
CV(%)		2.147	1.349	3.292	14.938	9.552	2.699	8.355	9.792	8.059	8.716

* - Significant at $P_{0.05}$ ** - Significant at $P_{0.01}$

B. Genetic variability

The efficiency of selection in a crop depends upon the genetic variability present within the population and/or among genotypes subjected to selection. The phenotypic variation found among genotypes is the sum of genotypic as well as environmental components (Table 2). So, a quantitative assessment of genetic variability in terms of heritable and non-heritable fractions is possible only when the phenotypic variation is partitioned into its genotypic and environmental components. The genotypic variances recorded were higher than its environmental variances indicating genotypic component of variation as a major contributor to total variation among studied traits. The estimates of PCV and GCV showed a range from days to maturity (2.88%, 3.88%) to seed yield per plant (26.89%, 28.27%), respectively. For all morpho-agronomic traits, the GCV was comparatively lower than PCV, inferring to significant role of environment on expression of these characters. However, higher magnitude of GCV and PCV was noted for single plant yield, number of pods/plant, number of clusters/plant and number of branches/plant. These experimental results were in accordance with findings of Chubatemsu *et al.*, (2017); Bishnoi *et al.*, (2017); Kondagari *et al.*, (2017); Bandi *et al.*, (2018); Blessey *et al.*, (2018); Sushmitharaj *et al.*, (2018); Sarvani *et al.*, (2020).

Table 2: Estimates of genetic parameters for seed yield and yield contributing traits in a set of 58 urdbean test genotypes.

Characters	Range	Mean	CV%	PCV%	GCV%	h^2_{bs} (%)	GA	GA (as %) of mean
Days to 50% flowering	44.5 - 55.5	50.09	2.15	4.62	4.09	78.43	3.74	7.47
Days to maturity	80.5 - 92.0	84.70	1.35	3.18	2.88	82.05	4.56	5.38
Plant height	23.45 - 56.70	36.20	3.29	18.64	18.34	96.88	13.46	37.19
No. of branches/plant	1.6 - 4.7	2.62	14.94	27.47	23.03	70.33	1.04	39.79
No. of clusters/plant	5.15 - 14.7	9.24	9.55	24.54	22.60	84.85	3.96	42.88
No. of pods/plant	16.75- 55.55	30.89	2.70	26.53	26.39	98.97	16.71	54.08
Pod length	3.27 - 5.62	4.31	8.36	13.36	10.44	61.09	0.72	16.81
No. of seeds/ pod	3.20 - 7.75	6.19	9.79	14.79	11.09	56.21	1.06	17.12
100-seed weight	3.51 - 6.23	4.56	8.06	14.67	12.26	69.83	0.96	21.10
Seed yield/plant	3.89 - 12.30	6.71	8.72	28.27	26.89	90.49	3.54	52.70

K value at 5% selection index = 2.06

C. Heritability and genetic advance

The efficiency of selection can further be increased by estimation of heritability and genetic gain of each character to next generation. According to Panse and Sukhatme (1957), a combination of moderate or high values of heritability and genetic advance substantiates the role of additive gene action in effective selection of the concerned characters. The estimates of heritability (in broad sense) was higher for all characters except seeds per pod. In conformity with the present findings, (Table 2) high heritability coupled with high genetic advance in number of pods/plant (98.9%,54.08%), plant height (96.88%, 37.19%), number of branches/plant (70.33%, 39.79%), number of clusters/plant (84.85%, 42.88%), seed yield/plant (90.49%, 52.70%) were also reported by Meshram *et al.*, (2012), Pushpa *et al.* (2013); Panigrahi *et al.*, (2014); Panda *et al.*, (2017). Traits like pod length, number of seeds/pod and 100-seed weight with high heritability and moderate genetic gain too provides ample scope for selection (Bishnoi *et al.*, 2017), while the rest of the characters showed high heritability and low genetic advance indicating the role of both additive and non-additive gene actions. This suggests that selection for such morpho-agronomic traits may not be much rewarding for obtaining appreciable genetic gain in the follow-up generation.

D. Genetic diversity

Genetic diversity found among parents are a pre-requisite contributing to one of the major factors of any crop improvement programme. Crossing diverse parents provides better chances of getting superior recombinants in the next generation. Hence, proper assessment and exploitation of genetic diversity among existing breeding material in any of the plant breeding programmes have been a necessity to fulfill the evolving needs for new and superior varieties of a crop. As per the recent investigation, the diversity found among parents in most of the crops including black gram at genetic level might not always show parallelism with geographical diversity, ploidy level or place of origin. This seems to be similar line of outcome to the previous findings of Patel *et al.*, (2014); Senthil (2018); Islam *et al.*, (2019). In the present investigation, cluster analysis using Tocher's method (Rao, 1952) depicted the grouping of 58 genotypes into eight distinct clusters (Table 3). Such clear genetically distant clustering pattern with appreciable genetic diversity in urdbean was also revealed by Mandal *et al.*, (2014); Priya *et al.*, (2021); Rajalakhsmi *et al.*, (2020).

Table 3: Clustering of 58 urdbean genotypes using Tocher's method.

Cluster no.	No. of genotypes	Genotypes
I	36	AZAD-1, AZAD-2, AZAD-3, BIRSA, COBG-632A, COBG-612, COBG-662, OBG-16, OBG-24, OBG-28, OBG-32, AKU-9901, SARALA-10, LBG-427, LBG-645, WBG-52 LBG-719, G-25-48, TU-3, TU-94-2, TU-10-13, MASH-1-1, PU-30-3, PU-31, PU-30-1, SERVER-1, SERVER-2, KU-25-1, NABINA, KALIA-2, PDU-1-7, PDU-1, WBG-108, TV01312, PEJUA, RBU-38
II	13	CO-5, MONIKA, COBG-593, KU-96-3, KU-1, TU-94-1, VG-218, TV01264, PU-98-14, TU-74-51, G-25-91, B-3-8-8, PU-19
III	01	TV01304
IV	01	SHEKHAR-1
V	03	SARALA-3, SARALA-16, PU-30-4
VI	02	VIXUR-17, V02034B-BL
VII	01	PU-30-16
VIII	01	PDU-1-9

Estimates of average intra-cluster distance (D^2 values) revealed that genotypes within few clusters had minor or negligible genetic divergence with respect to the ten quantitative characters, while wider and much heterogenic clusters were also observed. In accordance with the distance (D^2-value) between cluster pairs (Table 4, Fig. 1), highest inter-cluster distance was established between Cluster VI and VII (D^2 = 1765.15) followed by Cluster III and VI (D^2 = 1555.86), Cluster IV and VI (D^2 = 1396.32), Cluster I and VI (D^2 = 851.80), Cluster II and VII (D^2 = 764.99), Cluster V and VII (D^2 = 709.08) and Cluster V and VI (D^2 = 705.43), respectively, inferring higher possibility of obtaining promising recombinants in segregating generation when genotypes from distant cluster are crossed. While, lowest inter-cluster distance was observed between cluster IV and VI (D^2 = 40.68) followed by cluster III and IV, cluster III and VIII indicating high homology between the genotypes of the concerned clusters.

Estimated cluster means (data not shown) revealed considerable differences among eight clusters. Cluster VI showed highest cluster mean values for number of branches/plant, number of clusters/plant, number of pods/plant and seed yield/plant. Thus, picking genotypes from this cluster can be efficiently used in developing high yielding and superior genotypes. However, it showed lowest mean values for pod length and number of seeds/pod. On the other hand, Cluster - III, IV and VII had highest cluster mean values for pod length, 100-seed weight and number of seeds/pod respectively.

Table 4: Average intra- and inter-cluster distance (D^2 values) among a set of 58 urdbean test genotypes.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**78.16**	238.31	176.73	148.64	248.89	851.80	275.01	189.62
II		**62.14**	616.43	515.70	255.72	277.23	764.99	549.71
III			**0.0**	63.30	570.70	1555.86	77.16	188.67
IV				**0.0**	527.44	1358.70	46.52	212.10
V					**55.51**	705.43	709.08	258.68
VI						**40.68**	1765.15	1396.32
VII							**0**	293.57
VIII								**0**

Diagonal bold figures represent intra-cluster distances

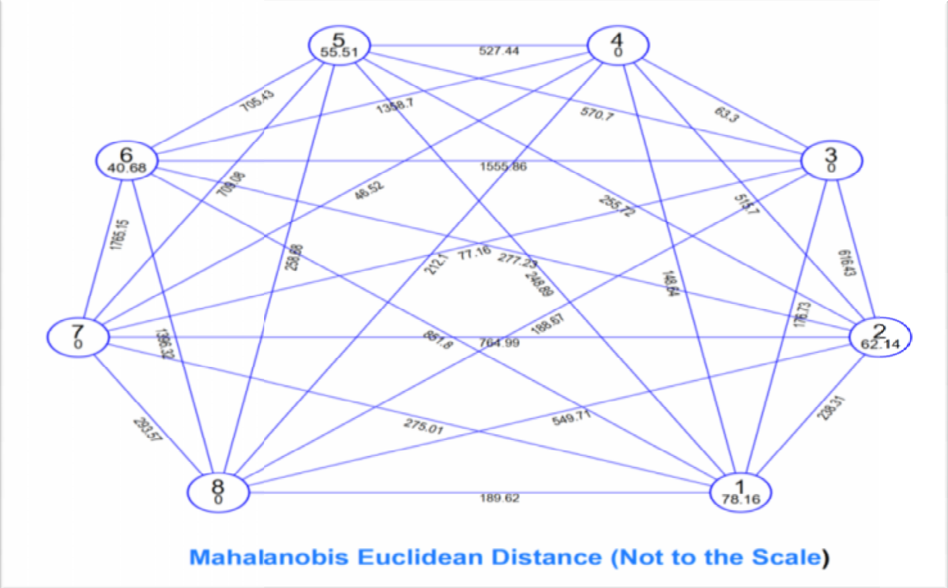

Fig. 1. Cluster diagram based on D^2 statistics showing mutual relationship among clusters comprising 58 urdbean test genotypes.

Seed yield/plant (59.47%) revealed the highest contribution to divergence followed by number of pods/plant and 100-seed weight (Table 5), while clusters/plant contributed the lowest (0.42%). As yield is a polygenic character, its value may be varied for a particular genotype when subjected to different environment in different agro-climatic zones. So, along with seed yield/plant, number of pods/plant and 100-seed weight should be considered for improving seed yield. These present findings are in accordance with previous findings of Kamannavar *et al.*, (2016); Vinod *et al.*, (2017); Kuralarasan *et al.*, (2018); Srividya *et al.*, (2018).

Table 5: Percent contribution of ten morpho-agronomic traits to genetic divergence.

Sr. No.	Characters	Rank	Per cent contribution (%)
1.	Days to 50% flowering	25	1.51
2.	Days to maturity	30	1.81
3.	Plant height (cm)	33	2.00
4.	No. of branches/plant	16	0.97
5.	No. of clusters/plant	7	0.42
6.	No. of pods/plant	429	25.95
7.	Pod length (cm)	23	1.39
8.	No. of seeds/pod	9	0.54
9.	100-seed weight (g)	98	5.93
10.	Seed yield/plant (g)	983	59.47
	Total	**1653**	**100**

CONCLUSION

The current investigation on variability and genetic diversity study in 58 urdbean genotypes revealed that there was ample variation in the material used for study. There were narrow differences between PCV and GCV in days to 50% flowering, days to maturity and plant height indicating lesser environmental influence on these characters. The fifty-eight genotypes were grouped into eight clusters based on D^2 statistics and non-hierarchical Euclidean cluster analysis implying presence of high degree of genetic diversity among them. Highest inter-cluster distance was observed between cluster VI and VII, whereas lowest in between cluster IV and VI. So, selection of genotypes from diversely related clusters with respect to maximum inter-cluster distance can give rise to better transgressive recombinants in the follow-up generations.

FUTURE SCOPE

The present findings based on genetic parameters and D^2 statistics paved the way for selection of elite germplasm lines with potential genotypic worth for yield and yield contributing traits. The selected test genotypes would serve as better parent materials for recombination breeding in urdbean.

Acknowledgement: The authors are highly thankful to the Department of Plant Breeding & Genetics, College of Agriculture, OUAT, Bhubaneswar for providing the plant materials for the present study.

Conflict of Interests. The authors declare that there is no conflict of interests.

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How to cite this article: Barik, B.R., Lenka, D., Agarwal, A.K., Mishra, A., Nayak, G. and Tripathy, S.K. (2021). Genetic Variation and Extent of Genetic Diversity in Urdbean [*Vigna mungo* (L.) Hepper]. *Biological Forum – An International Journal, 13*(3a): 556-561.