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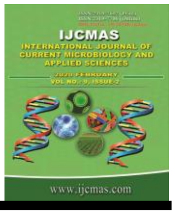

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Genetic Variability, Character Association and Divergence Study in Urdbean [*Vigna mungo* (L). Hepper]

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ABSTRACT

Urdbean is an important climate resilient pulse crop with excellent nutritional profile grown extensively in Indian subcontinent. The present investigation was conducted to study the genetic variability, association of the characters and diversity among 51 released varieties and advance breeding lines of urdbean considering yield and yield attributing traits. The experiment was conducted during *kharif* season of 2017 and 2018 in Randomized Block design maintaining two replications. Observation was recorded regarding nine yield and yield attributing traits for determining genetic variability, association of the characters and divergence among the tested genotypes. Significant variation was observed in terms of all the quantitative characters. Selection for the characters *viz*. plant height, branches plant^{-1}, no. of pod plant^{-1}, no. of seed pod^{-1} and 100 seed weight would be effective for improvement of seed yield in these populations. Cluster analysis divided the population into ten clusters and indicated a considerable amount of divergence within and between the clusters with detection of diverse parents for future breeding programme. Presence of significant genetic variability and diversity among the tested genotypes of urdbean would be conducive for obtaining superior progenies in future breeding programme.

Keywords

Genetic variability, Heritability, Correlation, Diversity, Urdbean

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Introduction

Urdbean (*Vigna mungo* (L). Hepper) is a self pollinated diploid grain legume (2n=2x=22) belongs to the Leguminaceae family with a genome size of 560 Mb (Arumuganathan and Earle, 1991). It is an important short duration pulse crop mainly grown in South Asian regions in different seasons under rainfed based agro-ecosystems (Gupta *et al.*, 2001) and now also started to grow in the Southern United States, West Indies, Japan and other tropics and subtropics (Delic *et al*., 2009). In India, urdbean is cultivated in an area of 3.06 million hectares with an average productivity of 555 kg ha^{-1} and production of 1.70 million tonnes (Annoymous, 2018). Being a short duration legume it can fit well with any cropping system and enrich soil fertility status for fallow crop. Despite of immense potential, the productivity of this crop in India is very low due to various constraints like non-availability of quality seed of high yielding varieties, pre-harvest sprouting, water logging and other abiotic and several biotic stresses. Thus, the crop requires due attention to increase its production and productivity.

The knowledge of nature and magnitude of correlation for characters of economic importance and cause and effects of relationship of yield and yield components for the available genotypes are of utmost essential which, helps in planning the future breeding programme for genetic improvement of any crop species (Reni *et al*., 2013; Panigrahi *et al*., 2014). Narrow genetic diversity is the main bottleneck for improving urdbean. Therefore, choice of diverse parents for hybridization is one of the important considerations for creating new genetic variability in this crop. Furthermore, monitoring the genetic variability within the gene pool of elite breeding material could make crop improvement more efficient by the directed accumulation of favoured alleles (Kanimozhi *et al*., 2009). Keeping these in the backdrop, the present study aimed to investigate the genetic variability, character association and divergence among 51 urdbean genotypes in terms of yield and yield attributing characters for identifying the important traits as well as diverse parents to be exploited for future breeding programme.

Materials and Methods

The present investigation was carried out during the *kharif* season of 2017 and 2018 at District Seed Farm (21.5^0 N latitude, 85^0 E longitude and altitude of 11.7 m above the Mean Sea Level), Bidhan Chandra Krishi Viswavidyalaya, Kalyani, Nadia, West Bengal. The soil of the experimental field at new alluvial zone is alluvial and sandy loam in texture having good water holding capacity (WHC), medium fertility status and neutral in reaction. Fifty one genotypes of urdbean including two checks (Sekhar-3, Uttara) collected from All India Co-ordinated Research Project on urdbean and other pulses (MULLaRP) were line sown following proper plant geometry with a row to row spacing of 40 cm × 10 cm between row to row and plant to plant respectively. The experiment was conducted in Randomized Complete Block Design (RCBD) with 2 replications. Standard package of practices were followed to raise the crop. Observation on various yield attributing traits as well as yield *viz*. days to 50% flowering, Plant height (cm), number of primary branches plant-^{1}, number of pods plant^{-1}, number of seeds pod^{-1}, pod length (cm), days to maturity, 100 seed weight (g) and seed yield plant^{-1} (g) were recorded considering five competitive randomly selected plants from each replications.

The pooled experimental data of two years (2017 and 18) were used for statistical analysis by using MS EXCEL and OPSTAT online software. The total variations among genotypes for different characters were tested for significance by 'F' test using analysis of variance technique, to find out the 'F' values from the table (Fisher and Yates, 1953). Phenotypic (σ^2p) and genotypic variance (σ^2g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) were estimated using standard procedure (Singh and Chaudhary, 1995). Heritability was calculated according to Singh and Chaudhary, 1995; Genetic advance was estimated by the formula described by Allard (1960) and Correlation coefficient was calculated by the formula suggested by Johnson *et al*., (1955) and Al. Jibouri *et al*., (1958). Path coefficient analysis was carried out according to Dewey and Lu (1959). The analysis of genetic divergence was done using

Mahalonobis (1936) D^2 statistics. The genotypes were grouped into different clusters, inter and intra cluster distances and mean performances of characters were also computed.

Results and Discussion

Frequency distributions for the traits were enumerated to group the cultivars into different categories (Figure 1). It was observed that 35 % of the genotypes were flowered within 38-42 days while, only 14% genotypes were identified as late flowering genotype and flowered within 46-50 days. Regarding pods plant^{-1} it was detected that 61% genotypes having no. of pods ranged between 8.5-23.5 whereas, only 8 % genotypes were having pods plant^{-1} more than 38 to 54. Furthermore, only 6% genotypes were having pod length of up to 6.55 cm, whereas, around 76% genotypes having pod length between 3.95-5.25cm. Among the tested genotypes only 4% of the genotypes matured beyond 82 days to 87 days. Regarding seed index, it was revealed that around 96 % of the genotypes having 100 seed weight of up to 4.4 g, whereas, only 6% genotypes were having bold seed with size ranged from 4.4-7.3 g. Finally, regarding yield plant^{-1} it was detected that only 4 % genotype yielded more than 11.81 g to 16.81 g.

The estimation of PCV (Table 1) ranged from 3.19 % for days to maturity to 50.08% in yield plant^{-1}, whereas for GCV it was 2.73 % to 47.72 % for the said characters respectively. The estimates of genotypic and phenotypic coefficient of variation (GCV and PCV) were high (>20%) for branches plant^{-1}, pod plant^{-1}, and for yield plant^{-1}. On the contrary, moderate GCV and PCV (10-20%) was observed in case of plant height, seeds pod^{-1} and for pod length. Characters like days to 50% flowering, branches plant^{-1}, pods plant^{-1} and 100 seed weight exhibited low difference between PCV and GCV thus confirmed that there was very less effect of environment with greater role of genetic factors for controlling these traits. Results were in conformity with the reports of Priya *et al.*, (2018) for PCV and GCV in case of days to 50 % flowering and no. of branches plant^{-1}, Gowsalya *et al.*, (2016) for no. of pods plant^{-1} and Kumar *et al.*, (2015) for 100 seed weight. Moreover, no. of branches plant^{-1}, no. of pods plant^{-1} and seed yield plant^{-1} showed presence of high heritability coupled with high GA as % of mean which indicated that there was preponderance of additive gene action governing these traits. Selection would be rewarding for improving these traits. The present study corroborated with the findings of Kanimoli *et al.*, (2013) for heritability and GA as % of mean in case of no. of branches plant^{-1}, Bandi *et al.*, (2018) in case of no. of pods plant^{-1} and Gowsalya *et al.*, (2016) for seed yield plant^{-1}. Whereas, the presence of high heritability with moderate to low GA as % of mean for days to 50 % flowering, no. of seeds pod^{-1}, days to maturity and 100 seed weight indicated the influence of non-additive gene action which indicates epistasis, dominance and genotypic and environmental interaction hence their response to selection would be poor (Usharani and Kumar, 2016). Exhibition of moderate heritability was the effects of significant influence of environments towards this character and the observation was earlier confirmed by Punia *et al.*, (2014). The results are in accordance with the findings of Toppo *et al.*, (2019) in urdbean, Das *et al.*, (2007) in greengram, Arshad *et al.*, (2002) in chickpea and Malik *et al.*, (2014) in soybean.

In the present study it was observed that for all the traits the genotypic correlation coefficient was higher than the phenotypic correlation coefficient thus confirmed less influence of environments towards influencing the expression of any characters (Figure 2). It was observed that at genotypic level, yield plant^{-1} exhibited significant positive relationship with plant height, no. of branches plant^{-1}, no. of pods plant^{-1}, no. of seeds pod^{-1} and 100 seed weight. At phenotypic level all these characters revealed significant positive correlation with yield except plant height thus confirmed the importance of selection of superior genotypes based on these characters would be meaningful for improving urdbean yield. Similar results were reported by Bharti *et al.*, (2014); Patidar *et al.*, (2017) and Suryawanshi *et al.*, (2018).

Table.1 Genetic parameters of nine yield and yield attributing traits in 51 genotypes of urdbean during *kharif* season of 2017 and 2018 (pooled)

Parameters	Mean	Range	GCV	PCV	Heritability	Genetic advance as % of mean
Days to 50% flowering	42.86	38-48.5	5.25	6.01	76.2	9.44
Plant height (cm)	46.55	29.6-73.65	17.25	19.6	77.4	31.25
Branches plant^{-1}	2.297	1.1-4.11	40.54	40.82	98.6	83.14
Pods plant^{-1}	21.28	8.5-47	40.48	41.7	94.2	80.95
Seeds pod^{-1}	6.15	4.5-8	10.86	14.55	55.7	16.75
Pod length (cm)	4.47	2.65-5.6	13.91	14.35	93.9	27.77
Days to maturity	76.55	71.5-82.5	2.73	3.19	73	4.80
100 seed weight (g)	4.14	3.74-4.61	4.62	4.73	95.4	9.42
Yield plant^{-1} (g)	5.03	1.81-12.98	47.72	50.08	90.8	93.59

Table.2 Genotypic path coefficient analysis of nine yield attributing traits in 51 genotypes of urdbean during *kharif* season of 2017 and 2018 (pooled)

	Days to 50% flowering	Plant height (cm)	Branches plant^{-1}	Pods plant^{-1}	Seeds pod^{-1}	Pod length (cm)	Days to maturity	100 seed weight (g)	Yield plant^{-1} (g)
Days to 50% flowering	-0.075	-0.003	0.001	0.027	-0.039	-0.002	0.063	0.002	-0.026
Plant height (cm)	-0.022	-0.011	0.001	0.148	0.138	-0.008	0.014	0.035	0.294*
Branches plant^{-1}	-0.004	0.003	0.013	0.323	-0.011	0.001	0.009	-0.012	0.318**
Pods plant^{-1}	-0.002	-0.002	0.005	0.827	0.062	-0.003	0.01	0.046	0.943**
Seeds pod^{-1}	0.009	-0.005	0.002	0.165	0.31	-0.014	-0.014	0.028	0.479**
Pod length (cm)	-0.008	-0.004	0.004	0.098	0.187	-0.023	0.006	0.016	0.272
Days to maturity	-0.066	-0.002	0.002	0.115	-0.06	-0.002	0.071	-0.014	0.044
100 seed weight (g)	-0.001	-0.003	-0.001	0.302	0.07	-0.003	-0.008	0.125	0.481**

Residual: 0.0642

Figure.1 Percent frequency distribution for nine yield and yield attributing traits in 51 genotypes of urdbean during *kharif* season of 2017 and 2018 (pooled)

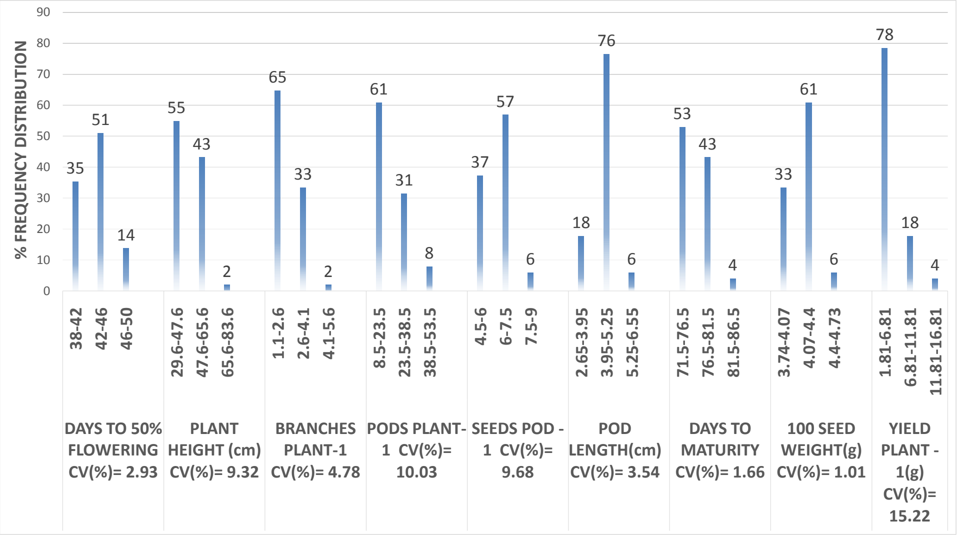
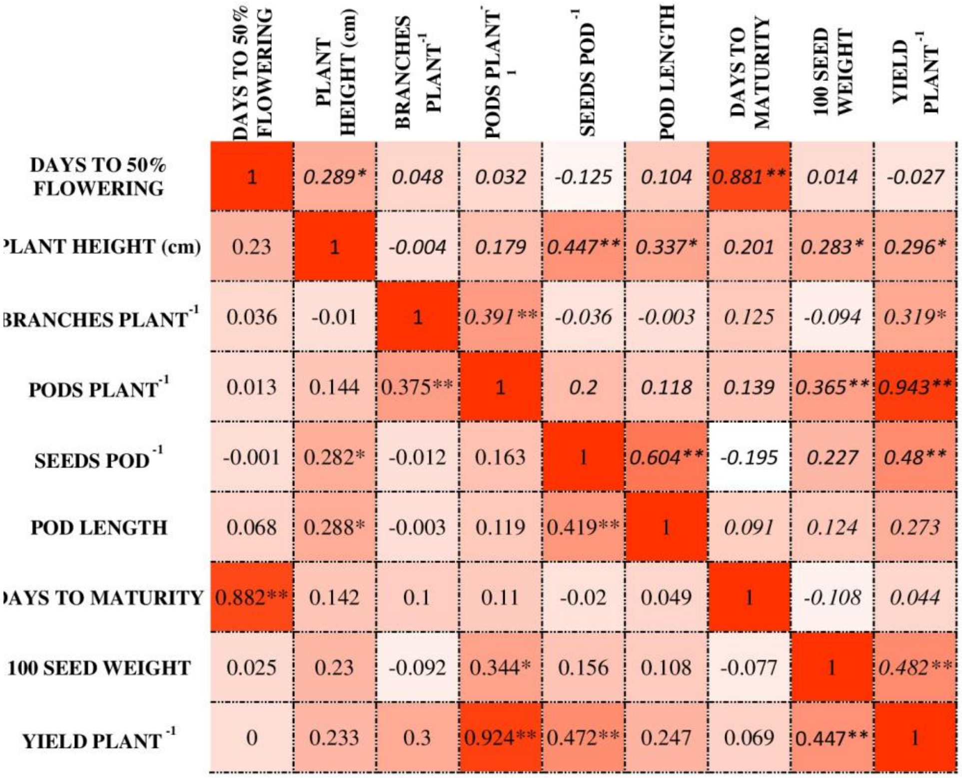


Figure.2 Genotypic (italics) and phenotypic correlations for yield and yield attributing traits in 51 genotypes of urdbean during *kharif* season of 2017 and 2018 (pooled)



	DAYS TO 50% FLOWERING	PLANT HEIGHT (cm)	BRANCHES PLANT^{-1}	PODS PLANT^{-1}	SEEDS POD^{-1}	POD LENGTH	DAYS TO MATURITY	100 SEED WEIGHT	YIELD PLANT^{-1}
DAYS TO 50% FLOWERING	1	_0.289*_	_0.048_	_0.032_	_-0.125_	_0.104_	_0.881**_	_0.014_	_-0.027_
LANT HEIGHT (cm)	0.23	1	_-0.004_	_0.179_	_0.447**_	_0.337*_	_0.201_	_0.283*_	_0.296*_
RANCHES PLANT^{-1}	0.036	-0.01	1	_0.391**_	_-0.036_	_-0.003_	_0.125_	_-0.094_	_0.319*_
PODS PLANT^{-1}	0.013	0.144	0.375**	1	_0.2_	_0.118_	_0.139_	_0.365**_	_0.943**_
SEEDS POD^{-1}	-0.001	0.282*	-0.012	0.163	1	_0.604**_	_-0.195_	_0.227_	_0.48**_
POD LENGTH	0.068	0.288*	-0.003	0.119	0.419**	1	_0.091_	_0.124_	_0.273_
AYS TO MATURITY	0.882**	0.142	0.1	0.11	-0.02	0.049	1	_-0.108_	_0.044_
100 SEED WEIGHT	0.025	0.23	-0.092	0.344*	0.156	0.108	-0.077	1	_0.482**_
YIELD PLANT^{-1}	0	0.233	0.3	0.924**	0.472**	0.247	0.069	0.447**	1

Figure.3 Dendrogram representing clustering of 51 urdbean genotypes based on Squared Euclidian distance matrix

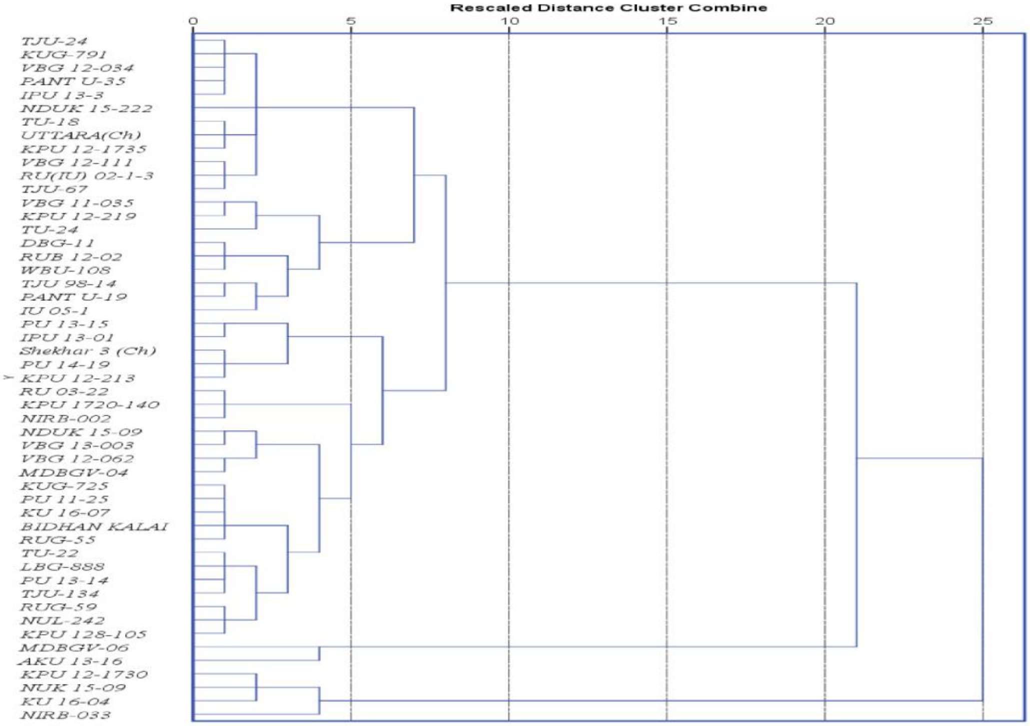
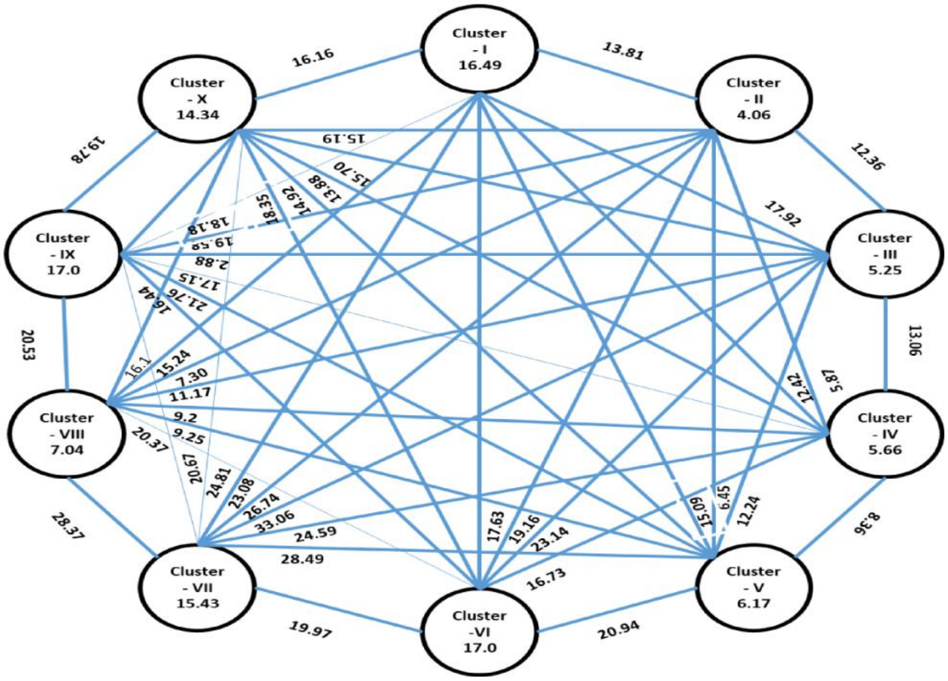


Figure.4 Intra and Inter-cluster distances of the 51 urdbean genotypes



The knowledge regarding association of yield attributing traits and their relative contribution shown by path analysis has practical significance in selection as path analysis splits the interrelationship between two characters in to direct and indirect effects (Verma *et al.*, 2015). Perusal of the data regarding genotypic path analysis revealed that no of pods plant^{-1}, 100 seed weight, seeds pod^{-1}, branches plant^{-1} and plant height exerted significant high positive direct effect on yield (Table 2). The residual effect in genotypic path coefficient (0.064) indicated that the nine characters included in this study explain the moderate percentage of variation in grain yield in this population. Similar findings were reported by Sohel *et al.,* (2016), Priya *et al.,* (2018), and Suryawanshi *et al.,* (2018).

Genetic improvement of any crop mainly depends upon the amount of genetic variability present in the population. Information on genetic diversity within and among closely related crop germplasm is essential for rational use of genetic resources as a parent for obtaining higher amount of heterotic expression in F_1s and broad spectrum of variability in subsequent segregating generations. In order to assess the genetic diversity among 51 genotypes of urdbean, D^2 statistic was used following the procedure given by Rao (1952). Since all the traits under study were correlated, they were transformed into uncorrelated linear combination through pivotal condensation method. All the genotypes of urdbean under study were distributed into 10 clusters such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters (Figure 3).

In the present study it was observed that cluster IX (12 genotypes) comprised of maximum number of genotypes followed by cluster I with 10 genotypes, cluster VI with 9 genotypes, cluster X with 6 genotypes whereas Cluster VII and VIII comprised of 3 genotypes each and cluster II, III, IV, V comprised of 2 genotypes each. Tendency to form clusters ignoring the geographical boundaries showed the regional isolation was not the only factor contributing to diversity in natural population (Das and Kumar, 2016). Formation of clusters among the genotypes of common geographic origin may be due to their parentage, developmental traits, past history of selection and different out-crossing rates (Arnold *et al*., 1996). Therefore, the kind of genetic diversity found among the genotypes belonging to same geographic origin might be due to difference in adoption, selection criteria, selection pressure and environmental conditions (Vivekananda and Subramanian, 1993).

The present study also revealed that the average intra cluster distance varied from 4.06 in cluster II to 17.002 in cluster VI and IX (Figure 4). The maximum intra cluster distance was observed between cluster VI and III (33.06) followed by cluster VII and V (28.491), cluster VIII and VII (28.37), cluster VII and II (26.74), and so on. This indicated considerable amount of divergence within and between clusters. Such highly divergent, high performing genotypes would be of great use in recombination breeding programme in order to get high heterotic recombinants. Keeping this in view, it could be concluded that genotypes from Cluster VI and III might be used as parents in the hybridization programme to generate breeding material with high diversity to get encouraging results. The results of this investigation collaborated with that of Kumar *et al.,* (2014).

From the present study it can be concluded that adequate genetic variability was present in the tested urdbean genotypes. For improving grain yield emphasis should be given towards selection based on plant height, branches plant^{-1}, no. of pod plant^{-1}, no. of seed pod^{-1} and 100 seed weight will be effective. Crossing involving genotypes from diverse group *viz*. VBG 12-111, RU(IU) 02-1-3 from cluster III with genotypes *viz*. Uttara, KPU 12-1730, KU 16-07, IU 05-1, RUG-55 etc. from cluster VI may produce wide spectrum of segregants and create opportunity for getting desirable transgressive segregants in future urdben breeding programme.

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