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Genetic diversity study for grain yield and its components in urdbean (*Vigna mungo* L. Hepper) using different clustering methods

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ABSTRACT

In the present study, 66 urdbean genotypes were evaluated for various agro-morphological traits during rainy season (kharif) 2012 at IIPR, Kanpur to assess the level of genetic diversity among the genotypes. Based on hierarchical average linkage clustering method and D^2 statistic the genotypes were grouped into seven clusters having significant inter-cluster distances. Shannon-Weaver's diversity index (H) and Simpson's index (1/D) was used to assess the phenotypic diversity for all eight yield attributes. The H index revealed moderate diversity for most of the traits. The average Shannon – Weaver's diversity index for all traits in whole population was 0.54 with the lowest value of 0.49 for biological yield per plant to highest value for grain yield per plant and pods per plant (0.58). The simple correlation coefficients showed significant positive correlation of grain yield per plant with plant height (0.44), clusters per plant (0.65**), pods per plant (0.77**) and biological yield per plant (0.70**). Based on the inter cluster D^2 value, genotypes with high inter cluster distances could be used in hybridization programme to generate diversity in breeding programme.**

Key words: Correlation, Cluster analysis, D^2 statistics, Shannon-Weaver diversity index, Urdbean, Yield and attributes

Urdbean (*Vigna mungo* L. Hepper 2n=2x=22), commonly known as black gram is an important pulse crop, widely cultivated and consumed throughout India (Singh and Ahlawat, 2005). It is the fourth most important pulse crop after chickpea, pigeon pea and green gram in terms of acreage and production in India. It is a short duration crop, cultivated throughout the year i.e. rainy season (kharif crop) and in spring / summer (rabi crop) in different parts of the country. In the year 2012-13, the total area under urdbean was 3.19 mha with 1.9 m tonnes of production and 595 kg/ha productivity (Department of Agriculture & Cooperation estimates, *Source:* agricoop.nic.in/ and AICRP on MULLaRP annual report*)*. The major urdbean producing states are Andhra Pradesh, Maharashtra, Madhya Pradesh, Uttar Pradesh and Tamil Nadu. Although in India urdbean is grown under a considerably large area, the average productivity is still very low as compared to other pulses. Improving productivity therefore is the major objective in any breeding programme of urdbean.

The availability of genetic diversity is an important prerequisite in crop improvement programme. However, the low genetic diversity remains one of the main bottlenecks for improving productivity in urdbean. Morphological, agronomic and physiological traits are conventionally used for estimating genetic diversity. The identification of diverse parents will be useful in combining desirable traits through recombination breeding. There are several methods available to assess the genetic divergence among genotypes. Multivariate analysis by means of Mahalanobis D^2 statistic (Mahalanobis 1936) is a powerful tool in quantifying the degree of divergence at genotypic level. Several workers have used this method to quantify the degree of divergence based on morphological traits in different leguminous crops (Khare and Singh 1992; Koul et al. 1997). Various clustering methods (hierarchical and non-hierarchical) are also used to group genotypes into different groups based on similarities/dissimilarities among members within and between groups. Also diversity analysis using Shannon-Weaver diversity index (H) and Simpson's index (D) based upon different traits represents trait diversity in the whole population or genotypes belonging to each cluster. The main objective of this study was to assess genetic diversity for various agro-morphological traits in a set of 66 urdbean genotypes and determine correlation among these traits.

MATERIALS AND METHODS

The experimental material for the present study comprised of 66 genotypes representing advance breeding lines, selections from local germplasm and released varieties having variation for various agro-morphological traits. The trial was conducted at Indian Institute of Pulses Research (IIPR), Kanpur during 2012 kharif season. The trial was sown in 3 compact blocks, with 22 entries in each block. The plot size was 5 rows of 3m length with the between and within row distance at 30 and 10cm, respectively. The recommended agronomic package of practices was followed to raise a healthy crop.

Data were collected for days to first heading, plant height, number of clusters/plant, number of pods / plant, seeds/

pod, biological yield/plant, grain yield /plant and grain yield/ plot. Data were recorded on five randomly selected plants for days to first flower, plant height, number of clusters per plant, number of pods per plant, number of pods per cluster, number of seeds per pod, seed yield per plant (g) and grain yield on plot basis. The average of five observations was used for analysis. The data were analysed to calculate descriptive statistics and coefficient of variation (CV) for all the traits. The data were subjected to hierarchical cluster analysis following average linkage techniques and Mahalanobis D^2 statistics using SAS statistical software version 9.3. At the same time Shannon-Weaver diversity index (H) and Simpson's index (D) were used to assess the phenotypic diversity among the accessions for individual traits on whole population and of different clusters (Shannon and Weaver 1963; Galwey 1995). The data were used to calculate simple correlation coefficient among traits (Snedecor and Cochran 1967) and its significance to measure the association among various traits.

RESULTS AND DISCUSSION

The results (Table 1) revealed comparatively high CV for most of traits except number of seeds per pod (7.60%) and days to first flower (11.9%). The high coefficient of variation was recorded for grain yield per plant (40.5%) followed by grain yield per plot (37%), biological yield per plant (38.9%), number of pods per plant (30.4%) and number of clusters per plant (29.2%). The results showed considerable diversity in the parental materials, especially for grain yield and its attributes. A wide range of values was observed for grain yield (100-761 gm/plot), number of pods per plant (13.9-63.4), biological yield/plant (6-45.8 gm), plant height (28.4-72.1) and number of pods / plant (13.9-63.4). The phenotypic variation on various agro-morphological traits has also been reported earlier by a number of workers (Chauhan et al. 2008; Shanthi et al. 2006) in urdbean and in mungbean (Appalaswamy and Reddy 2004); in cluster bean (Henry and Mathur 2007).

The use of genetically diverse parents in the crossing programme will be helpful in generating desirable recombinants in segregating generations for making further improvement. Based on hierarchical cluster analysis and D^2 statistics genotypes were grouped into seven clusters in such a way that within cluster diversity is minimized and between clusters diversity is maximized. The genotypes belonging to different clusters are given in Table 2.

The graphical representation of genotypes belonging to different clusters based on hierarchical average linkage method is given in Fig. 1. The clustering pattern revealed considerable differences between the groups. It was also observed that some of the local genotypes collected from similar geographical region fall into same cluster like Jalpaiguri selection and Jalpaiguri local1in cluster II; Barabanki local and Vigna selection (cluster III). Genotypes developed in the breeding programme at Indian Institute of Pulses Research (IPU nos.) were spread over different clusters which may be due to the fact that diverse parental materials from different sources were utilized in the hybridization programme to generate these advance breeding lines. However, some of the genotypes within a cluster were also from different geographical origin indicating that the geographical diversity is not necessarily related to genetic diversity. The similar finding on genetic diversity has been reported earlier (Verma et al. 1997; Dikshit and Swain 2002 and Umadevi 2007) as well.

Table 1. Mean, standard error, standard deviation, range and coefficient of variation of different traits

S. No.	Traits	Mean ± SE	Standard deviation	Range		Coefficient of Variation (CV %)
				Minimum	Maximum	
1	Days to first flower	37.9±0.55	4.5	30.0	51.0	11.9
2	Plant height (cm)	47.5±1.07	8.7	28.4	72.1	18.3
3	No. of clusters/plant	13.9±0.50	4.0	5.2	24.2	29.2
4	No. of pods / plant	32.0±1.2	9.7	13.9	63.4	30.4
5	Seeds/pod	7.1±0.06	0.54	5.7	10.1	7.6
6	Biological yield/plant (g)	18.1±0.87	7.0	6.0	45.8	38.9
7	Grain yield /plant (g)	6.4±0.32	2.6	2.2	16.0	40.5
8	Grain yield/plot (g)	452.5±20.6	167.3	100.0	761.0	37.0

Table 2. Clustering pattern of barley genotypes evaluated

Cluster No.	Number of genotypes	Genotypes
I	15	PDU103, VBN4, IPU94-1, YAKUBPUR EARLY, IPU99-31, IPU99-167, IPU12-20, IPU12-15, Bold seeded, IPU12-25, Shekhar2, IPU07-03, IPU12-12, IPU12-17, VB04-008
II	08	CO5, LBG20, VBN1, Jalpaiguri selection, Jalpaiguri local1, TU94-2, ADT3, DU1
III	04	Barabanki local, COBG653, *Vigna* selection, LBG17
IV	12	Bara Nabada, RTM10, YAKUBPUR2, IPU12-23, IPU12-09, IPU12-16, IPU12-10, PDU38, VBN7, SPS5, TU17-4, UH85-5
V	07	PU40, IPU33, UH04-4, BLB67-2, IPU12-18, IPU12-24, MASH114
VI	07	STY2468, IPU06-1, WBC108, IPU12-13, IPU98/34-2, IPU12-19, IPU12-21
VII	13	IPU12-22, TROMBEY URD, NODAI URD, IPU12-14, SPS39, IPU12-11, KUG216, PU06-20, PU31, IPU12-26, IPU02-43, IPU2000-01, IPU02-33

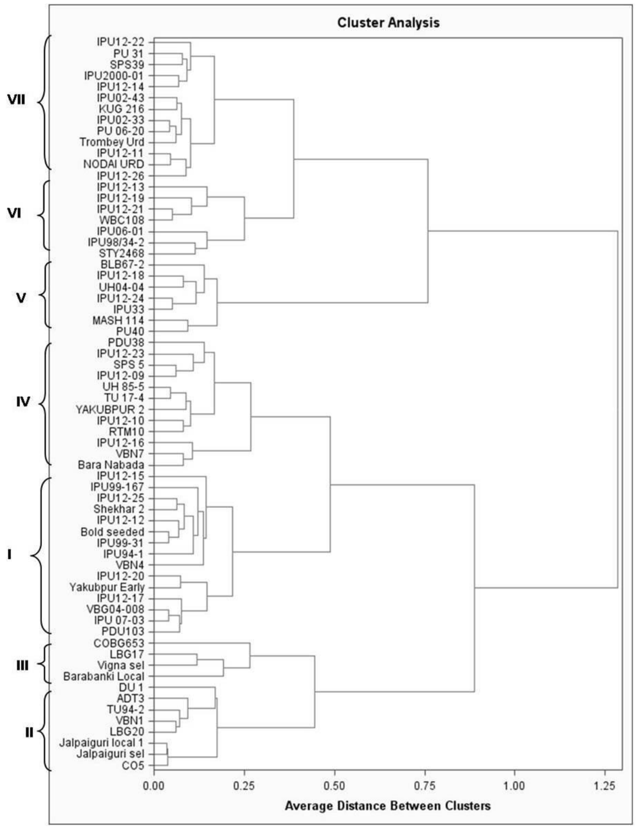

Figure 1. Clustering of urdbean genotypes based on average linkage clustering method

The mean and standard deviations of different clusters for each trait have been given in Table 3. The results showed that, cluster-V has entries with highest grain yield per plot followed by entries belonging to cluster-VI, VII and I. In case of grain yield / plant, cluster-III had the best performing genotypes followed by cluster-IV and II. While in case days to flower entries in cluster VI was earliest followed by cluster I and for biological yield / plant highest yielding genotypes fall into cluster III and lowest yielding were from cluster IV.

The clustering pattern revealed that the maximum number of genotypes were grouped in cluster I (15) followed by Cluster VII (13), IV (12), II (8), V & VI (7 each) and III (4). The analysis clearly indicates that a wide array of variability exists in the genetic materials which can be utilized in hybridization programme to diversify the breeding materials. The average inter cluster distances (D^2 statistics) between seven clusters groups are presented in Table 4. The maximum inter cluster distance was observed in between cluster III and V (735.8) followed by cluster II and V (512.4), III and VI (494.3), while lowest inter cluster distance was observed between cluster I and VII (18.6) followed by cluster VI and VII (18.7). The genotypes from those clusters showing high inter cluster differences, could be utilized in the hybridization programme as diverse parents are likely to produce wider genetic variability among the progenies of the segregating generations (Arunachalam and Bandyopadhyay 1984). The minimum inter cluster distance between clusters I and VII and cluster VI and VII reveals that the genotypes of these clusters were relatively closer. Each genotype within a cluster centre was closest to the cluster mean. There are genotypes superior for an individual trait which belong to different clusters indicating that no single cluster contained genotypes with all the desirable characters. This implies that none of the clusters possessed a genotype which could be designated as superior for all traits as such. However, the genotypes superior for specific characters may be selected for utilization in recombination breeding programme. The selected genotypes from diverse clusters may be utilized in breeding programme depending upon breeding objectives. The study on genetic diversity in urdbean has also been reported by number of workers earlier (Parmeswaappa and Patil 1994; Chauhan et al 2008).

Table 4. Mahalanobis inter cluster distances (D^2 statistic) between seven clusters in urdbean

Cluster	II	III	IV	V	VI	VII
I	92.3	197.8	26.5	173.0	68.2	18.6
II		22.5	21.9	512.4	314.8	186.8
III			83.0	735.8	494.3	330.3
IV				327.8	175.2	84.1
V					25.9	81.4
VI						18.7

To measure the diversity index of different traits, Shannon diversity index and Simpson index were calculated and are given in Table 5. The results indicated moderate overall Shannon-Weaver diversity index (H) and Simpson's index (D) for most traits except biological yield per plant and seeds per pod. The average H for the whole population was 0.54 with a minimum of 0.49 for biological yield per plant to highest for grain yield per plant and pods per plant (0.58). Among clusters, H was higher for plant height, seeds per pod, grain yield/plot in cluster I; number of clusters per plant, pods per plant, grain

Table 3. Means and standard deviation of within clusters for different traits

Traits	I	II	III	IV	V	VI	VII
Days to first flower	36.8±3.9	40.0±5.5	38.5±1.7	37.3±5.4	37.4±5.6	35.7±2.3	40.0±4.3
Plant height (cm)	44.2±7.9	52.7±9.7	50.0±5.5	46.0±9.5	49.6±9.8	44.8±9.4	49.3±7.2
No. of clusters/plant	12.9±3.3	14.0±5.6	16.0±7.3	12.7±3.4	14.4±3.2	16.3±5.0	14.0±3.1
No. of pods / plant	29.9±8.5	30.7±13.6	40.7±15.3	30.7±9.0	31.9±8.0	32.9±11.6	33.3±7.4
Seeds/pod	6.9±0.3	7.12±0.7	7.4±0.7	7.4±0.9	7.3±0.4	6.9±0.3	7.1±0.3
Biological yield/plant (g)	18.9±8.2	19.5±7.7	26.7±12.8	16.2±5.6	16.6±6.1	16.5±5.3	17.1±4.3
Grain yield /plant (g)	5.6± 1.4	6.5±3.5	9.1±4.8	6.5±3.1	6.4±2.5	6.0±2.5	6.4±1.7
Grain yield/plot (g)	448.5±25.6	238.9±14.6	142.0±30.0	341.2±30.0	741.1±19.2	622.7±30.4	539.7±19.1

yield per plant in cluster II; seeds per pod in cluster III; plant height, number of clusters per plant and grain yield per plot in cluster IV; days to flower, plant height, biological yield per plant and grain yield per plant in cluster V; plant height in cluster VI and pods per plant, grain yield per plant and grain yield per plot in cluster VII.

The overall average D was 0.68 with minimum for biological yield per plant (0.63) and maximum for clusters per plant, pods per plant and grain yield per plot (0.72). Simpson's index in each cluster was also compared with that of the whole population. The index among clusters were more or less in proportion to that of the whole collection, the values however, were little larger for most of the qualitative traits in clusters. The index D was higher for plant height, grain yield per plot in cluster I; number of cluster per plant, pods per plant, grain yield per plant in cluster II; seeds per pod in cluster III; plant height, number of cluster per plant, grain yield per plot in cluster IV; for all traits except number of clusters per plant in cluster V; for all traits except seeds per pod in cluster VI; pods per plant, number of clusters per plant, grain yield per plant and grain yield per plot in cluster VII. The similar study on genetic diversity using Shannon Weaver diversity index has been reported in mungbean (Bisht et al 1998) and chickpea (Upadhyaya 2003 and Upadhyaya et al. 2002).

To understand the nature of correlation between traits, data were analysed to determine the simple correlation coefficients among these traits (Table 6). The results showed significant positive correlation between grain yield per plant with plant height (0.44**), number of clusters per plant (0.65**), pods per plant (0.77**) and biological yield per plant (0.70). While significant positive correlation was found between plant height with days to first flower (0.43**), number of cluster per plant (0.35**), number of pods per plant (0.28*) and biological yield per plant (0.46**); between number of clusters per plant with number of pods per plant (0.81**), biological yield per plant (0.57**); between number of pods per plant with biological yield per plant (0.67**). This indicates that selection of genotypes with high biomass will be helpful in indirectly selecting genotypes with high yield and tall plant will have more clusters per plant, more pods and high biological yield. The similar findings has also been reported by Shanmugasundaram and Sreerangaswamy (1995) for seed yield per plant with pods per plant and clusters per plant while Pooran Chand (1999) and Kingshlin and Vanniyarasan (2000) for seed yield per plant with seeds per pod and 100-seed weight and Srividhya etal. (2005) for seed yield/plant with pods/plant, c1usters/plant, seeds/pod, 100-seed weight and biomass.

The present study showed that, moderate level of variability exists in the material for most of the traits for exploiting and developing improved cultivars. The identification of suitable donors for different traits will help in the development of better variety. Cluster analysis clearly differentiated genotypes into major groups for various useful traits. Based on distance between genotypes of different clusters, contrasting parents may be used in the hybridization programme for generation of wider variability and selection of superior segregants in the breeding programme. Designing a crossing programme by identifying genotypes of interest from different clusters will make the breeding process more directional and effective. The correlation studies among traits will help in simultaneous improvement of various traits by selecting few traits.

Table 5. Shannon-Weaver diversity index (H) and Simpson's diversity index (D) for various traits in clusters and whole population

Traits	Shannon-Weaver diversity index (H)								Simpson diversity index (D)							
	Overall	I	II	III	IV	V	VI	VII	Overall	I	II	III	IV	V	VI	VII
Days to first flower	0.55	0.46	0.53	0.24	0.25	0.55	0.47	0.45	0.69	0.58	0.66	0.38	0.58	0.69	0.65	0.63
Plant height (cm)	0.54	0.58	0.55	0.45	0.58	0.55	0.55	0.55	0.68	0.72	0.69	0.63	0.72	0.69	0.69	0.69
No. of clusters /plant	0.57	0.39	0.60	0.24	0.58	0.30	0.28	0.45	0.72	0.67	0.75	0.38	0.72	0.49	0.69	0.72
No. of pods / plant	0.58	0.50	0.57	0.24	0.55	0.42	0.43	0.57	0.72	0.61	0.72	0.38	0.69	0.57	0.69	0.71
Seeds/pod	0.50	0.55	0.30	0.60	0.13	0.43	0.26	0.47	0.65	0.68	0.66	0.75	0.17	0.69	0.41	0.58
Biological yield /plant (g)	0.49	0.28	0.32	0.24	0.51	0.55	0.55	0.32	0.63	0.46	0.69	0.38	0.63	0.69	0.69	0.67
Grain yield /plant (g)	0.53	0.52	0.60	0.24	0.45	0.55	0.42	0.57	0.66	0.64	0.75	0.38	0.55	0.69	0.57	0.71
Grain yield/plot (g)	0.58	0.57	0.55	0.24	0.59	0.43	0.43	0.58	0.72	0.71	0.69	0.38	0.74	0.69	0.69	0.72
Average	0.54	0.48	0.50	0.31	0.45	0.47	0.42	0.49	0.68	0.63	0.70	0.45	0.60	0.65	0.64	0.68

Table 6. Correlation coefficient and their significance among various traits

Traits	Plant height (cm)	No. of clusters/ plant	No. of pods / plant	Seeds /pod	Biological yield/ plant (g)	Grain yield / plant (g)	Grain yield/plot (g)
Days to first flower	0.43**	0.09	0.05	0.08	0.13	0.13	-0.09
Plant height (cm)		0.35**	0.28*	0.08	0.46**	0.44**	-0.06
No. of clusters /plant			0.81**	-0.04	0.57**	0.65**	0.04
No. of pods / plant				0.13	0.67**	0.77**	-0.05
Seeds/pod					0.03	0.22	-0.09
Biological yield /plant (g)						0.70**	-0.22
Grain yield /plant (g)							-0.16

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