

Original Research Article

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Estimation of Genetic Diversity in Local Grown Urdbean [*Vigna mungo* (L.) Hepper] Genotypes

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ABSTRACT

Urdbean is the important pulse crops grown throughout India. It is consumed in the form of 'dal' (whole or split, husked and un-husked) or perched. It is used as nutritive fodder specially for milk animals also as green manuring crop. This study aims for estimation of genetic variability in local grown genotypes of urdbean. Its measures allelic richness, expected heterozygosity and percent polymorphic loci. Present investigation studied 50 local genotypes of urdbean evaluated in randomized block design with two replications in kharif-2020 at Botany Section Farm, College of Agriculture, Dhule (MS). All 50 lines were evaluated for different morphological and agronomical traits. Result showed high diversity for most of traits under observations. Combined analysis of variance revealed that mean sum of square due to genotypes for all characters were highly significant and indicate presence of ample variability among genotype. The D^2 values between all possible pairs of fifty genotypes studied for seed yield per plant ranged from 61.69 (LCU-32, LCU-42) to 3994.94 (LCU-4, LCU-25). The significant differences due to genotypes with high range in D^2 value clearly indicated the presence of adequate diversity among the genotypes studied. Among yield contributing components, the number of seeds per pod (41.63%) contributed maximum for divergence, followed by pod length (28.31%). However, the contribution of protein content (12.73%), seed shattering (7.76%), plant height (2.94%), seed yield per plant (2.29%) and 100 seed weight (1.71%) were moderate. So, this trait suggested important indices for selection of superior genotypes of Urdbean in breeding programs.

Keywords

Genetic Diversity,
Urdbean,
self-pollinated
leguminous crop

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Introduction

Urdbean is one of the important pulse crops grown throughout the country during rainy season. It is a self-pollinated leguminous crop which contains 24 % protein, 60 %

carbohydrate, 1.3 % fat, 3.2 % minerals, 0.9 % fiber, 154 mg calcium, 385 mg phosphorus, 9.1 mg iron, arginine 520 mg, lysine 170 mg and small amount of Vitamin-B complex. It also contains 0.37 g riboflavin and 0.42 mg thiamin in per 100 g of urdbean. Urdbean is a

highly priced pulse, very rich in phosphoric acid. India currently represents the largest producer of urdbean accounting for more than 70 per cent of the global production. India is followed by Myanmar and Pakistan in urdbean production. In India during *Kharif* 2020, it covers area is up by 38.7 per cent at 8.77 lakh ha. Maharashtra has 1.79 lakh ha area under cultivation of urdbean Production of urdbean increased from 17.71(2011) to 23.3(2019) tones in India. Yield is multidimensional trait that encompasses several different properties and is affected by numerous factors. The development of superior variety can be based on the magnitude of genetic variability in the base material and the extent of heritability for desirable characters.

To begin with any crop improvement programme, the information of genetic variability in genetic system of particular crop is sought as pre-requisite. Although increased seed yield is the ultimate aim of the plant breeders, seed yield is a product of interaction of many component traits, which influence it directly or indirectly. Therefore, variability and diversity existing within each component traits must be exploited by selection to realize seed yield. Assessment of genetic diversity is a basic step in any crop improvement programme.

Materials and Methods

The 50 genotypes of urdbean were evaluated in a Randomized Block Design (RBD) with two replications during kharif-2020, at a distance of 30 X 10 cm with two replications.

The divergence analysis was carried out by D^2 statistic of Mahalanobis (1936) as described by Rao (1952). Analysis of variance for the individual characters was worked out as per Randomized Block Design to test the significances among the genotypes. The characters exhibited significant differences

were only used for further analysis of D^2 statistic. The analysis of covariance for pairs of characters, based on plot averages was carried out.

Mahalanobis's generalized distance (D^2)

$$D^2 = \sum_{ij} \sum_{pp} \lambda_{ij} \delta_i \delta_j$$

Where

\square_{ij} = The reciprocal matrix to common dispersion matrix

\square_i = Difference between the mean values of the two populations for the i^{th} character. ($\mu_{i1} - \mu_{i2}$)

\square_j = Difference between the mean values of the two populations for the j^{th} character. ($\mu_{j1} - \mu_{j2}$)

μ = Vector of mean value

Results and Discussion

The present investigation undertaken with view to genetic diversity and correlation coefficient of fifty diverse genotypes in urdbean. The genetically diverse parents are known to produce high heterotic effects and consequently give desirable recombinants in the breeding material or wide spectrum of transgressive sergeants in segregating generations. Multivariate analysis (D^2 statistic) measures the genetic variability quantitatively among a set of genotypes. The fifty genotypes under study were therefore, assessed for genetic diversity for a set of twelve characters. The calculated D^2 values were ranged from 61.69 to 3994.94. The lowest value between the pair of genotypes LCU-32 and LCU-42 while, the highest between the genotypes LCU-4 and LCU-25. Cluster formation was done by following Tocher's method as

described by Rao (1952). The fifty genotypes were grouped into 11 clusters. The cluster I was the largest having 18 genotypes, followed by clusters II, IV and III with 14, 6 and 5 genotypes, respectively, while clusters V, VI, VII, VIII, IX, X and XI was solitary (Table.2, Fig.1 and Fig.2).

Consequently, breeding program should be from diverse parents selected for crossing from different clusters. Greater is the distance between two clusters, wider is the genetic diversity in the genotypes. The 60 genotypes grouped into 17 clusters was reported by Shanthi, *et al.*, (2006), 109 genotypes grouped into 11 clusters was reported by Kumar, *et al.*, (2014), 52 genotypes grouped into 10 clusters was reported by Geethanjali, *et al.*, (2015), 64 genotypes grouped into 12 clusters was reported by Hadimani, *et al.*, (2016), 22 genotypes grouped into 5 clusters was reported by Vyas, *et al.*, (2018) and 100 genotypes grouped into 14 clusters was reported by Punithavathy, *et al.*, (2020). Thus, their grouping suggested considerable diversity in the material under investigation. The genotypes viz., LCU-1, LCU-2, LCU-4, LCU-17, LCU-19, LCU-26 and LCU-30 were mono-genotypic, indicating wide diversity from the rest as well as from each other suggesting that this genotype may have entirely different genetic architecture from the others. Wide range of diversity was also reported by, Kamannavar, *et al.*, (2015), Shamim and Pandey (2018), Vidya, *et al.*, (2018), Bhareti, *et al.*, (2019), Jayashree, *et al.*, (2019) and Chandrakar, *et al.*, (2020).

The averages inter and intra-cluster D^2 values are presented in Table 3. The maximum inter-cluster distance was found between cluster IV and IX (60.474), followed by cluster IV and X (60.211), cluster IV and VI (54.934) and cluster VII and X (54.444) whereas, minimum inter-cluster distance was found between

cluster V and VI (15.746). Considering the intra-cluster distance, cluster III had maximum intra-cluster distance (21.650) followed by cluster IV (21.263), II (18.776) and I (16.784) whereas, intra-cluster distance was not found in the cluster V, VI, VII, VIII, IX, X and XI as they were solitary clusters (Fig.1 and Fig.2). The maximum intra-cluster distance was observed in the cluster III ($D^2=21.650$), followed by cluster IV ($D^2=21.263$), II ($D^2=18.776$) and I ($D^2=16.784$) suggesting that genotypes included in these cluster might have different genetic architecture. The monogenic clusters showed zero intra-cluster distance. Maximum inter-cluster distance was observed between cluster IV and IX ($D^2=60.474$) suggesting that, genotypes included in these clusters might had entirely different genetic architecture (Table.3 and Fig.2). These observations confirming the results of Shanthi, *et al.*, (2006), Kumar, *et al.*, (2014), Geethanjali, *et al.*, (2015), Hadimani, *et al.*, (2016), Vidya, *et al.*, (2018), Bhareti, *et al.*, (2019), Jayashree, *et al.*, (2019) and Punithavathy, *et al.*, (2020). The minimum inter cluster distance was observed between cluster V and VI ($D^2=15.746$), followed by cluster VI and VIII ($D^2=16.978$), V and IX ($D^2=17.722$) and between cluster V and XI ($D^2=20.084$). The lower D^2 value between the clusters in the above cluster pairs suggested that the genetic constitution of the genotypes in one cluster is in close proximity with genotypes in other cluster of the pair. The number of seeds per pod (41.63%) contributed maximum for divergence, followed by pod length (28.31%). However, the contribution of protein content (12.73%), seed shattering (7.76%), plant height (2.94%), seed yield per plant (2.29%) and 100 seed weight (1.71%) were moderate. The contribution of number of pods per plant (0.40%), number of primary branches per plant (0.35%), number of days to 50 per cent flowering (0.33%) and days to maturity (0.25%) were negligible (Table 5).

Table.1 Analysis of variance for twelve characters in urdbean

Sr. No.	Characters	Mean sum of squares		
		Replication (1)	Treatment (49)	Error (49)
1	Days to 50% flowering	0.040	27.703**	2.693
2	Days to maturity	0.160	33.893**	3.405
3	Plant height (cm)	6.487	70.102**	2.154
4	Number of primary branches per plant	0.014	0.014**	0.036
5	Number of pods per plant	5.185	18.085**	3.721
6	Number of seeds per pod	0.003	0.659**	0.003
7	Pod thickness (mm)	0.013	0.150**	0.006
8	Pod length (cm)	0.004	0.202**	0.001
9	100 seed weight (g)	0.003	0.208**	0.012
10	Protein content (%)	0.008	1.237**	0.020
11	Seed shattering (%)	42.250	397.352**	10.617
12	Seed yield per plant (g)	3.140	5.128**	0.886

Table.2 Distribution of fifty urdbean genotypes into different clusters

Clusters	Number of genotypes in cluster	Name of genotypes
I	18	LCU-5, LCU-8, LCU-10, LCU-13, LCU-14, LCU-20, LCU-22, LCU-29, LCU-31, LCU-32, LCU-34, LCU-38, LCU-39, LCU-40, LCU-41, LCU-42, LCU-43, LCU-45.
II	14	LCU-6, LCU-7, LCU-9, LCU-11, LCU-12, LCU-15, LCU-16, LCU-18, LCU-21, LCU-36, LCU-37, LCU-44, LCU-46, LCU-48.
III	5	LCU-24, LCU-28, LCU-35, TAU-1, TPU-4.
IV	6	LCU-3, LCU-23, LCU-25, LCU-27, LCU-33, LCU-47.
V	1	LCU-26
VI	1	LCU-4
VII	1	LCU-2
VIII	1	LCU-30
IX	1	LCU-19
X	1	LCU-17
XI	1	LCU-1

Table.3 Average Intra and Inter-Cluster D² Values of Eleven Clusters in Urdbean

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	<u>16.784</u>	23.900	24.736	34.908	21.576	28.880	26.677	27.099	33.924	41.280	29.928
II		<u>18.776</u>	29.386	42.303	23.638	35.200	38.333	33.381	27.509	27.119	35.457
III			<u>21.650</u>	33.070	32.310	37.637	31.994	29.353	41.890	45.361	41.268
IV				<u>21.263</u>	48.035	54.934	42.778	49.578	60.474	60.211	53.679
V					<u>0.000</u>	15.746	26.240	20.826	17.722	34.647	20.084
VI						<u>0.000</u>	23.326	16.978	25.619	46.898	21.999
VII							<u>0.000</u>	23.498	39.760	54.444	23.218
VIII								<u>0.000</u>	30.143	46.500	29.775
IX									<u>0.000</u>	24.653	28.835
X										<u>0.000</u>	44.912
XI											<u>0.000</u>

(Underlined figures indicate intra-cluster D² value)

Table.4 Divergence classes DC 4

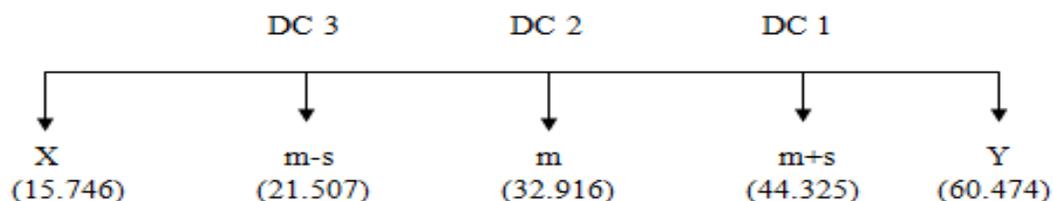


Table.5 Contribution of various twelve characters in genetic divergence of urdbean

S.No.	Characters	Contribution (%)
1	Days to 50% flowering	0.33
2	Days to maturity	0.25
3	Plant height	2.94
4	No. of primary branches per plant	0.35
5	No. of pods per plant	0.40
6	No. of seeds per pod	41.63
7	Pod thickness	1.31
8	Pod length	28.31
9	100 seed weight	1.71
10	Protein content	12.73
11	Seed shattering	7.76
12	Seed yield per plant	2.29
	Total	100

Fig.1 Cluster formation of fifty genotypes by Tocher`s method in urdbean

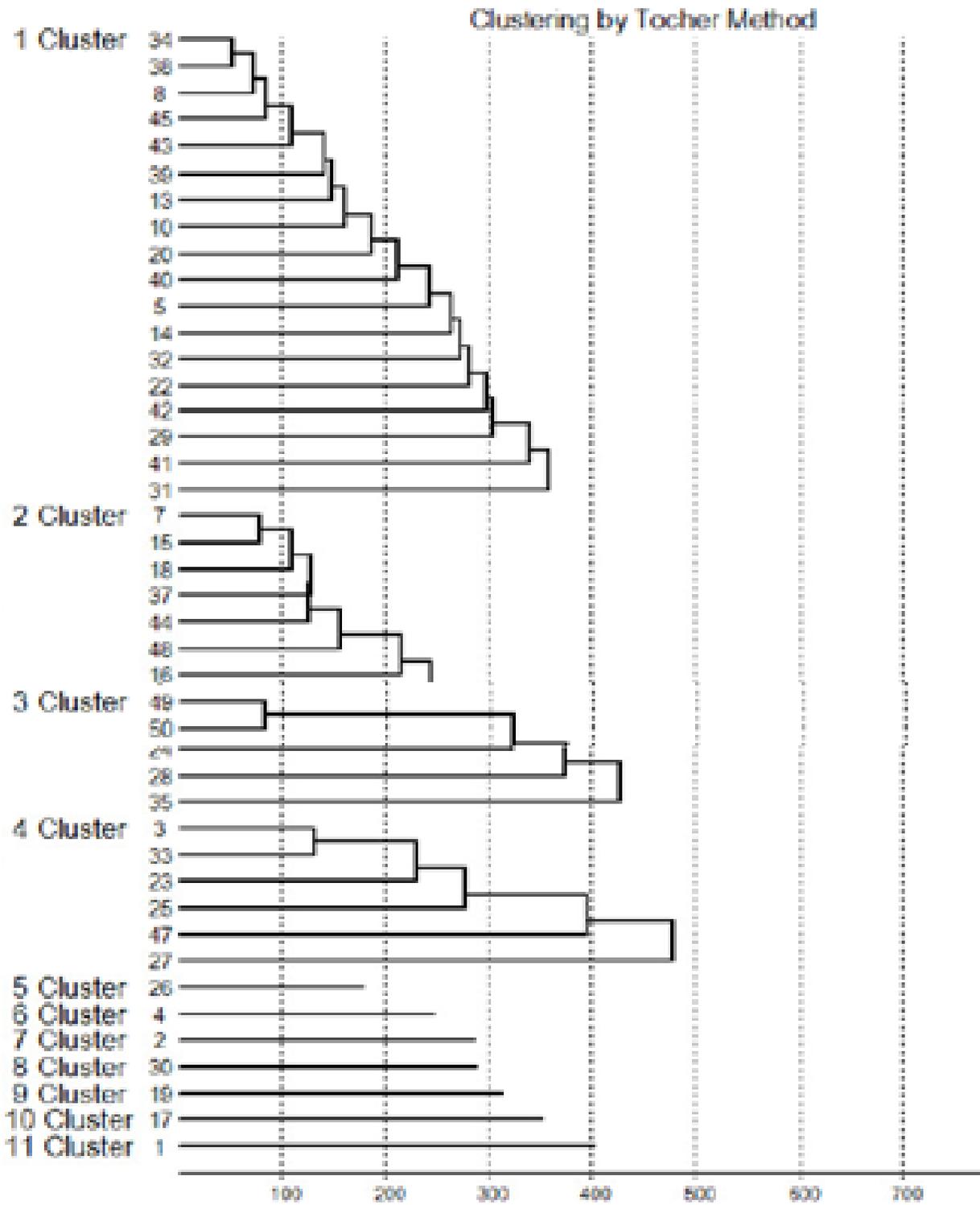
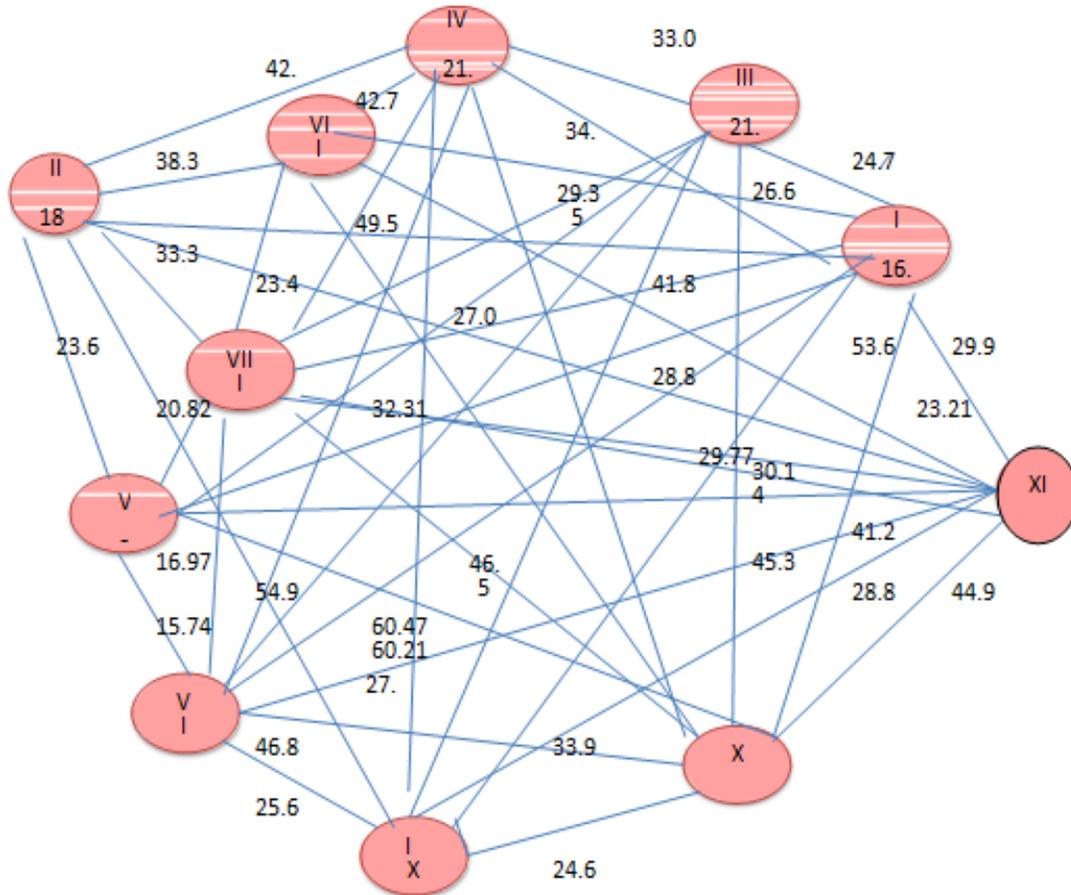


Fig.2 Cluster diagram of fifty genotypes in urdbean (Scale not to measure.....)



Grouping of clusters pairs into the divergence classes (DC) are presented in Table 4. On the light of discussion, initial choice of parents should be made from the cluster combinations falling in the divergence classes DC2 and DC3.

While, crossing among the genotypes of a cluster, the per se performance of the genotypes for different traits such as earliness (days to 50 per cent flowering and days to maturity), number of pods per plant, number of seeds per pod, 100-seed weight, protein content, seed shattering and seed yield per plant should be taken into account for funneling desirable transgressive segregants after hybridization.

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