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GENETIC DIVERSITY ANALYSIS FOR SEED YIELD AND ITS COMPONENT CHARACTERS IN URDBEAN (*VIGNA MOU* (L.) HPER)

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Abstract

Forty-six genotypes were subjected to genetic diversity studies for seed yield and its component characters using Mahalanobis's D^2 statistic. The analysis of variance indicated significant differences among 46 genotypes for all the 14 characters. Forty-six genotypes were grouped into nine clusters, out of which cluster-II had the maximum number of genotypes (16), followed by cluster-III (10), cluster-I (9) and cluster-IV (6). The rest of the clusters *i.e.* cluster-V, VI, VII, VIII and IX, each possessed single genotype. The inter-cluster distances surpassed the intra-cluster distances, expressing existence of stupendous diversity among the entries. The cluster-III and IV have the greatest diversity among their genotypic groups consequently these genotypes can potentially be utilized in varietal development programmes. Highest inter-cluster distance was noted between cluster-IV and VII followed by cluster-VII and VIII, and cluster-VI and VII, indicating ample of diversity available among them, Therefore, the genotypes of these clusters can be used as parents for crossing in hybridization programme to obtain desirable and excellent segregants. Protein content was the greatest contributor towards genetic divergence followed by number of clusters per plant and number of pods per cluster, suggesting direct selection of these characters.

Introduction

Urdbean (Chromosome number 2n = 22) is one among the highly valuable pulses of India. . It enriches soil fertility, improves the soil structure and is used as green fodder for cattle (Parveen *et al.* 2011), apart from serving as great source of protein in food. Genetic improvement and development of high yielding varieties are dependent upon genetic variability (Lal *et al.* 2017) as it provides base for selection. Since urdbean is a self-pollinating legume crop, it faces lack of exploitative genetic variability. Thus, creation of variability in such a crop stands as a challenge for breeders. Hybridization system of breeding furnishes a liberty to create large extent of genetic variability in self-pollinating crops. Choice of diverse and elite genotypes, as parental lines, is a very important aspect of hybridization programme. Therefore, assessment of genetic diversity among genotypes is the first step and serves as key to select such elite and diverse parents that can yield excellent and worthwhile segregants followed to crossing. Among all, Mahalanobis's D^2 statistic followed by Rao's analysis is appropriate and popularly used technique to assess genetic diversity for classifying the genotypes. Keeping in view the above facts, the 46 genotypes of urdbean were subjected to genetic diversity studies in the present investigation.

Materials and Methods

The research was conducted involving forty-six genotypes of urdbean during *kharif* 2018 at Botany field, Dept. of GPB, RCA, Udaipur, India. The design adopted for the experiment was randomized block design with three replications. 14 characters were investigated including seed yield per plant, *viz.* days to 50 per cent flowering, days to 75 per cent maturity, plant height,

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number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, biological yield per plant, 100-dry seed weight, harvest index and protein content. Average values of the characters over three replications were used for statistical analysis. Standard technique of D^2 statistic presented by Mahalanobis (1936) was followed to assess genetic divergence among the test genotypes and Tocher method given by Rao (1952) was adopted for grouping of genotypes into different clusters.

Results and Discussion

The analysis of variance indicated significant differences among the forty-six genotypes for all the 14 characters. Grouping of the genotypes into nine clusters is represented in Table 1. Cluster-II had the maximum number of genotypes *i.e.* 16, followed by cluster-III with 10 genotypes, cluster-I with 9 genotypes and cluster-IV with 6 genotypes (Fig. 1). The rest of the clusters *i.e.* cluster-V, VI, VII, VIII and IX, each possessed single genotype. The intra and inter cluster distances are presented in Table 2. The inter-cluster distances surpassed the intra-cluster distances. It expressed existence of stupendous diversity among the entries. More or less similar results were reported by Reddy *et al*. (2018) and Panwar *et al*. (2019).

Table 1. Cluster composition.

Cluster	Total no. of genotypes	Genotypes
Cluster 1	9	MPU-41, MPU-43, MPU-42, MPU-26, MPU-34, MPU-40, MPU-24, MPU-14, MPU-37
Cluster 2	16	MPU-13, MPU-29, MPU-6, MPU-44, MPU-31, MPU-39, MPU-10, MPU-19, MPU-35, MPU-28, MPU-3, MPU-4, MPU-11, MPU-8, MPU-15, MPU-9
Cluster 3	10	MPU-16, MPU-20, MPU-22, MPU-5, MPU-17, MPU-18, MPU-30, MPU-25, MPU-1, MPU-46
Cluster 4	6	MPU-12, MPU-33, MPU-7, MPU-32, MPU-45, MPU-27
Cluster 5	1	MPU-21
Cluster 6	1	MPU-2
Cluster 7	1	MPU-38
Cluster 8	1	MPU-36
Cluster 9	1	MPU-23

The range of intra-cluster distance was noticed from 0.00 to 10.46. Highest intra-cluster distance was displayed by cluster-III (10.46) followed by Cluster-IV (10.43). The high intra-cluster distance indicated more heterogeneity among the genotypes of the cluster. Similar findings about high intra-cluster distances were made by Panigrahi *et al*. (2014), Panwar *et al*. (2019) and Vara Prasad *et al*. (2020). Lowest intra-cluster distance was displayed by cluster-V, VI, VII, VIII and IX since these clusters are monogenotypic. The low intra-cluster distance indicated more homogeneity among the genotypes of the cluster, hence not recommended for hybridization breeding programmes. Similar findings about low intra-cluster distances were made by Panwar *et al*. (2019) and Vara Prasad *et al*. (2020).

The range of inter-cluster distances was noticed from 8.56 to 23.92. Highest inter-cluster distance was noted between cluster-IV and VII (23.92) followed by cluster-VII and VIII (22.43), and cluster-VI and VII (22.03). The cluster pairs displaying high inter-cluster distances indicate

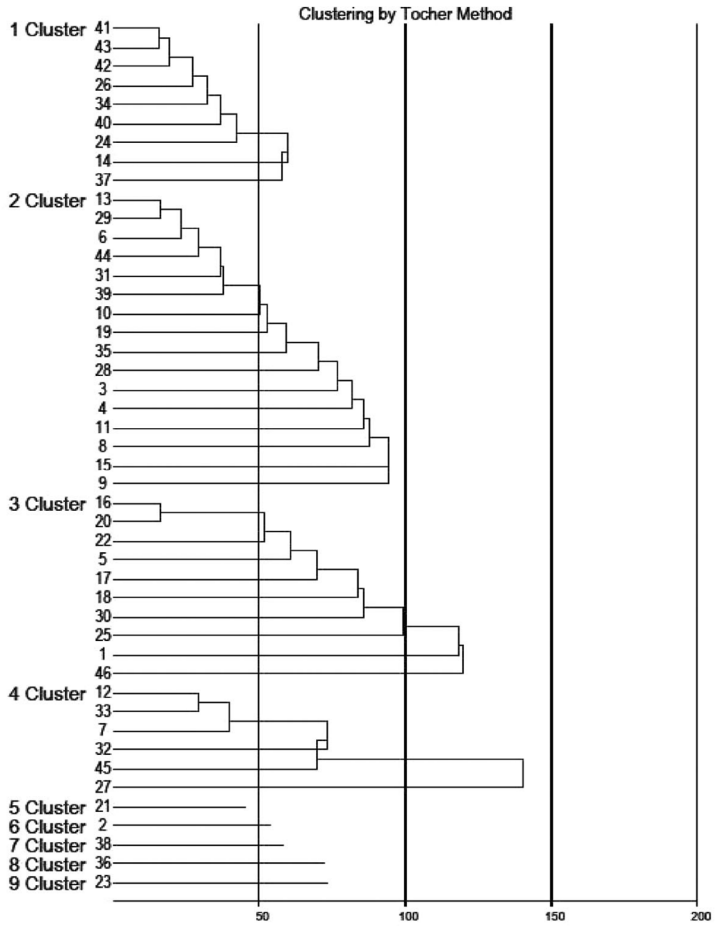

Fig. 1. Clustering of Genotypes by Tocher Method.

Table 2. Average Intra and Inter Cluster Distances.

	Group 1	Group 2	Group 3	Group 4	Group 5	Group 6	Group 7	Group 8	Group 9
Group 1	**7.18**	13.39	14.35	16.56	10.05	16.39	15.11	11.79	13.03
Group 2		**9.00**	12.60	12.05	15.61	10.96	17.57	17.60	16.01
Group 3			**10.46**	18.12	19.29	15.79	12.17	20.95	11.98
Group 4				**10.43**	16.68	14.19	23.92	17.65	20.84
Group 5					**0.00**	16.47	21.13	10.00	18.37
Group 6						**0.00**	22.03	21.41	21.17
Group 7							**0.00**	22.43	8.56
Group 8								**0.00**	18.79
Group 9									**0.00**

Bold numbers: Intra-cluster distance.

ample of diversity available among them, Therefore, the genotypes of these clusters can be utilized as parents for crossing in hybridization programme to obtain desirable and excellent segregants. Analogous outcomes were reported by Panigrahi *et al*. (2014), Sabesan *et al.* (2018), Senthilkumar (2018) and Vara Prasad *et al*. (2020). Lowest inter-cluster distance was noted between cluster-VII and IX (8.56) followed by cluster-V and VIII (10.00), and cluster-I and V (10.05). The low inter-cluster distance expresses low levels of diversity among the genotypes of such clusters and may have followed similar evolutionary stages during their development. Analogous results were reported by Sabesan *et al.* (2018) and Senthilkumar (2018).

Table 3. Relative contribution of each character towards divergence.

Source		Times ranked 1st	Contribution %
1	D to 50% flowering	9	0.87 %
2	D to 75% maturity	4	0.39 %
3	Plant height	63	6.09 %
4	No. of clusters/ plant	81	7.83 %
5	No. of pods/ cluster	76	7.34 %
6	No. of PB/ Plant	66	6.38 %
7	No. of pods/ plant	5	0.48 %
8	Pod length/ plant	45	4.35 %
9	No. of seeds/ pod	13	1.26 %
10	Seed Index	58	5.60 %
11	Bio. Yield/ plant	72	6.96 %
12	Seed yield/ plant	51	4.93 %
13	H.I.	2	0.19 %
14	Protein %	490	47.34 %

Results of the proportionate contribution of each character towards divergence represented in Table 3 showed that protein content was the greatest contributor, with 47.34% contribution, towards genetic divergence followed by number of clusters per plant (7.83%) and number of pods per cluster (7.34%), whereas, harvest index had the lowest contribution (0.19%) towards genetic divergence. Those characters that have displayed maximum contribution towards genetic divergence should be considered for direct selection. Analogous outcomes for number of clusters per plant were reported by Sabesan *et al.* (2018) and Senthilkumar (2018).

The cluster means of all the 14 characters presented in Table 4 revealed that analysis of data had appreciable contrast among the clusters for most of the characters investigated. Similar observation was made by Reddy *et al*. (2018). Cluster-I displayed maximum mean for days to 75 per cent maturity, while Cluster-III displayed maximum mean for days to 50 per cent flowering. Cluster-VI displayed maximum mean for seed index. Cluster-VII displayed maximum mean for eight characters *i.e.* number of clusters per plant, number of primary branches per plant, number of pods per plant, pod length per plant, number of seeds per pod, biological yield per plant, seed yield per plant and harvest index. Cluster-VIII displayed maximum mean for number of pods per cluster and protein content, and lowest mean for days to 50 per cent flowering, days to 75 per cent maturity and plant height. Cluster-IX displayed maximum mean for plant height.

The present investigation of genetic diversity among 46 genotypes of urdbean disclosed appreciable contrast among the clusters for most of the characters investigated. The cluster-III

(10.46) and IV (10.43) have the greatest diversity among their genotypes consequently these genotypes can potentially be utilized in different breeding programmes for developing new varieties. The cluster-VII disclosed high inter-cluster distance with cluster-IV (23.92), VIII (22.43) and VI (22.03). Therefore the genotypes of these clusters can be used as parents in such hybridization programmes where excellent and preferable segregants are desired, and also, introduction of variability is vital. Protein content was the greatest contributor, with 47.34% contribution, towards genetic divergence followed by number of clusters per plant (7.83%) and

Table 4. Cluster means for fourteen characters.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9
D to 50% flowering	37.63	37.48	38.87	37.94	38.33	36.67	37.67	36.33	38.00
D to 75% maturity	72.52	69.79	72.17	71.28	70.33	69.33	71.67	64.67	70.33
Plant height	35.45	34.45	41.64	30.80	28.27	38.18	39.40	24.93	42.70
No. of Clusters/plant	9.64	9.84	12.96	8.17	6.84	7.87	16.29	6.22	15.30
No. of Pods/cluster	3.02	3.19	3.14	2.97	3.07	2.43	3.35	3.44	3.38
No. of P.B./plant	3.19	3.05	3.21	2.72	2.61	3.25	3.49	2.55	2.59
No. of Pods/plant	29.22	31.41	40.65	23.57	21.00	19.73	54.73	21.45	52.07
Pod length/plant	4.35	4.31	4.50	3.98	4.20	4.43	4.49	4.30	4.46
No. of seeds/pod	6.56	6.58	6.63	5.94	6.00	7.00	7.67	5.67	6.33
Seed Index	4.24	4.39	4.21	3.92	5.03	5.41	4.43	3.22	3.82
Bio. Yield/plant	18.89	19.11	23.32	16.65	16.30	18.93	24.80	15.94	21.42
Seed yield/plant	4.61	5.16	6.93	3.43	4.20	4.90	7.70	4.33	5.80
H.I.	24.49	26.86	29.84	20.66	25.87	26.04	31.40	27.33	27.07
Protein %	23.70	21.37	22.20	20.84	23.79	20.65	23.95	24.18	23.83

number of pods per cluster (7.34%). Therefore, these characters should be considered for direct selection. The genotype MPU-38 of cluster-VII can prove itself excellent in hybridization breeding for improving number of clusters per plant, number of primary branches per plant, number of pods per plant, number of seeds per pod, biological yield per plant, seed yield per plant and harvest index. Therefore, MPU-38 can be considered as a unique genotype regarding seed yield improvement breeding programmes. The cluster-IX having genotype MPU-23 can be utilized for developing tall varieties of urdbean, whereas MPU-36 of cluster-VIII can be utilized for developing dwarf varieties as well as for improving number of pods per cluster and protein content. The crop improvement programmes aimed at improving number of pods per cluster and protein content, and developing early flowering and early maturity varieties may involve MPU-36 from cluster-VIII as a promising parent.

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