RESEARCH ARTICLE Legume Research- An International Journal, Volume 44 Issue 2: 158-163 (February 2021)

Divergence studies of blackgram (*Vigna mungo* L) for selection of drought tolerant genotypes under rainfed conditions of North Western Himalayas in J & K, India

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10.18805/LR-4083

ABSTRACT

The present investigation was aimed at ascertaining the nature and magnitude of genetic diversity among a set of twenty five blackgram genotypes through Mahalanobis D^2 method. Field experiments were conducted continuously during *Kharif* 2016 and 2017 to examine the selection indices and genetic divergence among twenty five black gram genotypes under rainfed conditions. This study assessed the drought response of twenty five genotypes of blackgram grown in a randomized block design (R.B.D.) during *Kharif* 2016 and 2017. The genotypes under study fall into six clusters. The cluster-V contained the highest number of genotypes (06) followed by cluster-VI (05) and Cluster-III (05) and cluster IInd and IVth each contained 04 genotypes. It is suggested that the recombinant should be made between genotypes of cluster V, III and VI for enhancing the seed yield potential of crop as well as improving important economic traits to develop a high yielding variety or cultivar for rainfed areas in future breeding programme. On the basis of selection indices scores, genotypes are arranged in the order of merit and top 05 or 10% of total used genotypes may be selected for further breeding programmes. The genotype Uttara (262.31) gained maximum selection indices score followed by genotypes NP 16 (255.37), PU 99 (251.90), UH86-4(251.09) and No.13/11(246.86) and these genotypes shall also be utilized for future breeding programme.

Key words: Blackgram, Heritability, Selection indices, Variability.

INTRODUCTION

Pulses are the major source of dietary protein. Blackgram [*Vigna mungo* (L.) Hepper], popularly known as black gram in India, is an important short duration pulse crop and self pollinating diploid (2n=2x=22) with a small genome size estimated to be 0.56pg/1C (574 Mbp) (Gupta *et al*., 2008). In India, black gram occupies 12.7 per cent of total area under pulses and contribute 8.4 per cent of total pulses production (Swathi *et al.* 2013). Blackgram (*Vigna mungo* L.) which belongs to leguminaceae family is a very important pulse crop especially in Jammu region of state Jammu and Kashmir, India. It is consumed in the form of split pulse as well as is whole pulse, which an essential supplement of cereal based diet. It is also ground into flour and used to make cakes, bori, bread and porridge. Besides, it is used as a nutritive fodder especially for milch cattle. It is also used as green manuring crop. It contains about 24% protein, 60% carbohydrates, 1.3% fat and is the richest among the various pulses in phosphoric acid, being 5 to 10 times richer than in others (Modern techniques of raising field crop).

Like other pulses, it also enriches the soil fertility, improves the soil structure and used as green fodder for cattle. In Jammu, it is mainly grown on sandy soil which is very low in organic matter content. Lack of stable varieties for higher seed yield/plant for rainfed areas is a major bottleneck for growing of this crop (Parveen *et al*. 2011). The productivity of urdbean in India is 451 kg/ha but very low in Jammu (336 kg/ha). In addition, being an important source of human food and animal feed**,** it also plays an important role in sustaining soil fertility by improving soil physical properties and fixing atmospheric nitrogen. Drought tolerance in seed yield/plant of black gram is a complex trait. An effective screening method with well defined traits for selecting drought tolerant genotypes under field conditions is necessary for breeding drought tolerant lines / genotypes (Devasirvatham *et al*. 2013).

The present productivity level of black gram in J & K as well as in India is very low as compared to International level. Efforts to genetically improve the crop are still at low ebb. Further, it has been the least studied crop among the pulses and no International system under the CGIAR has this as a mandate crop (Ghafoor *et al*. 2000). The proper

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How to cite this article: Kumar, S., Kumar, A., Jamwal, S., Abrol, V., Singh, A.P., Singh, B. and Kumar, J. (2021). Divergence studies of blackgram (*Vigna mungo* L.) for selection of drought tolerant genotypes under rainfed conditions of North Western Himalayas in J & K, India. Legume Research. 44(2): 158-163. DOI: 10.18805/LR-4083.

Submitted: 19-09-2018 **Accepted:** 07-12-2018 **Online:** 05-06-2019

estimate of nature and magnitude of diversity in a crop is essential to infer about extent of variation available for seed yield and its component traits. The selection of highly genetically divergent parents is expected to throw superior and desirable segregants following crossing (Bhatt, 1973).

Assessment of genetic divergence or similarity among the genotypes would help in identification of genotypes that may be used in cross breeding programme for producing transgressive segregants. Limited systematic breeding programmes for breeding superior genotypes have been taken up for developments of high yielding genotypes in blackgram have been initiated. Vast scope lies for genetic improvement of blackgram through genetic diversity study done to understand the diversity in different genotypes for assessment and creation of diverse line for further breeding. Hence, a study on selection indices and divergence studies of *Vigna mungo* L. for drought tolerant genotypes under rainfed field conditions of north western himalayas in J & K, India in 25 genotypes of blackgram was taken up with the view of selecting parents for hybridization programme.

MATERIALS AND METHODS

The experimental materials for the present investigation comprised of 25 diverse genotypes of black gram received (Table 1) from ICAR-Indian Institute of Pulses Research, Kanpur, (U.P.).

Table 1: List of 25 black gram genotypes and their source of collection.

Name of genotypes	Source	Cultivation
IPU99-16	ICAR-IIPR Kanpur	Being in cultivation
JU-468	ICAR-IIPR Kanpur	Important Strain
IPU-2-43	ICAR-IIPR Kanpur	Being in cultivation
Uttara	ICAR-IIPR Kanpur	Being in cultivation
Mash-114	ICAR-IIPR Kanpur	Being in cultivation
UR82-14	ICAR-IIPR Kanpur	Important Strain
SPS-38	ICAR-IIPR Kanpur	Important Strain
Mash-338	ICAR-IIPR Kanpur	Being in cultivation
PU-99	ICAR-IIPR Kanpur	Being in cultivation
IPU-96-1	ICAR-IIPR Kanpur	Being in cultivation
Pant 31	ICAR-IIPR Kanpur	Being in cultivation
IPU96-6	ICAR-IIPR Kanpur	Being in cultivation
STTZ-834	ICAR-IIPR Kanpur	Germplasm line
NKD 4-2	ICAR-IIPR Kanpur	Germplasm line
PL-4158	ICAR-IIPR Kanpur	Germplasm line
UH86-4	ICAR-IIPR Kanpur	Being in cultivation
DUS-19	ICAR-IIPR Kanpur	Being in cultivation
PLU499-52	ICAR-IIPR Kanpur	Being in cultivation
No. 13/11	ICAR-IIPR Kanpur	Germplasm line
PGRU-99022	ICAR-IIPR Kanpur	Being in cultivation
Mash479	ICAR-IIPR Kanpur	Being in cultivation
PU-19	ICAR-IIPR Kanpur	Being in cultivation
T-9	ICAR-IIPR Kanpur	Being in cultivation
No.40	ICAR-IIPR Kanpur	Germplasm line
NP-16	ICAR-IIPR Kanpur	Being in cultivation

The experiment were conducted in randomized block design at the experimental farm of Advanced Centre for Rainfed Agriculture (ACRA) Dhiansar of SKUAST-Jammu during *Kharif* 2016 and 2017. Each entry was represented by 5 rows of 3.0 meter row length with a spacing of 30 cm × 10 cm. fertilizer doses of 20:40:20 kg NPK ha^{-1} was applied and need based plant protection measures were followed. The pooled mean values of three replications were used for statistical analysis. The observations were recorded on eight quantitative traits *viz.,* days to 50% flowering, days to maturity, plant height, number of primary branches $plant^{-1}$, number of seeds pod^{-1}, pod length, 1000 seed weight and seed yield $plant^{-1}$. Assessment of genetic divergence was done by using Mahalanobis D^2 (Mahalanobis, 1936) statistic and the genotypes were grouped into different clusters following Tocher's method as described by Rao (1952). Average intra and inter cluster distances were determined using GENRES version 3.11, 1994 Pascal Intl. Software as suggested by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

The analysis of variance (Table 2) showed highly significant differences among the genotypes for the pooled analysis with respect to all the characters under studied indicated high genetic variability and is an indication of the fact that in spite of highly interactive with environments, the genotypic differences among the genotypes was highly significant across the environments.

Genetic diversity

For a successful breeding programme, the diversity of parents is of utmost importance, since the crosses made between the parents with maximum genetic divergence are more likely to yield desirable recombinants in the progenies. However, it is desirable to select suitable genetically divergent parents based on information about the genetic variability and genetic diversity present in the available germplasm.

The Mahalonobis D^2 values have grouped the 25 genotypes of black gram to six distinct clusters on the basis of clustering by K method and four clusters as per Tocher's method shown in Table 3 and Fig 1. The estimates of average intra- and inter-cluster distances for six clusters (Table 4) revealed that the genotypes present within a cluster have good genetic divergence from each other with respect to aggregate effect of eight characters under study, while greater genetic diversity was observed between the genotypes belonging to different clusters.

The maximum inter cluster distance was between cluster II and IV (160.19) followed by cluster V and VI (152.47) suggesting that the crosses involving varieties from these two clusters would give desirable recombination. While the minimum inter cluster distance of 49.98 was recorded between cluster IV and V indicating that genotypes of these clusters had maximum number of gene complexes and genotypes of these clusters were genetically close. Such genotypes can also be used in breeding programmes for developing biparental crosses between the most diverse and

closest groups to break the undesirable linkages between yield and its associated traits (Haddad *et al.* 2004).

High or optimum genetic divergence is desired between the parents for hybridization since the chances of obtaining good segregants by crossing the little diverse genotypes belonging same cluster is very low. In order to increase the possibility of isolating good segregants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances.

Genotypes in cluster II and IV are highly divergent followed by those in cluster V and VI and cluster IV and VI. Hybridization programme involving parents from these clusters is expected to give higher frequency of better segregates or desirable combinations for development of useful genetic stocks or varieties.

Table 2: Analysis of variance and estimates of mean, PCV, GCV, ECV, heritability $(h^2)_{bs}$ and genetic advance (GA) for different morphological traits in urdbean.

Source of variation	df	Days to 50% flowering (days)	Plant height (cm)	Primary branch per Plant	Pod length (cm)	Seed per Pod	Days to maturity	1000 Seed weight (gms)	Grain yield per Plant (gms)
Environments	1	2.23	5.19	0.01	0.35	0.07	6.57	19.58	0.26
Genotype	24	4099.51**	20684.04**	106.11**	15.98*	147.14**	3962.43***	1284.74***	247.08**
Error	125	64.78	304.14	5.01	4.71	7.51	249.09	165.83	14.52
CD (0.05)		1.31	1.78	0.22	0.22	0.28	1.61	1.32	0.39
General Mean		53.359	60.709	4.736	4.567	6.137	82.525	38.364	5.604
PCV (%)		10.19	19.88	18.53	8.26	16.87	6.55	8.25	24.03
GCV (%)		9.96	19.71	18.04	7.09	16.39	6.31	7.68	23.24
ECV (%)		2.152	2.569	4.230	4.252	3.995	1.711	3.002	6.082
Heritability $(h^2)_{bs}$		95.5	98.3	94.8	73.5	94.4	93.2	86.8	93.6
GA (5%)		10.7	24.44	1.71	0.57	2.01	10.37	5.66	2.6

*, **&*** Significant at .05%, 0.01% and 0.001% level, respectively.

Table 3: Distribution of 25 genotypes of urdbean in clusters.

Clusters by K Method	No. of genotypes	Names of genotypes	Clusters by Tocher Method	No. of genotypes	Names of genotypes
Cluster-I	1	JU468	Cluster-I	22	IPU-2-43, Mash-114, STTZ-834, PL-4158, Mash-479, Mash-338, Pant-31, DUS-19, IPU-96-1, UH-86-4, PLU-499-52, UH-82-14, SPS-38, PU-99, IPU-96-6, PGRU-99022, NP-16, NKD-4-2, PU-19, T-9, No.-40, No. 13/11
Cluster-II	4	IPU-2-43, Mash-338, Pant 31, Mash-479	Cluster-II	1	Uttara
Cluster-III	5	SPS38, NKD 4-2, PL4158, DUS19, No. 40	Cluster-III	1	JU468
Cluster-IV	4	Uttara, UH86-4, No. 13/11, NP16	Cluster-IV	1	IPU99-16
Cluster-V	6	Mash114, UH82-14, IPU96-1, STTZ834, PGRU99022			
Cluster-VI	5	IPU99-16, PU99, PLU499-52, PU19, T-9			

Table 4: Average inter and intra-cluster distance D^2 statistics.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	38.22	62.39	63.17	98.85	91.47	103.01
Cluster 2	-	0.00	94.72	160.19	95.73	111.40
Cluster 3	-	-	0.00	64.94	59.81	108.40
Cluster 4	-	-	-	0.00	49.98	134.77
Cluster 5	-	-	-	-	0.00	152.47
Cluster 6	-	-	-	-	-	0.00

Cluster V recorded lowest mean value for days to 50% flowering (42.75) and Cluster III recorded highest days to 50% flowering (59.50). Cluster III recorded the lowest days to maturity (70.50) followed by Cluster II (70.65) and Cluster V (74.43). Cluster II showed the highest seed yield/plant (7.38g) followed by Cluster IV (7.10g) and VI (6.68g). Maximum number of seeds/pod was exhibited by cluster VI (10.48) and minimum by Cluster IV (5.78). Cluster IV exhibited highest plant height (88.08cm) followed by Cluster V (85.57) and Cluster III. Similarly maximum number of primary branches were exhibited by Cluster III and followed by Cluster VI. Cluster II (5.25) exhibited the highest pod length followed by Cluster V (Table 5).

Cluster I recorded more number of primary branches (4.83), Cluster VII recorded highest mean value for days to maturity, Cluster VI highest test weight (45.60) and highest seed yield by cluster II (7.38) (Table 6). Genotypes of Clusters II and III can be utilized for development of early maturing varieties while those of clusters IV and VI in the development of medium duration varieties. Highest mean number seeds/pod in genotypes of Cluster VI may be utilized directly for adaptation and parents for the development of high yielding varieties. Lowest mean height of genotypes of cluster II can be utilized for the development of dwarf and bushy varieties of urdbean.

D^2 statistic indicates the characters contributing to divergence (Table 6). Maximum contribution towards genetic divergence is exhibited by plant height (40.33), followed by grain yield/plant (15.33g) and days to 50% flowering (15.00%). These three characters together recorded for more than 70% of the total divergence in the twenty five genotypes studied.

Principal component analysis

The eigen values (variances), per cent variability, cumulative per cent variability and component loading of the different characters are given in Table 6. The PCA analysis gives the information about the clusters of traits explaining the maximum variability in the genotypes under rainfed conditions. The canonical variate analysis revealed that in the both vectors (Vector I and Vector II) days to 50% flowering (0.39 and 0.46), number of primary branches/plant (0.43 and 0.37), seeds /pod (0.05 and 0.04) and days to maturity (0.39 and 0.12) were positive. Such results indicated that these characters contributed maximum towards divergence of the genotypes. In vector I, II III and IV days to maturity played significant roles. In vector III, plant height and in vector IV, days to 50% flowering, pod length, seeds/pod, 1000 seed weight and seed yield/plant were positive which indicated that these characters also played significant roles.

Selection indices

On the basis of selection indices scores genotypes are arranged in the order of merit and then the top 05 or 10% of total used genotypes may be selected for further breeding programmes. The genotype Uttara (262.31) gained maximum selection indices score (Table 6) followed by genotypes NP 16(255.37), PU99 (251.90), UH86-4(251.09)

Table 5: Cluster Mean for 8 agro-morphological characters of 25 genotypes of Urdbean.

Clusters/Traits	DF	PH	PBR	PL	S/P	DTM	1000 SW	GY/P
Cluster 1	54.04	57.85	4.83	4.53	5.87	83.88	38.09	5.51
Cluster 2	46.63	52.05	3.35	5.25	6.47	70.65	37.03	7.38
Cluster 3	59.50	75.53	5.57	4.63	6.60	70.50	37.03	4.60
Cluster 4	49.52	88.08	4.65	4.45	5.78	85.33	38.73	7.10
Cluster 5	42.75	85.57	3.45	4.85	6.65	74.43	38.92	4.15
Cluster 6	54.75	59.57	4.75	4.47	10.48	84.67	45.60	6.68

DF (days to 50% flowering), PH (Plant height), PBR (Primary branches per plant), DTM (days to maturity), PL (Pod length) S/P (Seeds per pod), 1000 SW (1000-Seed weight), GY/P (Seed yield per plant).

Table 6: Latent vectors and percent contribution of different characters to genetic diversity for 08 component characters of 25 genotypes of urdbean.

Traits	Vector 1	Vector 2	Vector 3	Vector 4	Contribution %	Times Ranked First
Eigene value (Root)	2.39	1.81	1.37	0.83	-	-
% Var. Exp.	29.89	22.60	17.16	10.36	-	-
Cum. Var. Exp.	29.89	52.49	69.65	80.01	-	-
Days to 50% flowering	0.39	0.46	0.00	0.02	15.00	45
Plant height	0.16	-0.51	0.21	-0.49	40.33	121
No. of primary branches	0.43	0.37	-0.10	-0.45	9.67	29
Pod length	-0.49	0.06	-0.14	0.27	0.67	2
Seeds per pod	0.05	0.04	-0.78	0.07	8.33	25
Days to maturity	0.39	0.12	0.36	0.63	6.00	18
100 Seed weight	0.32	-0.53	-0.03	0.26	4.67	14
Grain yield per plant	0.37	-0.29	-0.42	0.17	15.33	46

and No.13/11(246.86) and these genotypes shall be utilized in future breeding programme.

Mean performance

On the basis of pooled mean data of both the years *i.e.* during *kharif* 2016 and 2017, variety No. 13/11 gave maximum yield/plant (9.58) which is 25% higher in yield than the standard check Uttara (7.38) under varying agro climates during the period of study. During *kharif* 2016 rainfall was less than the optimum in reproductive stage of crop but in *kharif* 2017, rainfall was lesser during vegetative stage as compared to later years (Fig 2). However the varieties

Table 7: Mean performance and simultaneous selection of 25 genotypes under rainfed conditions.

Genotypes	DF	PH (cm)	PBR	PL (cm)	S/ Pod	DTM	1000-SW (gms)	GY/ P (gms)	SI Score
IPU99-16	59.50	75.53	5.56	4.33	6.60	70.50	37.03	4.60	
JU-468	42.75	85.56	3.45	4.85	6.65	74.43	38.91	4.15	239.94
IPU-2-43	44.45	66.63	4.21	4.61	6.61	74.20	37.28	4.40	223.30
Uttara(SC)	49.51	88.08	4.65	4.45	5.78	85.33	38.73	7.10	262.31
Mash-114	60.26	59.78	5.15	4.63	5.43	92.45	33.21	4.70	245.01
UH82-14	61.76	51.65	6.25	4.68	6.05	86.08	35.65	5.13	236.65
SPS-38	57.38	59.25	4.56	4.36	5.93	83.26	38.16	5.00	237.17
Mash-338	46.83	48.21	3.55	5.41	6.45	81.83	37.18	5.20	212.86
PU-99	58.80	69.81	4.30	4.58	5.81	85.65	37.25	5.66	251.90
IPU-96-1	57.55	46.73	5.16	4.40	5.90	82.45	36.43	6.85	223.64
Pant 31	46.63	52.05	3.35	5.25	6.46	70.65	37.03	7.38	207.26
IPU96-6	53.50	42.01	6.21	4.20	6.15	82.43	37.50	5.33	215.56
STTZ-834	54.84	43.33	6.05	4.13	6.60	82.83	37.55	4.33	222.90
NKD4-2	51.58	53.70	4.50	4.13	5.65	85.73	38.26	6.33	228.12
PL-4158	54.81	59.30	4.63	4.48	5.60	85.40	35.78	3.33	231.39
UH86-4	54.75	59.56	4.75	4.46	10.48	84.66	45.60	6.68	238.73
DUS-19	53.28	53.66	4.23	4.50	5.53	88.00	40.41	5.10	235.44
PLU499-52	54.66	56.40	4.23	4.35	6.30	86.50	43.75	6.70	239.43
No. 13/11	55.00	61.98	4.43	4.38	5.53	85.83	39.80	9.58	246.86
PGRU-99022	62.50	59.53	6.05	5.00	6.36	86.33	37.10	5.21	246.20
Mash479	50.13	53.93	3.43	4.43	5.28	80.83	36.23	4.55	215.95
PU-19	48.41	71.06	4.31	4.01	4.93	81.21	36.90	6.48	246.16
T-9	47.41	69.25	4.71	4.76	6.31	81.00	35.83	5.70	35.27
No.40	53.00	55.65	5.18	4.91	5.60	84.83	44.30	5.30	237.53
NP-16	54.63	75.00	5.43	4.50	5.86	80.66	43.16	5.26	255.37
CV	2.15	2.56	4.23	4.25	3.99	1.71	3.00	6.08	-
CD 5%	1.31	1.78	0.22	0.22	0.28	1.61	1.31	0.38	-
SE	0.46	0.63	0.08	0.07	0.10	0.57	0.47	0.13	-

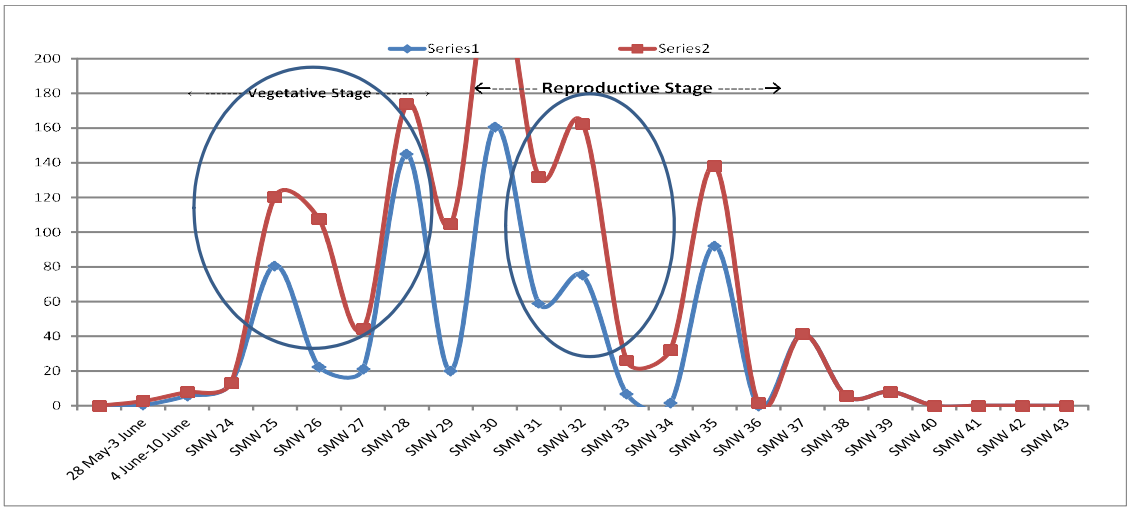

Fig 1: Weather data during the entire crop season.

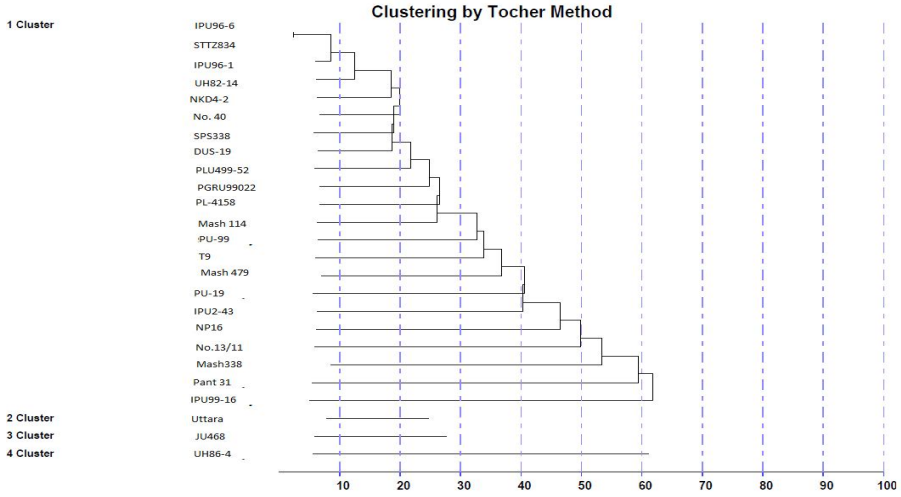

Fig 2: Variance dendogram of urbean genotypes by clustering (Tocger Method).

Pant 31 (7.10) and IPU 96-1(6.85) were at par in seed yield/ plant as compared to check but these varieties were younger than Uttara and less prone to diseases and should be replaced with Uttara under rainfed conditions (Table 7) for increasing the productivity of urdbean.

Impact of weather

From the Fig 1, it is observed that in *Kharif* 2016 rainfall was less during vegetative stage (series 1) *i.e*. from leaf formation to prior anthesis and there was more rainfall during reproductive stage (series 2) *i.e*. from anthesis to maturity of seeds than the optimum rainfall (60-75cm) for good seed yield which causes the flowers dropping and very meager amount of fertilization was taken place which ultimately results in low yield of the all varieties under rainfed conditions. In *kharif* 2017, rainfall is comparatively higher both in vegetative (series 1) and reproductive stages (series 2) as compared to *kharif* 2016. But under rainfed conditions, on pooled mean bases in both the years some of the varieties were possessed good seed yield by different varieties namely No**.** 13/11(9.58 gms/pl), Pant 31(7.38 gms/pl), Uttara (7.10gms/pl) and PU 19(6.48gms /pl). These varieties therefore are recommended to grow under rainfed conditions for good seed yield.

CONCLUSION

From the present study, it was concluded that the Cluster-V contained the highest number of genotypes (06) and cluster I contained the lowest (01). Cluster-VI produced the highest mean value for days to maturity. The inter-cluster distances were much higher than the intra-cluster distances. Cluster-V exhibited the highest intra-cluster distance while the lowest distance was observed in Cluster-IV and V. The highest inter-cluster distance was observed between cluster-II and IV while the lowest was between Cluster-I and II. Considering all the characters, it is suggested that the genotypes Uttara (262.31) gained maximum selection indices score followed by genotypes NP 16 (255.37), PU99 (251.90), UH86-4 (251.09) and No.13/ 11(246.86) could be used as parents for future breeding programmes to develop high yielding varieties of urdbean.

REFERENCES

Bhatt, G.M. (1973). Comparison of various methods of selecting parents for hybridization in common bread wheat (*Triticum aestivum* L.). Australasian Journal of Agriculture Science. 24: 457-464.

Devasirvatham, V., Gaur, P.M., Mallikarjuna, N., Raju, T.N., Trethwan, R.M., Tan, D.K. (2013). Reproductive biology of chickpea response to heat stress in the field is associated with the performance in controlled environments. Field Crop Research. 142: 9-19.

Ghafoor, A., Ahmad, Z. and Sharif, A. (2000). Cluster analysis and correlation in blackgram germplasm. Pakistani Journal of Biological Science. 3(5): 836-839.

Gupta, S.K., Subramanian, J. and Gopalakrishna, T. (2008). Construction of a genetic linkage map of blackgram based on molecular markers and comparative studies. Genome. 51: 628-637.

Hadad, N.I., Boggo, T.P. and Muchibauer, F.J. (2004). Genetic variation of six agronomic characters in three lentil crosses. Euphytica. 31: 113-120.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. Proceedings of National Institute of Sciences. (Indian) 2: 49-55.

Parveen, S.I., Reddi Sekhar, M., Mohan Reddy, D. and Sudhakar, P. (2011). Correlation and path coefficient analysis for yield and yield components in blackgram [*Vigna mungo* (L.) Hepper]. International Journal of Applied Biology and Pharmaceutical Technology. 2(3): 619-625.

Rao, C.R. (1952). Advanced Statistical Methods in Biometrical Research. John Wiley and Sons. New York. pp. 236-272.

Singh, R.K. and Chaudhary, B.D. (1977). Biometrical Methods on Quantitative Ggenetic Analysis. Kalyani Publishers. New Delhi. pp. 215-218.

Swathi, S., Senthil, N., Vinod Kumar, V., Sathish, S., Jagadeesh N.S. and Raveendran, M. (2013). Proteome data base-black gram proteome. American Journal of Experimental Agriculture. 3(4): 971-976.