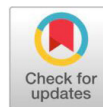


## Research Article

## Open Access

# Analysis of Divergence at different Developmental Stages under Drought Stress in green gram (*Vigna radiata* (L.) R. Wilczek)



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## ABSTRACT

Drought is the major problem that causes severe reduction in yield as the plant faces severe moisture and temperature stresses. To enhance the area of mungbean cultivation under drought prone region it is important to understand the response of mungbean for different morphophysiological and biochemical traits under drought condition in order to formulate effective breeding programme. In the current investigation, Twenty-five genotypes of mungbean were evaluated in randomized block design with three replications along with three levels of water stress i.e. Control, drought stress at the vegetative stage, and drought stress at the reproductive stage during the summer season of 2020 & 2021. When all the characters were considered simultaneously, significant differences among twenty-five genotypes were observed as the 'V' statistic value was highly significant. During both the years under control and stress conditions, these twenty-five mungbean were grouped into six clusters. The intra-cluster  $D^2$  values ranged from 0.00 to 21.86 under the control condition, while it was 0.00 to 36.77 under drought at the vegetative stage condition and 0.00 to 29.62 under drought at the reproductive stage condition. Under control and drought at vegetative stage condition, during both the years, leaf area contributed the maximum to the diversity by taking first rank out of 300 combinations respectively while in drought at reproductive stage condition, seed yield & 100 seed weight contributed the maximum to the diversity during summer 2020 & 2021 respectively. Selection of divergent parents based on these characteristics might be useful in the formulation of a breeding program for drought tolerance as well as it will help in obtaining a large number of transgressive segregants in subsequent generations.

**Keywords:** Cluster, Divergence, Drought,  $D^2$  statistic, Genetic diversity, Intercluster distance, Intracluster distance, Mungbean, 'V' statistic, Wilk's ' $\lambda$ ' criterion.

## INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek,  $2n=22$ ] is the third most important short-season summer grain legume cultivated in India. It is nutritionally rich and can thrive under drought conditions. The phenomenon of drought is always associated with higher moisture and temperature stress which can lead to severe yield reduction. In the current era of climate change there is need to develop mungbean variety that can thrive under moisture stress. Several breeding programs were formulated for drought tolerance in mungbean but till now, the progress is not significant. The response of mungbean varieties varies for different morphophysiological and biochemical traits under drought conditions depending upon the growth stage on which drought has been induced, stress duration, and genotype of the crop. Hence, understanding the response of mungbean towards drought will expand the area of legume cultivation in drought-prone region. A large amount of genetic diversity has been reported in mungbean which indicates huge potential for genetic improvement of the crop. The genetic variability present among the different genotypes may arise either due to

geographical separation or due to genetic barriers to crossability. The success of any breeding program depends largely on the selection of parents showing high genetic diversity for traits of interest.

$D^2$  statistic [8] is one of the formidable techniques to measure genetic diversity in plant breeding. The genetic base of a crop plays an important role in crop improvement, as the wider the genetic base more is the genetic diversity. Therefore, knowledge about genetic diversity plays a crucial aid in formulating crop improvement strategies which can be obtained by the selection of genetically diverged parents. In this technique, divergence is measured at two levels viz., intra-cluster and inter-cluster which helps to select genetically divergent parents for utilization in hybridization programmes. For the selection of parents on the basis of  $D^2$  statistic, it becomes important to consider three points viz., i) the relative contribution of each character to the total genetic divergence, ii) the choice of clusters with the maximum statistical distance, and iii) the selection of one or a few genotypes from such clusters. Among germplasm functions, Evaluation of germplasm collection has the highest priority. Germplasm enhancement embraces those activities required to aggregate useful genes and gene combinations into usable phenotypes [3]. Thus the present study was done to find out the genetic variability among different plant traits, direct and indirect contributions of these traits towards yield and to identify better combinations as selection criteria for developing high-yielding drought tolerant mungbean genotypes.

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## MATERIAL & METHODS

Twenty-five mungbean genotypes were evaluated in randomized block design in three levels of stress i.e. Control, drought stress at vegetative stage and drought stress at the reproductive stage having three replications each during the summer season 2020 & 2021 at the Research Farm, ICAR Research Complex for Eastern Region Research Centre, Plandu, Namkum, Ranchi. A recommended agronomic package of practices was adopted for the experiment except for irrigation. Irrigation was done as per the recommended package of practices in control Plot, while for stress at the vegetative stage and reproductive stage, irrigation was restricted at 25 days after sowing and 35 days after sowing respectively by removal of irrigation for 15 days. The genotype performance was assessed by recording observations on the following fifteen attributes from five randomly selected plants from each row for Plant height (cm), Primary branches per plant, Clusters per plant, Pods per plant, Seeds per pod, 100 seed weight (g), Seed yield per plant (g), Harvest index (%), Relative water content (%), Leaf area (cm<sup>2</sup>), Proline content (%), Protein content (%) and chlorophyll content. Days to 50 % flowering and days to maturity was recorded on the basis of plant population. Genetic divergence was analyzed using Mahalanobis D<sup>2</sup> [7] statistics. The test of significance for the correlated variables had been done following Rao, 1948 [11] using Wilk's ' $\lambda$ ' criterion [18]. Grouping of genotypes into different clusters was done by using Tocher's method as described by Rao, 1952 [12]. The contribution of individual trait towards genetic divergence was quantified on the basis of coefficient of variation at genotypic and inter-cluster levels as per Vavilov, 1951 [17].

## RESULT AND DISCUSSION

Genetic divergence analysis is an important tool for selection of genetically diverse parents in order to obtain high-yielding genotypes for a successful and efficient hybridization program. The significance of Wilks " $\Lambda$ " criterion (statistic) value was tested by X<sup>2</sup> at 360 degrees of freedom. The value of 'V' statistic was 1110.17, 946.54, 1110.17, 1007.55, 1110.25 and 1149.19 in control during 2020, control during 2021, drought at the vegetative stage during 2020, drought at the vegetative stage during 2021, and drought at the reproductive stage during 2020, a drought at the reproductive stage during 2021 respectively. The 'V' statistic value was highly significant (table 1) which indicated significant differences among twenty-five genotypes when all the characters were considered simultaneously and thus can be considered for divergence study.

The twenty-five mungbean genotypes were grouped into six clusters during both the years under control and stress conditions. Under control condition, during the summer of 2020 Cluster I was the largest with twelve genotypes followed by Cluster II with nine genotypes, cluster III, cluster IV, cluster V, and cluster VI with one genotype respectively, while during 2021, cluster II was the largest with eleven genotypes followed by cluster III with seven genotypes, cluster I with four genotypes, cluster IV, cluster V and cluster VI with one genotype respectively (table 2 and Figure 1-2). In case of drought at vegetative stage, Cluster II was the largest with fourteen genotypes followed by Cluster I with seven genotypes, cluster III, cluster IV, cluster V and Cluster VI with one genotype each in the year 2020, while Cluster III was the largest with nine genotypes followed by cluster II with seven genotypes, cluster I with five genotypes, cluster V with two genotype and cluster IV

and cluster VI with one genotype respectively during 2021 (table 3& Figure 3-4). During the year 2020, under drought at reproductive stage condition, Cluster I was the largest with thirteen genotypes followed by Cluster II with six genotypes, cluster III with three genotypes, cluster IV, cluster V, and Cluster VI with one genotype each, while during 2021 cluster I was the largest with fourteen genotypes followed by cluster II with seven genotypes, cluster III, cluster IV, cluster V and cluster VI with one genotype respectively which is illustrated in table 4 and figure 5-6.

Under control condition during 2020, intra-cluster D<sup>2</sup> values ranged from 0.00 to 21.86. Among the clusters, cluster II had the maximum intra-cluster distance (21.86) while clusters III, IV, V, and VI recorded zero values as they included only single genotype in each cluster. The maximum inter-cluster D<sup>2</sup> was recorded between cluster III and cluster IV (72.52) followed by cluster III and cluster II (61.34) while the minimum D<sup>2</sup> value was found between cluster I and cluster III (25.09) followed by cluster IV and cluster VI (25.80). During the year 2021 under similar (control) conditions, intra-cluster D<sup>2</sup> values ranged from 0.00 to 20.70. Cluster III had the maximum intra-cluster distance (20.70) while clusters IV, V, and VI recorded zero values as they included only a single genotype in each cluster. The maximum inter-cluster D<sup>2</sup> was recorded between cluster IV and cluster V (232.82) followed by cluster V and cluster II while the minimum D<sup>2</sup> value was found between cluster I and cluster V (21.45) followed by cluster II and cluster VI (29.64) (table 5). Based on the cluster composition and inter-cluster distance, the genotype may be selected from clusters II, III and IV during 2020 and II, V and IV during 2021 in order to create variation through hybridization which will result in generation of segregating population under control condition [13; 6; 15; 9; 14; 1].

Under drought stress at vegetative stage condition during the year 2020, intra-cluster D<sup>2</sup> values ranged from 0.00 to 36.77. Cluster II had the maximum intra-cluster distance (36.77) while clusters III, IV, V and VI recorded zero values as they included only a single genotype in each cluster. The maximum inter-cluster D<sup>2</sup> was recorded between cluster II and cluster VI (376.17) followed by cluster VI & III (267.01) while the minimum D<sup>2</sup> value was found between cluster III and cluster V (35.41) followed by cluster IV and cluster VI (37.96). During the year 2021 under similar stress condition, intra-cluster D<sup>2</sup> values ranged from 0.00 to 25.97, cluster III had the maximum intra-cluster distance (25.97) while clusters IV and VI recorded zero. The maximum inter-cluster D<sup>2</sup> was recorded between cluster IV and cluster V (195.34) followed by cluster V & cluster III (155.90) while the minimum D<sup>2</sup> value was found between cluster IV and cluster VI (20.34) followed by cluster I and cluster IV (26.93) (table 6). Selection of genotypes from clusters II, VI and III (reported in the year 2020) and clusters IV, V and III (cluster reported in the year 2021) would result in achieving drought tolerant segregating population after hybridisation [ 5; 13; 6; 15; 1].

In the year 2020 under drought stress at reproductive stage condition, intra-cluster D<sup>2</sup> values ranged from 0.00 to 29.62 and cluster I had the maximum intra-cluster distance (29.62) The maximum inter-cluster D<sup>2</sup> was recorded between cluster III and cluster VI (371.76) followed by cluster VI & cluster I (217.21) while the minimum D<sup>2</sup> value was found between cluster II and cluster V (50.38). During the year 2021 under similar stress condition, intra-cluster D<sup>2</sup> values ranged from 0.00 to 33.57. Cluster I had the maximum intra cluster distance (33.57) The maximum inter-cluster D<sup>2</sup> was recorded between cluster II and

cluster VI (552.08) followed by cluster VI and cluster I (357.79) while the minimum  $D^2$  value was found between cluster I and cluster III (48.44) (table 7). This clearly indicated that in order to breed for drought tolerance genotypes must be selected from clusters VI, III and I during 2020 and 2021 respectively [5; 13; 6; 15;1].

Under control condition, during 2020 Cluster mean showed considerable difference for the various characters studied. Cluster V was early flowering as well as maturing with maximum plant height, number of Primary Branches per plant, leaf area and chlorophyll content. Cluster IV had highest number of clusters per plant, Number of pods per plant and protein content. Seed per pod, 100 seed weight, harvest index, proline content and seed yield per plant was highest in cluster III. The relative water content was maximum in cluster VI. For most of the characters studied, cluster III recorded the highest values and cluster II recorded the lowest. During the year 2021, Cluster IV was early flowering, early maturing, depicted the maximum number of clusters per plant, pods per plant, Seed per pod, 100 seed weight, harvest index, proline content, leaf area, chlorophyll content and seed yield per plant. Cluster V genotypes had maximum plant height and number of Primary Branches per plant. The maximum amount of protein and relative water content was observed for cluster VI. For most of the characters studied, cluster IV recorded highest values and cluster V recorded the lowest (table 8). The cluster mean of different clusters enables to identify the character to be chosen for hybridization program. Hence under control condition, genotypes must be selected from cluster III during 2020 and cluster IV during 2021 as they have higher mean for most of the traits under investigation which will result in improvement of the aforementioned traits [13; 9; 16; 4; 2; 10].

Under drought at vegetative stage condition, during the year 2020, Cluster V & VI was early flowering and maturing. Cluster I genotypes had maximum plant height. Cluster VI had maximum number of Primary Branches per plant, cluster per plant, pods per plant, seed per pod, 100 seed weight, harvest index, proline content, leaf area, chlorophyll content and seed yield per plant. The maximum amount of protein was observed for cluster II. The relative water content was maximum in cluster III. For most of the characters studied, cluster VI recorded highest values and cluster II & cluster III recorded the lowest. Under similar stress condition during the year 2021, Cluster V was early flowering and early maturing with highest number of cluster per plant, pods per plant, 100 seed weight, proline content, relative water content, leaf area, chlorophyll content and seed yield per plant. Cluster VI genotypes had maximum plant height. The number of Primary Branches per plant and harvest index was maximum in cluster IV. The maximum amount of protein was observed for cluster VI. Cluster V recorded the highest values and clusters III & IV recorded the lowest for most of the characters studied (table 8). If the occurrence of drought coincides with the vegetative stage, then for hybridization, genotypes must be selected from cluster VI and III during 2020 and 2021 respectively as they have high cluster mean under drought stress induced at vegetative stage [5; 13; 6; 15; 1].

Under drought at reproductive stage condition during the year 2020, Cluster V was early flowering and early maturing. Cluster III genotypes had maximum plant height, protein content and relative water content. Number of Primary Branches per plant, cluster per plant, Seed per pod, 100 seed weight, proline content and leaf area was highest in cluster VI. The number of pods per plant, harvest index, chlorophyll content and seed yield per

plant was maximum in cluster IV. For most of the characters studied, cluster VI recorded the highest values and cluster III recorded the lowest. During the year 2021, Cluster IV & VI were early flowering and early maturing. Cluster III genotypes had maximum plant height. Cluster V had the highest Primary Branches per plant and protein content. The highest number of clusters per plant, pods per plant, 100 seed weight, proline content, relative water content, leaf area, chlorophyll content and seed yield per plant was observed in cluster VI Seed per pod was highest in cluster II. The highest harvest index was recorded for the genotypes of cluster IV (table 8). If the occurrence of drought coincides with the reproductive stage, then in the breeding program for drought tolerance genotypes must be selected from cluster VI and cluster II for hybridization during 2020 and 2021 respectively. This cluster depicted a higher cluster mean for most of the traits under drought stress induced at the reproductive stage [5; 13; 6; 15; 1].

Under control and drought at vegetative stage condition, during both the years ie. 2020 and 2021, leaf area contributed the maximum to the diversity by taking first rank out of 300 combinations respectively while in drought at reproductive stage condition, during the year 2020, seed yield contributed the maximum to the diversity. In the year 2021, 100 seed weight contributed the maximum to the diversity by taking first rank out of 300 combinations (table 9) [13]. These findings confirmed that selection of divergent parents for based on these characteristics might be useful in the formulation of breeding programme for drought tolerance as well as large number of transgressive segregants may be obtained in subsequent generations. Thus on the basis of inter-cluster distance, cluster means, characters with high contribution to  $D^2$  values, dendrogram and by comparing the mean values of the all the genotypes; the following five genotypes viz., Samrat, IPM 2-05, Banka Local Mung, Pusa Vishal, KL 4 and GM 99-3 would give most desirable result in the formulation of future breeding program for drought tolerance in mungbean.

## CONCLUSION

Genetic divergence enables to select genetically diverse parents in order to obtain high-yielding genotypes for a successful and efficient hybridization programme under drought stress condition. The 'V' statistic value was highly significant indicating significant differences among twenty-five genotypes. The twenty-five mungbean genotypes were grouped into six clusters during both the years under control and stress conditions. Under control condition cluster I & II was the largest during 2020 & 2021 respectively. Based on the cluster composition and inter-cluster distance, the genotype may be selected from clusters II, III and IV during 2020 and II, V and IV during 2021 under control conditions in-order to obtain better transgressive segregants. Under drought stress at the vegetative stage condition and drought stress at the reproductive stage condition, cluster II and I was the largest during 2020 while cluster III & I was the largest respectively. Selection of genotypes from clusters II, VI and III (reported in the year 2020) and cluster IV, V and III (cluster reported in the year 2021) would result in achieving drought tolerant segregating population after hybridization in case of drought stress induced at vegetative stage. While for drought stress induced at the reproductive stage condition selection of genotypes from cluster VI, III, and I during 2020 and 2021 respectively, would be effective for drought tolerance breeding. Under control condition, selection of genotypes from cluster III during 2020

and cluster IV during 2021 will result in improvement of the aforementioned traits as they have higher mean for most of the traits under investigation. If the occurrence of drought coincides with the vegetative stage, then for hybridization, genotypes must be selected from clusters VI and III during 2020 and 2021 respectively while for drought stress at the reproductive stage, genotypes must be selected from cluster VI and cluster II for hybridization during 2020 and 2021 respectively as these clusters depicted higher mean for traits associated with drought. Under control and drought at vegetative stage condition, leaf area contributed the maximum to the diversity by taking first rank out of 300 combinations respectively during both the years while in drought at reproductive stage condition, during the year 2020, seed yield contributed the maximum to the diversity while in 2021, 100 seed weight contributed the maximum to the diversity by taking first rank out of 300 combinations. Thus selection on the basis of these traits would be rewarding. Therefore on the basis of inter-cluster distance, cluster means, characters with high contribution to  $D^2$  values, and dendrogram and by comparing the mean values of the all the genotypes; the following five genotypes viz., Samrat, IPM 2-05, Banka Local Mung, Pusa Vishal, KL 4 and GM 99-3 would give most desirable result in formulation of future breeding programme for drought tolerance in mungbean.

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**DISCLOSURE STATEMENT:** The authors declare that there is no conflicts of interest to report regarding the present study.

**Table 1: Analysis of variance for dispersion in twenty five mungbean genotypes under control, drought at vegetative stage and drought at reproductive stage during summer 2020 & 2021**

Source of variation	Degrees of freedom	Mean sum of squares					
		C Y1	C Y2	V Y1	V Y2	R Y1	R Y2
Genotype	24	8.83E07**	3.79E07**	2.28E05**	2.39E08**	8.21E05**	4.21E06**
Error	47	5.33E-01	1.68E-01	4.11E-05	3.22E-01	1.47E-04	3.52E-04
Total	71	2.98E07	1.28E07	7.73E04	8.11E07	2.77E05	1.42E06

CY1- Control condition during summer 2020, CY2- Control condition during summer 2021, VY1- Drought at vegetative stage condition during summer 2020, VY2- Drought at vegetative stage condition during summer 2021, RY1-Drought at reproductive stage condition during summer 2020, RY2- Drought at vegetative stage condition during summer 2020

\*\* - Significant at 1.0 per cent level of probability, \* - Significant at 5.0 per cent level of probability

**Table 2: Cluster composition of twenty five mungbean genotypes (Tocher's method) in control condition during summer 2020 & 2021**

Control condition during 2020		
Cluster no.	No. of genotypes	Genotypes
I	6	HUM 16, MH 565, Meha, PM 5, GM 99-125, ML 818, LGG 524, Pusa Vishal, IPM 409-4, KL4, Banka Local mung, Pusa 1081
II	4	IC 314326, MH 96-1, IPM 430-1, HUM 12, MH 805, IPM 2-14 IPM 2-3, Pant Mung, IPM 205-07
III	1	Samrat
IV	7	PusaBaishakhi
V	3	MH 921
VI	4	IC 39403
Control condition during 2021		
Cluster no.	No. of genotypes	Genotypes
I	4	IC 314326, HUM 12, IPM 430-1, MH 96-1
II	11	Pusa 1081, ML 818, IPM 205-7, GM 99-125, Meha, LGG 524, HUM 16, PM 5, Pusa Vishal, Banka Local Mung, MH 921
III	7	IC 39403, MH 565, IPM 2-14, IPM 2-3, Pant Mung, IPM 409-4, KL 4
IV	1	Samrat
V	1	MH 805
VI	1	PusaBaishakhi

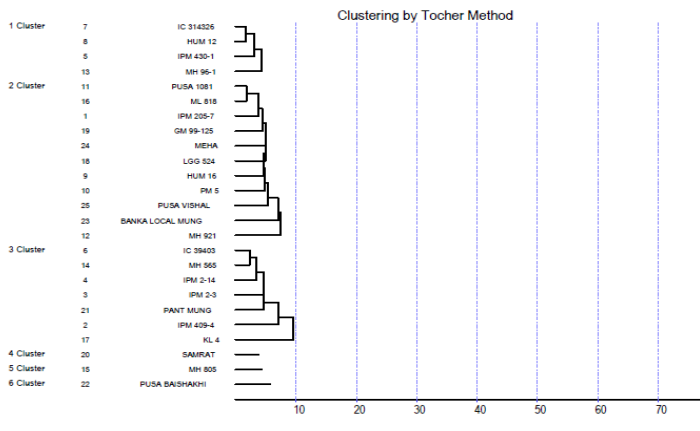


Figure 1: Dendrogram of twenty five mung bean genotype obtained through Tocher's method of classification under control condition during summer 2020

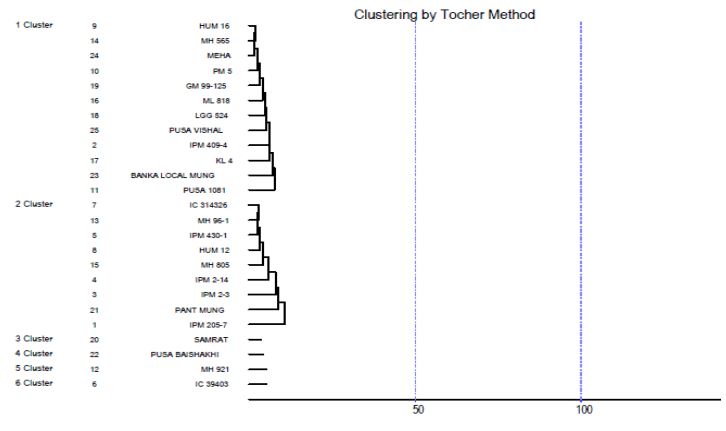


Figure 2: Dendrogram of twenty five mung bean genotype obtained through Tocher's method of classification under control condition during summer 2021

Table 3: Cluster composition of twenty five mungbean genotypes (Tocher's method) in drought at vegetative stage condition during summer 2020 & 2021

Drought at vegetative stage condition during 2020		
Cluster no.	No. of genotypes	Genotypes
I	7	LGG 524, Pusa Vishal, GM 99-125, Meha, MH 921, Pusa 1081, IPM 205-7
II	14	MH 805, Pant Mung, PusaBaishakhi, IPM 2-3, IPM 2-14, IC 39403, IC 314326, HUM 12, IPM 409-4, MH 96-1, ML 818, HUM 16, MH 565, IPM 430-1
III	1	PM 5
IV	1	Banka Local Mung
V	1	KL 4
VI	1	Samrat
Drought at vegetative stage condition during 2021		
Cluster no.	No. of genotypes	Genotypes
I	5	IPM 409-7, ML 818, Pusa 1081, HUM 12, IC 314326
II	7	GM 99-125, Meha, LGG 524, MH 921, PM 5, Pusa Vishal, KL 4
III	9	MH 565, MH 805, MH 96-1, HUM 16, Pant Mung, IC 39403, PusaBaishakhi, IPM 2-3, IPM 2-14
IV	1	IPM 430-1
V	2	Samrat, Banka Local Mung
VI	1	IPM 205-7

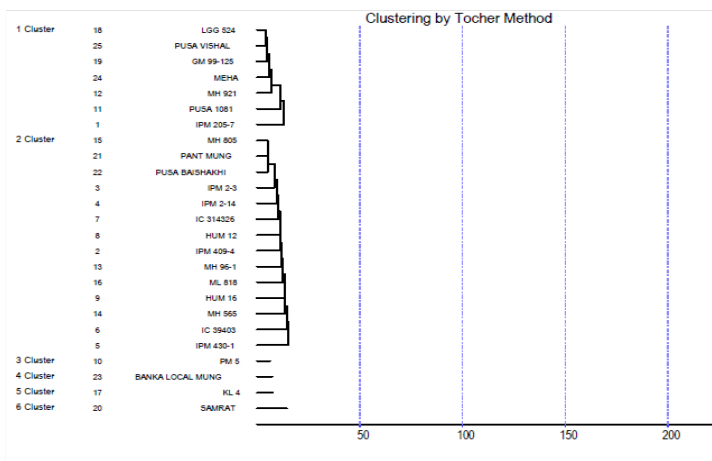


Figure 3: Dendrogram of twenty five mung bean genotype obtained through Tocher's method of classification under drought at vegetative stage condition during summer 2020

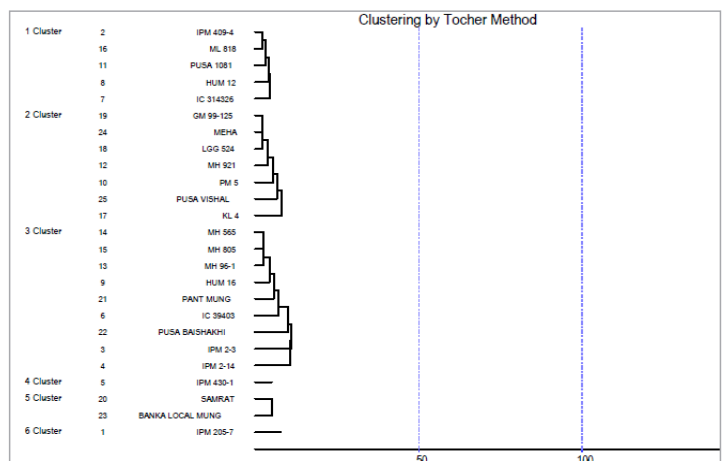
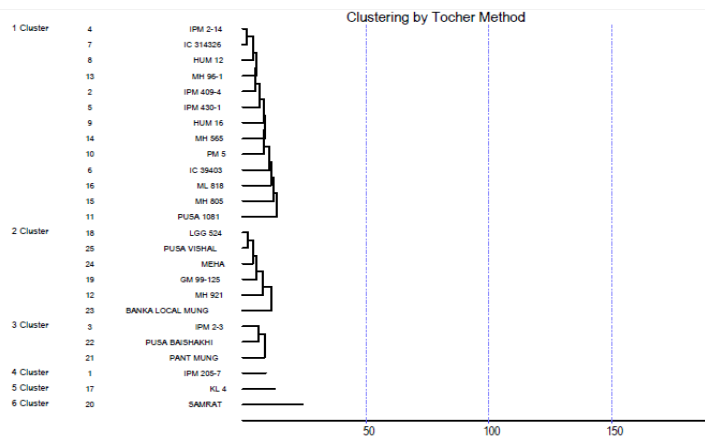


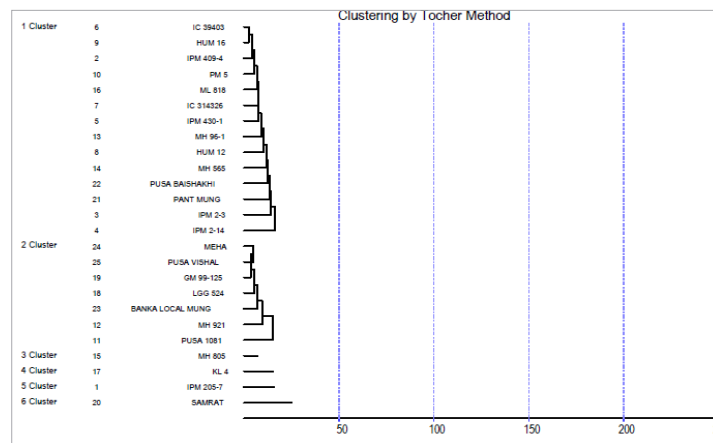
Figure 4: Dendrogram of twenty five mung bean genotype obtained through Tocher's method of classification under drought at vegetative stage condition during summer 2021

**Table 4: Cluster composition of twenty five mungbean genotypes (Tocher's method) in drought at vegetative stage condition during summer 2020 & 2021**

Drought at reproductive stage condition during 2020		
Cluster no.	No. of genotypes	Genotypes
I	13	IPM 2-14, IC 314326, HUM 12, MH 96-1, IPM 409-4, IPM 430-1, HUM 16, MH 565, PM 5, IC 39403, ML 818, MH 805, Pusa 1081
II	6	LGG 524, Pusa Vishal, Meha, GM 99-125, MH 921, Banka Local Mung
III	3	IPM 2-3, PusaBaishakhi, Pant Mung
IV	1	IPM 205-7
V	1	KL 4
VI	1	Samrat
Drought at Reproductive stage condition during 2021		
Cluster no.	No. of genotypes	Genotypes
I	14	IC 39403, HUM 16, IPM 409-7, PM 5, ML 818, IC 314326, IPM 430-1, MH 96-1, HUM 12, MH 565, PusaBaishakhi, Pant Mung, IPM 2-3, IPM 2-14
II	7	Meha, Pusa Vishal, GM 99-125, LGG 524, Banka Local Mung MH 921, Pusa 1081
III	1	MH 805
IV	1	KL 4
V	1	IPM 205-7
VI	1	Samrat



**Figure 5: Dendrogram of twenty five mung bean genotype obtained through Tocher's method of classification under drought at reproductive stage condition during summer 2020**



**Figure 6: Dendrogram of twenty five mung bean genotype obtained through Tocher's method of classification under drought at reproductive stage condition during summer 2020**

**Table 4: Cluster composition of twenty five mungbean genotypes (Tocher's method) in drought at vegetative stage condition during summer 2020 & 2021**

Control 2020							Control 2021						
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6		Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	<b>16.81</b>	37.40	25.09	46.72	26.27	29.02	Cluster 1	<b>12.36</b>	88.44	35.37	162.61	21.45	76.96
Cluster II		<b>21.86</b>	61.34	31.52	59.00	32.87	Cluster II		<b>17.30</b>	40.41	35.08	151.22	29.64
Cluster III			<b>0.00</b>	72.52	26.05	58.68	Cluster III			<b>20.70</b>	93.26	76.26	35.46
Cluster IV				<b>0.00</b>	43.87	25.8	Cluster IV				<b>0.00</b>	232.82	77.81
Cluster V					<b>0.00</b>	33.72	Cluster V					<b>0.00</b>	139.45
Cluster VI						<b>0.00</b>	Cluster VI						<b>0.00</b>

Diagonal bold indicate intra cluster distance while remaining indicate inter cluster distance

**Table 6: Average inter and intra cluster distance in twenty five mung bean genotypes under drought at vegetative stage condition during summer 2020 & 2021**

Drought at vegetative stage during 2020							Drought at vegetative stage during 2021						
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6		Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	<b>29.61</b>	85.57	65.02	68.80	56.85	165.56	Cluster 1	<b>13.17</b>	38.71	29.28	26.93	119.10	33.49
Cluster II		<b>36.77</b>	53.26	193.58	58.11	376.17	Cluster II		<b>18.62</b>	51.79	73.17	56.77	47.31
Cluster III			<b>0.00</b>	115.32	35.41	267.01	Cluster III			<b>25.97</b>	37.39	155.90	47.47
Cluster IV				<b>0.00</b>	120.83	37.96	Cluster IV				<b>0.00</b>	195.34	20.34
Cluster V					<b>0.00</b>	255.79	Cluster V					<b>13.44</b>	132.01
Cluster VI						<b>0.00</b>	Cluster VI						<b>0.00</b>

Diagonal bold indicate intra cluster distance while remaining indicate inter cluster distance

**Table 7: Average inter and intra cluster distance in twenty five mung bean genotypes under drought at reproductive stage condition during summer 2020 & 2021**

Drought at reproductive stage during 2020							Drought at reproductive stage during 2021						
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6		Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	<b>29.62</b>	67.91	54.84	62.53	55.40	217.21	Cluster 1	<b>33.57</b>	121.65	48.44	87.17	104.07	357.79
Cluster II		<b>25.78</b>	150.19	50.48	50.38	78.97	Cluster II		<b>29.42</b>	233.30	116.28	76.37	101.00
Cluster III			<b>28.78</b>	138.25	120.01	371.76	Cluster III			<b>0.00</b>	117.90	214.95	552.08
Cluster IV				<b>0.00</b>	74.43	121.59	Cluster IV				<b>0.00</b>	180.03	262.12
Cluster V					<b>0.00</b>	132.49	Cluster V					<b>0.00</b>	207.15
Cluster VI						<b>0.00</b>	Cluster VI						<b>0.00</b>

Diagonal bold indicate intra cluster distance while remaining indicate inter cluster distance

**Table 8: Cluster mean for fifteen quantitative and biochemical parameters in mung bean under control, Drought at Vegetative condition, Drought at Reproductive condition during summer 2020 & 2021**

Cluster mean during summer 2020 under control condition															
	DFF	DM	PH	PBP	CPP	PPP	SPP	100 SW	HI	PRT	PRL	RWC	LA	CC	SY
Cluster 1	43.92	69.28	44.51	2.98	8.43	15.56	10.32	4.26	0.63	4.92	2.09	80.58	71.50	43.63	6.22
Cluster 2	51.19	76.33	44.56	2.82	7.50	13.22	9.46	4.20	0.56	6.50	1.60	79.23	49.89	40.07	5.29
Cluster 3	39.33	64.33	46.76	3.77	11.51	21.26	12.05	4.66	0.76	4.16	2.62	76.66	60.71	46.39	8.50
Cluster 4	54.00	79.00	46.75	3.98	27.11	17.98	9.15	4.16	0.63	10.11	1.65	83.19	69.14	39.91	7.19
Cluster 5	37.33	62.67	48.88	3.99	10.37	19.70	10.29	4.28	0.68	8.84	2.44	77.67	77.31	44.66	7.88
Cluster 6	47.00	72.00	40.42	3.05	7.62	13.50	10.47	4.36	0.73	9.63	1.81	86.13	61.29	46.14	5.40
Cluster mean during summer 2021 under control condition															
	DFF	DM	PH	PBP	CPP	PPP	SPP	100 SW	HI	PRT	PRL	RWC	LA	CC	SY
Cluster 1	50.83	75.83	41.41	2.68	7.21	13.27	9.94	4.26	0.70	5.23	2.12	77.97	42.18	40.31	5.31
Cluster 2	45.67	71.15	45.32	3.23	9.35	17.23	10.17	4.31	0.70	5.39	2.55	80.52	80.36	44.19	6.89
Cluster 3	46.95	71.95	41.61	2.88	6.31	12.60	10.02	4.07	0.70	5.56	2.11	84.45	58.71	42.74	5.04
Cluster 4	36.67	63.67	46.75	3.91	11.82	22.87	10.95	4.73	0.82	4.48	3.38	83.29	94.89	48.17	9.15
Cluster 5	49.67	74.67	49.17	2.09	5.75	10.88	8.64	4.33	0.37	6.90	1.63	74.44	32.46	39.96	4.35
Cluster 6	51.33	76.33	45.08	4.02	7.81	15.45	8.97	4.17	0.59	10.25	1.79	86.38	74.58	40.90	6.1
Cluster mean during summer 2020 under drought at vegetative stage condition															
	DFF	DM	PH	PBP	CPP	PPP	SPP	100 SW	HI	PRT	PRL	RWC	LA	CC	SY
Cluster 1	36.67	59.95	39.24	1.53	6.22	8.72	6.46	3.55	0.35	2.51	3.60	70.69	39.94	45.56	2.46
Cluster 2	41.33	63.98	35.74	1.37	3.21	4.72	5.17	3.11	0.34	4.01	2.33	73.46	32.01	41.75	1.33
Cluster 3	33.67	58.67	34.43	1.45	3.67	4.97	4.74	2.89	0.27	1.64	3.83	76.40	38.85	46.64	1.40
Cluster 4	33.67	57.67	36.45	1.54	6.21	11.43	7.12	3.61	0.53	3.43	4.14	70.43	62.51	45.18	3.22
Cluster 5	30.67	54.00	33.59	1.47	3.11	6.73	5.74	3.55	0.40	1.98	3.08	68.53	37.11	40.33	1.90
Cluster 6	30.67	55.67	38.77	1.87	8.07	14.59	7.39	4.07	0.56	1.53	4.46	70.27	73.42	47.45	4.11
Cluster mean during summer 2021 under drought at vegetative stage condition															
	DFF	DM	PH	PBP	CPP	PPP	SPP	100 SW	HI	PRT	PRL	RWC	LA	CC	SY
Cluster 1	42.27	65.87	31.67	1.46	3.68	6.91	5.58	3.17	0.32	2.19	2.66	69.46	36.58	41.78	1.95
Cluster 2	33.76	58.48	37.49	1.48	5.35	6.94	6.22	3.58	0.61	3.28	3.50	73.83	44.73	44.11	1.95
Cluster 3	39.78	62.78	37.36	1.31	2.63	4.74	4.94	2.98	0.15	3.67	2.61	75.21	30.14	41.64	1.33
Cluster 4	45.67	69.00	31.22	1.21	3.20	7.60	6.04	3.40	0.72	3.00	2.49	74.13	22.93	39.28	2.14
Cluster 5	33.00	56.17	35.43	2.01	7.80	10.20	7.77	3.98	0.57	3.73	4.15	76.62	66.91	48.83	2.87
Cluster 6	42.67	66.33	40.09	1.29	7.00	9.48	5.31	3.73	0.38	4.80	2.81	75.36	34.03	43.03	2.67
Cluster mean during summer 2020 under drought at reproductive stage condition															
	DFF	DM	PH	PBP	CPP	PPP	SPP	100 SW	HI	PRT	PRL	RWC	LA	CC	SY



<b>Cluster 1</b>	45.72	69.33	37.45	1.95	2.98	5.33	5.25	3.20	0.27	4.13	2.74	73.35	41.38	41.50	1.50
<b>Cluster 2</b>	40.00	63.83	41.16	2.34	5.71	7.45	6.41	3.63	0.26	4.22	4.07	74.66	56.05	46.57	2.10
<b>Cluster 3</b>	49.78	69.11	42.85	1.29	1.59	2.69	4.40	2.59	0.08	6.35	1.82	76.91	40.11	35.08	0.76
<b>Cluster 4</b>	35.00	76.33	39.71	1.88	4.95	12.48	6.34	3.54	0.49	4.63	2.51	71.73	50.93	38.16	3.52
<b>Cluster 5</b>	34.33	59.00	36.03	2.12	2.23	6.32	5.31	3.76	0.30	3.14	3.74	68.62	54.52	38.19	1.78
<b>Cluster 6</b>	36.33	61.33	41.21	2.48	7.87	11.89	6.98	4.07	0.40	3.07	4.82	70.29	83.24	49.04	3.35
<b>Cluster mean during summer 2021 under drought at reproductive stage condition</b>															
	<b>DFE</b>	<b>DM</b>	<b>PH</b>	<b>PBP</b>	<b>CPP</b>	<b>PPP</b>	<b>SPP</b>	<b>100 SW</b>	<b>HI</b>	<b>PRT</b>	<b>PRL</b>	<b>RWC</b>	<b>LA</b>	<b>CC</b>	<b>SY</b>
<b>Cluster 1</b>	47.24	70.17	36.84	1.73	2.52	5.14	5.14	3.05	0.33	3.93	2.70	73.59	39.43	39.81	1.45
<b>Cluster 2</b>	42.29	65.76	39.89	2.22	5.49	7.52	6.39	3.64	0.30	3.63	3.69	73.19	58.44	44.87	2.12
<b>Cluster 3</b>	46.00	67.33	43.40	1.50	1.15	3.66	4.51	2.88	0.13	3.43	2.29	72.45	27.39	36.80	1.03
<b>Cluster 4</b>	34.67	58.67	30.58	1.99	2.23	6.38	5.69	3.23	0.74	5.68	4.63	73.16	58.07	39.41	1.80
<b>Cluster 5</b>	48.33	79.00	42.21	1.29	4.83	10.91	4.75	3.48	0.36	5.96	2.35	77.45	51.26	41.11	3.07
<b>Cluster 6</b>	34.67	59.67	40.98	2.73	7.84	11.01	5.14	3.93	0.37	5.17	4.79	79.69	82.96	51.98	3.10

DFE- Days to 50% flowering, DM- Days to maturity, PH- Plant height, PBP- Primary branches per plant, CPP- Clusters per plant, PPP- Pods per plant, SPP- Seed per pod, 100 SW- 100 Seed weight, HI- Harvest index, PRT- Protein content, PRL- Proline content, RWC- Relative water content, LA- Leaf area, CC- Chlorophyll content, SY- Seed yield per plant

**Table 9: Contribution of different quantitative characters to diversity in mungbean under control, drought at vegetative stage and drought at reproductive stage during summer 2020 & 2021**

Sl. No.	Characters	2020						2021					
		control		V		R		control		V		R	
		TRF	% contribution	TRF	% contribution	TRF	% contribution	TRF	% contribution	TRF	% contribution	TRF	% contribution
1	DFE	46	15.33%	46	15.33%	0	0%	30	10%	41	13.67%	17	5.67%
2	DM	0	0%	0	0%	49	16.33%	3	1%	6	2%	17	5.67%
3	PH	0	0%	0	0%	0	0%	0	0%	5	1.67%	0	0%
4	PBP	0	0%	0	0%	1	0.33%	4	1.33%	0	0%	5	1.67%
5	CPP	41	13.67%	41	13.67%	8	2.67%	0	0%	17	5.67%	20	6.67%
6	PPP	2	0.67%	2	0.67%	21	7%	4	1.33%	0	0%	2	0.67%
7	SPP	9	3%	9	3%	21	7%	1	0.33%	13	4.33%	0	0%
8	100 SW	5	1.67%	5	1.67%	55	18.33%	6	2%	41	13.67%	92	30.67%
9	HI	0	0%	0	0%	0	0%	0	0%	0	0%	0	0%
10	PRT	10	3.33%	10	3.33%	14	4.67%	6	2%	14	4.67%	9	3%
11	PRL	0	0%	0	0%	2	0.67%	1	0.33%	0	0%	2	0.67%
12	RWC	25	8.33%	25	8.33%	18	6%	24	8%	23	7.67%	18	6%
13	LA	139	46.33%	139	46.33%	26	8.67%	194	64.67%	130	43.33%	68	22.67%
14	CC	19	6.33%	19	6.33%	9	3%	25	8.33%	9	3%	17	5.67%
15	SY	4	1.33%	4	1.33%	76	25.33%	2	0.67%	1	0.33%	33	11%

DFE- Days to 50% flowering, DM- Days to maturity, PH- Plant height, PBP- Primary branches per plant, CPP- Clusters per plant, PPP- Pods per plant, SPP- Seed per pod, 100 SW- 100 Seed weight, HI- Harvest index, PRT- Protein content, PRL- Proline content, RWC- Relative water content, LA- Leaf area, CC- Chlorophyll content, SY- Seed yield per plant  
TRF- Times ranked first, V- Drought at vegetative stage, R- Drought at reproductive stage

## REFERENCES

1. Ahmad A., Razvi S. M., Rather M. A., Ahmad M., Zaffar G., Ganie S. A., Mir M. R. and Hakeem K. R. (2016). Estimation of Genetic Divergence in Mung Bean (*Vigna radiata* L.) under Temperate Ecology of Kashmir. *RRJBS*, 5(1): 30-34.
2. Das A, Biswas M, Ghosh K and Das K. (2010). Genetic divergence in green gram (*Vigna radiata* L. Wilczek). *J of Agronomy*. 9(3):126-30.
3. Evgenidis G., Traka- Mavrona E. and Koutsika-Sotiriou M. (2011). Principal component and cluster Analysis as a tool in the Assessment of Tomato Hybrids and Cultivars. *International Journal of Agronomy*. 1-7.
4. Gokulakrishnan, J., Sunil Kumar. B and Prakash, M. (2012). Studies on genetic diversity in mungbean (*Vigna radiata* L.). *Legume Research*. 35(1): 50-52.
5. Islam M. R., Kamal M. M., Hossain M. F., Hossain J., Azam M. G., Akhtar M. M., Hasan M. K., Al-Ashkar I., Almutaisi K. F., Sabagh A. E. L., Rahman M. A., Iqbal M. A., and Islam M. S. (2022). Drought tolerance in mung bean is associated with genotypic divergence, regulation of proline, photosynthetic pigment and water relation. *Phyton-International Journal of Experimental Botany*. DOI: 10.32604/phyton.2023.025138.
6. Joshi, D.P., Parmar, L.D., Meena, R.K. and Chaudhary, G.K. (2022). Estimation of Genetic Diversity in Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes Grown in Gujarat. *Legume Research*. 45(7): 828-833. DOI: 10.18805/LR-4836.
7. Mahalanobis P.C. (1928). On the generalised distance in statistics. *Proceedings of the National Academy of Sci.*, 19: 201-208.
8. Mahalanobis P.C. (1936). On the generalized distance in statistics. *Proceedings National Academy of Science India*, 249-55.
9. Murugan S., Jeevitha S., Karthikeyan R., Vignesh M., Malarkodi A., Tirumalai R., Nainu A. J., Ananadan R. and Prakash M. (2018). Estimation of morphological and molecular genetic diversity in blackgram [*vigna mungo* (L.) Hepper] under YMV hotspot regime, *Horticultural Biotechnology Research*, 4: 06-09
10. Rahim, M.A., Mia, A.A., Mahmud, F., Zeba, N and Afrin, K.S. 2010. Genetic variability, character association and genetic divergence in mungbean (*Vigna radiata*(L).Wilczek). *Plant Omics Journal*. 3(1): 1-6.
11. Rao C.R. (1948). The utilization of multiple measurements in problems of biological classification (with discussion). *J. Roy. Statist. Soc., Series BIO*, 159-193.
12. Rao, C.R. (1952). *Advance Statistical Methods in Biometric Research*. John Wiley and Sons. Inc., New York.
13. Reyes J. A. O., Delfin E. F., Reyes M. E. C. and Ocampo E. T.M. (2022). Physiological and yield responses of selected mungbean genotypes to terminal drought. *Philippine Journal of Science*, 151 (2): 739-750
14. Sen M. and D.K.De (2017). Genetic divergence in mung bean. *Legume Research*, 40 (1) : 16-21.
15. Sirisha A. B. M., Banu S. K. H. and Saritha H. (2020). Genetic Divergence Studies using Mahalanobis D Square Analysis in *Sesame (Sesamum indicum L.)* Germplasm. *Int.J.Curr.Microbiol.App.Sci*, 9(8): 2224-2229
16. Sri vidya S., Sabesan T. and Saravanan K. (2018). Genetic divergence studies in blackgram (*vigna mungol.*) For yield and quantitative traits. *Journal of Phytology*, 10: 24-26
17. Vavilov, N. I. (1951). The origin, variation, immunity and breeding of cultivated plants, *Chronica Botanica*, 13.
18. Wilks, S.S. 1932. Certain generalization in the analysis of variance. *Biometrics*. 24: 471.