Original Research Article

ASSESSMENT OF GENETIC DIVERSITY IN GREEN GRAM [*Vigna radiata*(L.) Wilczek] FOR QUANTITATIVE AND QUALITATIVE TRAITS

ABSTRACT: The current study, "Assessment of genetic diversity in green gram [*Vigna radiata* (L.) Wilczek] for quantitative and qualitative traits" was carried out during the *kharif* of 2022 at the College of Agriculture, Dhule.The experimental materials consisted local collection of 42 mungbean genotypes which were evaluated in a randomized block design (RBD) with two replications, representing various eco-geographic regions for twelve different characters and studies of genetic divergence were carried out.The genetic diversity among landraces is determined by the range of D^2 values which varied from 44.68 (MG-2022-15 and MG-2022-30) to 1678.53 (MG-2022-18 and MG-2022-31) for each genotype, showing adequate variance. Based on D^2 levels, the 42 genotypes were split up into 16 groups with notable genetic differences. Cluster I and III were the largest, with 11 and 10 genotypes each. It was adjacent to Clusters II, which had eight genotypes.Based on inter-cluster means and per se performance, breeding programs may employ the following effective genotypes *viz*., MG-2022-31, MG-2022-42, MG-2022-21, MG-2022-40, MG-2022-39, MG-2022-14, MG-2022-11, MG-2022-18, MG-2022-02, MG-2022-25, and MG-2022-24 to further enhance grain yield and its contributing characters in mungbean.

KEYWORDS: Genetic diversity, mungbean, cluster, genotypes,

INTRODUCTION: The present study was conducted as it provides a quantitative assessment of the link between geographic and genetic diversity based on generalized distance and is useful for assessing the degree of genetic divergence. Due to their greater protein content than any other crop grown, pulses are one of the most important food crops in the world. India is the biggest producer, importer, and consumer of pulses worldwide. India is the biggest producer, importer, and consumer of pulses worldwide. Mungbean has been consumed in the form of common traditional food worldwide (Berihun*et al.*, 2017). It is a good source of protein, folate as well as iron in comparison to other legumes (Keatinge*et al.*, 2011). The seeds of mungbean constitute protein (24-28%), oil (1.0-1.5%), ash (4.5–5.5%), fiber (3.5-4.5%) and carbohydrates (62–65%) on dry weight basis.In India, greengram was grown on over 31.15 lakh acres in 2019–2020.

Mungbean is an excellent rotation crop in a rice-based cropping system because of its low input requirements, short crop duration, and strong worldwide demand. Mungbean is regarded as the hardiest pulse crop and is a significant pulse crop. Known most popularly as "poor mans meat," mungbean is the main source of protein for a substantial portion of the global vegetarian population.

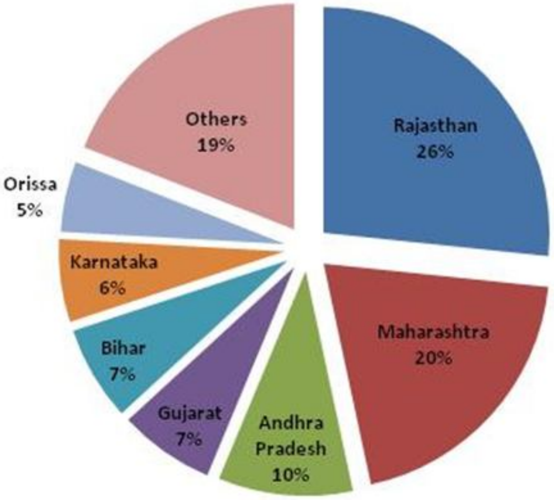

Figure 1: State-wise share of mungbean production in India (Anonymous, 2019)

The states that produced the most mungbean were Madhya Pradesh (1.57 lakh ha), Rajasthan (20.89 lakh ha), Karnataka (4.40 lakh ha), Maharashtra (3.94 lakh ha), and Orissa (1.48 lakh ha) (see figure 1). In 2020–21, the total area covered by green gram in India was approximately 35.79 lakh hectares, compared to 30.75 lakh hectares during the same period in 2019–20 (Anonymous, 2020). The study of diversity within a species is genetic diversity. More diversity increases the likelihood of choosing suitable genotypes for hybridization. The ability to estimate parental diversity may be aided by direct chemical examination of genetic material or gene products (Thorat *et al.,* 2023).

MATERIAL AND METHODS: The experimental materials for the present investigation included 42 genotypes of mungbean representing different eco-geographic regions, source of material was Assistant Pulse Breeder, Oilseed Research Station, Nimkhedi- Jalgoan and local collection from Dhagdaon. The 42 genotypes were evaluated in a Randomized Block Design (RBD) with two replications during *kharif* – 2022 at a spacing of 30 cm x 10 cm. Plants were evaluated for diverse characters like days for 50 % maturity, days to maturity, plant height (cm), number of pods per plant, pod length (cm), pod thickness (mm), number of clusters per plant, number of pods per cluster, number of seeds per pod, 100 seed weight (g), protein content (%), and seed yield per plant (g).

By calculating the organic nitrogen using the Kjeldahl technique described by Hawk et al. (1954), the protein content of dry seed was ascertained. Five plants were chosen for each genotype, and their seeds were bulked and ground in a grinder. At the Department of Soil Science, College of Agriculture, Dhule, 0.2 g of ground samples were subjected to a wet digestion procedure for nitrogen content analysis. Using the mean data from various sources, the analysis of variance for various characteristics was conducted using the Panse and Sukhatme (1995) approach. Diversity analysis will be done as per procedure given by Mahalanobis (1936) and clustering will be done by following the procedure of Rao (1952).

RESULTS AND DISCUSSION: Genetic diversity provides the foundation for trait improvement and adaptation to changing environmental conditions. Evaluation of germplasm resources has enabled breeders to identify valuable traits and select suitable parents for hybridization (Aswini *et al.*, 2023).The genetic diversity among the landraces is decided on the basis of the range of D^2 values among genotypes and high significant differences among the genotypes. Analysis of variance revealed extremely significant genotype differences for all characteristics in the current investigation, as shown in table 1.

Estimates of the population mean, range, and coefficient of variation were applied to the observations. There were notable differences across the genotypes, as evidenced by the large mean sum of squares for all attributes resulting from treatments.However, the replication-related differences were not statistically significant, suggesting that the experiment's land was uniform. High variation was present in all twelve characters that were examined. For seed yield per plant, D^2 values for all feasible pairs of 42 genotypes varied from 44.68 (MG-2022-15 and MG-2022-30) to 1678.53 (MG-2022-18 and MG-2022-31).

The Tocher's method for cluster formation was given by Rao (1952). The formation of clusters (figure 3) and finding out intra and inter-cluster divergence is aimed at making available basis for selection of parents for further hybridization programs. In table 2 averages inter and intra-cluster D^2 values are given. The cluster XIII and XIV (16.57) shown maximum inter-cluster distance, followed by cluster XV and XVI (15.75), cluster XII and XV (15.47), cluster XIII and XV (15.01) while minimum inter-cluster distance was found between cluster IV and V (3.52). In case of intra-cluster distance, cluster III had maximum intra-cluster distance (6.1) followed by cluster II (5.4), and cluster I (4.8). Whereas intra-cluster distance was not shown by clusters IV, V, VI, VII, VIII, IX, X, XI, XII, XIII, XIV, XV, XVI were solitary clusters (Fig. 3).

Mean performance of sixteen clusters for twelve characters are presented in table 3. Mean performance for character seed yields is the highest in cluster XVI (8.5 g) and cluster XV (3.64 g) was inferior among all the clusters. Cluster XI early flowered early matured, good in height but less in clusters per plant and 100 seeds weight resulted inferior in yield. The cluster mean for days to 50 per cent flowering was maximum of 38.75 days (cluster X), while for days to maturity, highest mean value was 77.50 days (cluster VII, VIII, XIII). The 56.83 cm (cluster VII) having maximum height among all clusters. A mean value for number of pods per plant was maximum for cluster XII (16.9), whereas mean value for pod length was maximum for cluster IV (9.18 cm).The highest mean performance for number of clusters per plant was observed in 4.97 (cluster X) and for number of pods per cluster is 5.95 (cluster XV). In case of seeds per pod, the highest mean value given by cluster XVI (11.31), 8.5 g is mean performance for 100 seeds weight and shown by cluster XVI. The highest mean value for protein content was found in cluster IX (24.53 per cent).

Using data collected, genetic divergence was determined for twelve characters of all the forty two genotypes in mungbean. From these 12 characters, the number of seeds per pod (46.57%) contributed maximum for divergence, followed by 100 seeds weight (24.27%) and number of clusters per plant (8.71%). However, the contribution of plant height (5.92%), number of pods per cluster (5.69%), Seed yield per plant (4.99%), pod thickness (2.67%) were moderate.

The contribution of pod length (0.47%), protein content (0.35%), days to 50% flowering (0.12%), days to maturity (0.12%), and number of pods per plant (0.12%) were negligible

Theclustering pattern indicates that, genotypes from different sources were clubbed into one groupandalsogenotypesofsamesourceformingdifferentclustersindicatingnorelationshipbetween geographical diversity and genetic divergence (Barate*et al.* 2020).The range of D^2 values across genotypes and the high significant difference between genotypes are used to determine the genetic diversity among landraces. The D^2 values demonstrated sufficient variation across the genotypes and varied from 44.68 (MG-2022-15 and MG-2022-30) to 1678.53 (MG-2022-18 and MG-2022-31). Solitary clusters included IV, V, VI, VII, VIII, IX, X, XI, XII, XIII, XIV, XV, and XVI. On the basis of diversity analysis, the best possible genotypes were taken which were desirable for specific character and are mentioned in table 5.

The findings suggests that there is substantial genetic diversity available among the genotypes. The genetic diversity was not to be necessarily associated with geographical origin. It was associated with genetic architecture of the genotypes. Also, the genotypes with more protein content, early flowering and maturing, maximum plant height with long and thick pod size, having more number of seeds per pod and better seed weight can give maximum yield in mungbean. On the basis of best suitable local genotypes for each trait, possible cross combinations are given in table 4 which can be further exploited to get desirable progenies.

SUMMARY AND CONCLUSIONS: The study's findings indicate that 42 genotypes were divided into 16 clusters, with cluster I having the most genotypes- 11 in all. All 42 genotypes were categorised into 16 clusters with significant genetic difference based on D^2 values. With 11 and 10 genotypes apiece, cluster I and III were the biggest, followed by cluster II, which had 8 genotypes each. With a D^2 value of (6.1), cluster III was the most divergent, followed by clusters II and I (5.4 and 4.8, respectively). This implies that the hybridisation algorithm has enough room to choose a variety of parents from these clusters in order to produce mungbean recombinants with a number of desired traits. It can be concluded that, MG-2022-31, MG-2022-42, MG-2022-21, MG-2022-40, MG-2022-39, MG-2022-14, MG-2022-11, MG-2022-18, MG-2022-02, MG-2022-25, and MG-2022-24 are effective genotypes that can be used in breeding programs to further improve grain yield and its contributing characters in mungbean based on inter-cluster means and per se performance.

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Table1:Analysisof variancefortwelvecharacters in mungbean

Sr. No.	Characters	Meansumof squares		
		Replication (1)	Genotypes (41)	Error (41)
1	Daysto 50%flowering	3.24	1.81**	1.10
2	Daysto maturity	4.30	2.07**	1.07

3	Plantheight(cm)	3.52	67.88**	13.80
4	Numberofclustersper plant	0.15	1.28**	0.17
5	Numberofpods per cluster	0.01	2.92**	0.20
6	Numberofpods per plant	0.17	7.18**	3.42
7	Numberofseedsper pod	0.52	3.95**	0.09
8	Podlength	0.00	1.10**	0.50
9	Podthickness	0.22	0.21**	0.06
10	100 seedsweight	0.00	1.34**	0.06
11	Proteincontent	2.29	2.29**	1.02
12	Seedyieldperplant	0.10	2.53**	0.36

* ,**significant at 5 and 1 per cent level, respectively.
Valuesin parenthesisindicates thedegrees offreedom.

Table2:Averageintraandinter-clusterD^2 valuesof twelveclustersinmungbean

Characters	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**	**XII**	**XIII**	**XIV**	**XV**	**XVI**
I	4.84	6.90	7.90	6.53	6.64	5.84	7.42	6.43	5.91	7.86	8.02	8.45	10.38	8.13	11.18	8.43
II		5.40	8.67	10.35	10.49	8.83	11.10	10.35	7.63	11.32	6.90	11.66	14.42	11.23	9.31	8.87
III			6.10	8.90	9.26	11.29	7.82	7.83	10.23	8.8	6.97	9.89	10.17	7.72	8.34	13.65
IV				0	3.52	7.00	7.11	5.19	7.26	5.59	11.00	6.67	7.84	5.23	13.72	11.47
V					0	6.54	6.90	6.23	6.83	6.87	11.97	4.60	8.07	5.06	14.48	10.86
VI						0	9.30	8.04	5.19	8.98	11.43	8.76	11.98	10.12	14.95	5.53
VII							0	3.66	10.32	5.75	9.5	8.28	4.86	6.77	11.96	13.08
VIII								0	9.27	4.51	8.97	8.72	5.81	6.28	12.16	12.22
IX									0	10.98	11.07	8.24	12.88	9.63	13.76	6.20
X										0	9.68	9.21	6.38	6.37	12.79	13.62
XI											0	13.41	12.73	11.11	5.64	12.56
XII												0	8.77	5.89	15.47	12.67
XIII													0	6.40	15.01	16.57
XIV														0	12.74	14.41
XV															0	15.75
XVI																0

Table3: Meanperformanceofsixteenclustersfortwelvecharactersinmungbean

Characters	Days to50 % flowering	Days tomaturity	Plantheight(cm)	No. ofclustersperplant	No. ofpodspercluster	No. ofpodsperplant	No. ofseedsperpod	Podlength(cm)	Podthickness(mm)	100 seedsweight(g)	Protein content (%)	Seedyieldperplant(g)
I	37.05	76.00	48.25	3.83	3.90	13.07	9.33	8.03	4.65	5.23	22.72	6.01
II	36.88	75.63	43.30	3.13	4.59	13.83	10.79	7.76	4.48	4.53	22.50	6.10
III	36.55	76.08	48.49	3.09	5.59	16.58	8.52	7.38	4.25	3.97	21.68	5.35
IV	38.00	75.50	44.30	3.85	3.92	13.40	7.71	9.18	5.46	5.08	22.34	4.98
V	38.50	75.00	43.87	3.86	5.02	15.77	7.55	8.67	4.62	5.76	22.86	6.22
VI	37.50	76.00	45.85	4.93	2.73	13.60	9.58	8.22	4.98	6.36	23.00	6.95
VII	38.00	77.50	56.83	4.35	4.06	15.40	7.20	7.34	4.00	5.51	21.99	5.51
VIII	36.00	77.50	55.15	4.79	3.27	14.50	7.69	8.96	4.68	5.12	23.42	5.16
IX	37.50	75.00	49.45	3.25	4.72	14.90	9.69	7.63	5.15	5.60	24.53	7.65
X	38.75	75.00	41.97	4.97	2.32	13.63	7.45	7.74	4.62	4.86	21.44	3.85
XI	36.50	75.50	50.02	3.35	3.43	13.60	10.02	7.39	4.18	3.73	22.10	4.18
XII	37.50	76.00	39.48	3.00	5.93	16.90	7.09	6.38	4.61	5.92	21.18	6.81
XIII	38.00	77.50	51.45	3.70	3.63	12.73	5.64	6.94	4.28	5.38	23.00	3.88
XIV	37.00	75.50	42.68	3.43	5.60	16.20	6.93	6.99	4.55	4.75	24.36	4.61
XV	37.50	76.25	53.16	2.90	5.95	13.30	10.37	6.45	4.10	3.02	21.00	3.64
XVI	38.00	75.00	51.42	4.53	3.11	13.90	11.31	8.56	4.76	6.54	23.23	8.50
AVERAGE	37.45	75.94	47.85	3.81	4.24	14.46	8.55	7.73	4.59	5.09	22.58	5.59

Figure 2:Clusterdiagramof fortytwo genotypesin mungbean

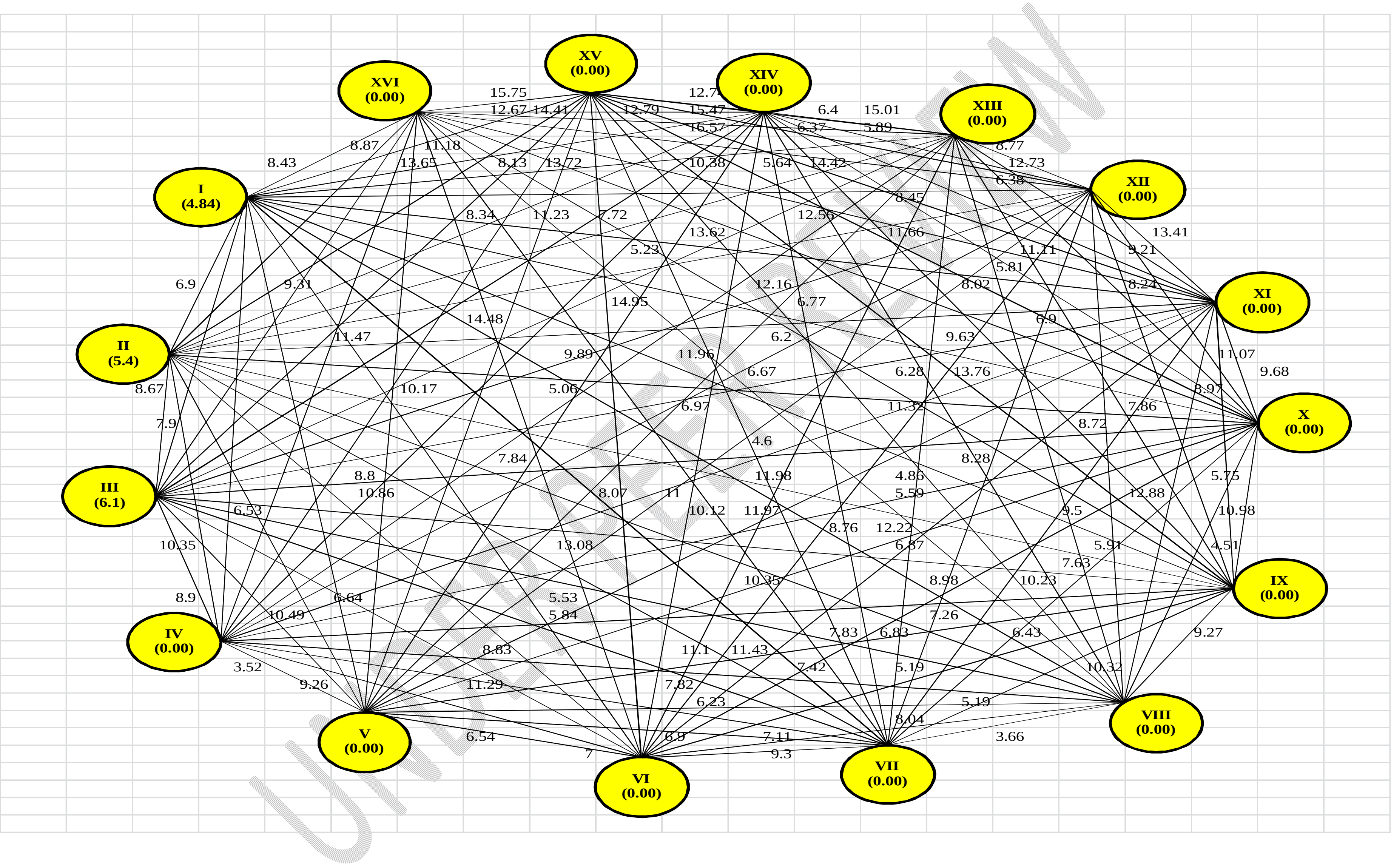

Table4:Tentativesuggestedcrossing programmeinfuture for improvement in mungbean

Sr. No.	Characterstobeimproved		Clustercombination withinter-cluster distance	Genotypespossible	Possiblecrosses
1	Earliness	Daysto50percentflowering	VIII×XI(8.97)	MG-2022-42 MG-2022-02	MG-2022-42× MG-2022-02
		Days tomaturity	IV×V(27.090)	MG-2022-39 MG-2022-23	MG-2022-39×MG-2022-23
2	Plantheight		VII×VIII(3.66)	MG-2022-25 MG-2022-42	MG-2022-25×MG-2022-42
3	Numberofclustersperplant		VI×X(8.98)	MG-2022-34 MG-2022-24	MG-2022-34× MG-2022-24
4	Numberofpods per cluster		XII × XV (15.47)	MG-2022-14 MG-2022-04	MG-2022-14×MG-2022-04
5	Numberofpods per plant		III × XII (9.89)	MG-2022-21 MG-2022-14	MG-2022-21×MG-2022-14

6	Numberofseedsper pod	II × XVI (8.87)	MG-2022-40 MG-2022-31	MG-2022-40 × MG-2022-31
7	Podlength(cm)	VIII ×IV(5.19)	MG-2022-42 MG-2022-39	MG-2022-42×MG-2022-39
8	Podthickness(mm)	IX ×IV(7.26)	MG-2022-11 MG-2022-39	MG-2022-11×MG-2022-39
9	100 seedsweight(g)	VI×XVI(5.53)	MG-2022-34 MG-2022-31	MG-2022-34×MG-2022-31
10	Protein content(%)	XIV×IX(9.63)	MG-2022-31 MG-2022-11	MG-2022-31 × MG-2022-11
11	Seedyieldperplant(g)	IX×XVI(6.2)	MG-2022-11 MG-2022-31	MG-2022-11 ×MG-2022-31

Table5:Tableincludinglistofgenotypeswithdesirablecharacters

Genotypes	Characters	Genotypes	Characters
MG-2022-31	Numberofseedsperpod,Seedyield perplant	MG-2022-42	Pod length
MG-2022-42	Plantheight, Pod length	MG-2022-40	Numberofseedsperpod
MG-2022-21	Numberofpods per plant	MG-2022-39	Days to 50 percent flowering,pod length, podthickness
MG-2022-31	Seed yieldperplant	MG-2022-42	Days to 50 per cent flowering, Plant height
MG-2022-14	Number of pods per cluster , Number of pods per plant	MG-2022-31	Days to maturity,Protein content,numberof clusters per plant,number of seedsper pod, 100 seedsweight,Seed yieldperplant
MG-2022-11	Proteincontent	MG-2022-11	Daystomaturity,proteincontent
MG-2022-18	Days to 50 per centflowering	MG-2022-11	Days to maturity, Seed yield per plant
MG-2022-42	Days to 50 per cent flowering, Days to maturity	MG-2022-24	Number ofclustersperplant

Figure 3:AclusterformationofffortytwogenotypesbyTocher'smethodinmungbean.