# GENETIC DIVERSITY IN MUNGBEAN (*VIGNA RADIATA* (L.) WILCZEK GERMPLASM

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## Abstract

Genetic diversity was studied in diversified mungbean germplasm by using Metroglyph analysis. Forty mungbean genotypes originating from Pakistan, Thailand and India were used in the present study. Different morphological and economic traits like plant height, clusters per plant, pods per plant, hundred seed weight, biological yield, seed yield and harvest index exhibited considerable genetic variability. Metroglyph analysis distributed mungbean genotypes into 8 groups. Group I and II, consisted of only one genotype each and were found to be distant from all other groups. Groups VII and VIII were the largest groups consisting of 10 genotypes each. The range of total mean index score varied from 12.6 to 17.0. Maximum index scores were obtained by groups I, II and III. In all the three groups, biological yield and seed yield contributed more to index scores. Highest index score of 18 was attained by NM 6368(46-40-4) (Genotype No. 13, Group VIII) and VC 3945A (Genotype No. 35, Group VII) followed by Mung-88 (Genotype No. 8, Group II) and VC-3476 (Genotype No. 33, Group III) with index score of 17. Lowest index score of 10 was attained by 3 genotypes viz., KPS-2, VC2984B and NM-94. VC-6369(53-97) (Genotype No. 39, Group I) of Thailand origin and Mung-88 (Genotype No. 8, Group II) of Pakistan origin were identified as the most important genotypes exhibiting an index score of 16 and 17, respectively. On the basis of this grouping it may be concluded that an effective hybridization program may include the genotypes of group I, II, VII and VIII to produce better segregants that may be used for the development of high yielding mungbean varieties.

## Introduction

Mungbean (*Vigna radiata* (L.) Wilczek is a major Kharif pulse crop in Pakistan. It is being grown on an area of 218 thousand hectares with an annual production of 138.46 thousand tons with an average of 636 kg per hectare (Anon., 2008). It is regarded as quality pulse due to its excellent digestibility and rich protein (25-28%), especially when combined with cereals (Thirumaran & Seralathan 1988). It is an important source of readily available proteins in cereal-based diet of the people of Pakistan, South Asia and Southeast Asian countries. It is also consumed as boiled dry beans. Moreover, it is regarded as fodder for livestock and also incorporated in soil for enriching organic matter. At Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad, Pakistan the mungbean improvement programme is in progress since 1974 by using induced mutations and conventional breeding techniques. These efforts have resulted in the development of 10 varieties of mungbean by using local and exotic germplasm, (mostly from Asian Vegetable Research and Development Centre (AVRDC), Thailand). Out of these 10 varieties, NM-92, NM-98 and NM-2006 occupied 70% of the total area under mungbean crop in the Punjab Province.

In the experiment local and exotic genotypes of diverse origin were used and an attempt was made to generate information for the selection of genotypes to broaden the

genetic base, which is a pre-requisite in any plant breeding programme for the evolution of high yielding and disease resistant varieties. The major objectives of this investigation were to classify the available mungbean germplasm into distinct groups on the basis of their genetic diversity by using metroglyph analysis and to identify diverse genotypes useful in hybridization programme for the development of better recombinants that will lead to the evolution of varieties with improved plant traits. Study of genetic diversity using data for grain yield and related traits has already been done in *Sorghum bicolor L.* (Nath *et al*., 1985) using Metroglyph (Anderson, 1957) and Canonical Variate Analysis. The efficiency of the Metroglyph and canonical variate techniques in distinguishing extremely diverse genotypes was confirmed. Several other researchers have studied genetic divergence in wheat (Martynov *et al*., 2006; Peleg *et al*., 2005), sorghum (Mehdi & Asghar 1999), rice (Bharawadraj *et al*., 2001; Cheema *et al*., 2004; Mahapatra *et al*., 1995), cotton (Ponitha & Raveendram 2000), turmeric (Chandra *et al*., 1997) and mungbean (Bish *et al*., 1998; Sharma *et al*., 1996; Thulasidas 1984).

## Materials and Methods

Experiment was conducted at Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad, Pakistan during spring (March-April) 2006. The experimental material consisted of 40 mungbean genotypes having different origins viz., Pakistan, Thailand and India. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications having a plot size of 4.8 $m^2$ by keeping row to row distance of 30 cm and plant to plant distance of 10 cm. Four plant rows were sown per entry. Normal agronomic practices were followed. At maturity, 5 guarded plants from two central rows were selected at random from every genotype in each replication and data on different traits were recorded. Biological yield was recorded after sun drying of plant materials for 7 days (constant weight was taken). Genotype names, origin and mean values of different traits are given in Table 1.

The mean data were subjected to the analysis of variance following Steel *et al*., (1997). The Metroglyph technique was performed following Anderson (1957) who proposed this method to study the patterns of morphological variations in crop species. This method was also used by many other scientists for classificatory analysis in various crops (Sadiq *et al*., 2004). This method involves the mean values of characters. The two most variable traits (seed yield per plot and seed weight) were depicted on X and Y-axes, respectively which resulted in a scatter diagram. All traits were represented as rays on the glyph, and each glyph represented a genotype. Rays for a certain trait occupied the same position on each glyph. All characters were represented by different length of ray (no ray for minimum, half ray for medium and full ray for maximum). The length of ray assigned to the trait depended upon the index score of genotypes for that trait (1 for lower value, 2 for medium and 3 for highest value). The performance of genotype was indicated by total index score of genotype, which was the sum of the index values with regard to all characters. The index values 1, 2, 3 meant lower to higher value of worth of a genotype/variety. The grouping of genotypes was carried out on the basis of sum of net index scores of all the genotypes in that group. For plant height, desirability was lower magnitude; therefore higher score (3) was given to the genotypes showing less height. For all other traits desirability was linked with higher magnitude, so high score was given to the genotypes exhibiting greater mean values of these traits (Table 3).

Table 1. Origin and mean phenotypic values of various traits contributing to genetic divergence in forty genotypes of mungbean.

| Sr. No. | Genotypes | Origin | Plant height (cm) | Clusters/ plant | Pods/ plant | 100-seed weight (g) | Biological yield/plot (g) | Seed yield/plot (g) | Harvest index (%) |
|---|---|---|---|---|---|---|---|---|---|
| 1. | AEM-96 | Pakistan | 65.33 | 11.00 | 38.33 | 3.90 | 1766.67 | 356.67 | 20.17 |
| 2. | BASANTI | India | 46.00 | 10.33 | 29.67 | 3.28 | 900.00 | 160.00 | 17.50 |
| 3. | BINA MUNG-2 | // | 53.00 | 12.00 | 32.33 | 3.73 | 1200.00 | 170.00 | 14.17 |
| 4. | CO-3 | // | 49.67 | 12.33 | 33.67 | 3.25 | 1533.33 | 266.67 | 17.37 |
| 5. | KPS-1 | Thailand | 49.67 | 10.33 | 26.00 | 5.79 | 900.00 | 200.00 | 22.23 |
| 6. | KPS-2 | // | 50.67 | 11.00 | 28.33 | 4.74 | 700.00 | 160.00 | 22.67 |
| 7. | ML-613 | India | 66.67 | 13.67 | 35.00 | 3.73 | 1466.67 | 206.67 | 14.07 |
| 8. | MUNG-88 | Pakistan | 66.33 | 11.67 | 39.33 | 3.81 | 1300.00 | 663.33 | 44.30 |
| 9. | NM 42-16-1-1 | // | 48.00 | 10.67 | 31.33 | 4.13 | 900.00 | 216.67 | 24.05 |
| 10. | NM 4320-5 | // | 50.67 | 10.33 | 24.33 | 5.28 | 1166.67 | 203.33 | 18.57 |
| 11. | NM 4331-4 | // | 48.00 | 10.00 | 28.67 | 4.71 | 1066.67 | 240.00 | 29.30 |
| 12. | NM 4350-2 | // | 48.33 | 7.33 | 24.33 | 6.68 | 1100.00 | 273.33 | 24.93 |
| 13. | NM 6368 (46-40-4) | // | 34.00 | 11.00 | 40.33 | 4.98 | 900.00 | 290.00 | 32.37 |
| 14. | NM 94 | // | 37.67 | 6.67 | 21.33 | 4.53 | 300.00 | 63.33 | 21.10 |
| 15. | PAK-17 | // | 46.33 | 9.33 | 22.67 | 5.79 | 766.67 | 240.00 | 31.67 |
| 16. | PDM-11 | India | 53.33 | 13.00 | 37.33 | 3.65 | 800.00 | 133.33 | 15.37 |
| 17. | PUSA-9072 | // | 69.00 | 11.00 | 33.33 | 3.23 | 1200.00 | 206.67 | 17.17 |
| 18. | SML-134 | // | 42.00 | 12.33 | 32.00 | 4.14 | 566.67 | 123.33 | 22.50 |
| 19. | VC-1000A | Thailand | 46.33 | 10.00 | 32.33 | 5.07 | 1033.33 | 193.33 | 18.73 |
| 20. | VC-2184 | // | 42.67 | 10.33 | 28.00 | 4.51 | 900.00 | 203.33 | 22.63 |

Table 1. (Cont'd.).

| Sr. No. | Genotypes | Origin | Plant height (cm) | Clusters/ plant | Pods/ plant | 100-seed weight (g) | Biological yield/plot (g) | Seed yield/plot (g) | Harvest index (%) |
|---|---|---|---|---|---|---|---|---|---|
| 21. | VC-2307A | // | 45.33 | 8.67 | 21.67 | 6.21 | 1433.33 | 230.00 | 16.03 |
| 22. | VC-2523A | // | 46.67 | 11.00 | 24.33 | 6.05 | 700.00 | 180.00 | 25.50 |
| 23. | VC-2528 | // | 49.33 | 10.33 | 21.33 | 6.15 | 766.67 | 120.00 | 16.05 |
| 24. | VC-2719A | // | 47.33 | 9.00 | 22.33 | 5.47 | 800.00 | 223.33 | 27.83 |
| 25. | VC-2754A | // | 45.00 | 10.33 | 24.00 | 5.04 | 1333.33 | 260.00 | 19.43 |
| 26. | VC-2768B | // | 46.33 | 8.67 | 19.67 | 5.62 | 566.67 | 120.00 | 21.10 |
| 27. | VC-2771A | // | 43.33 | 9.00 | 27.67 | 6.06 | 800.00 | 180.00 | 22.50 |
| 28. | VC-2984A | // | 50.00 | 7.33 | 23.67 | 5.11 | 1000.00 | 240.00 | 23.93 |
| 29. | VC-2984B | // | 47.00 | 10.67 | 26.67 | 4.76 | 700.00 | 120.00 | 17.07 |
| 30. | VC-3061A | // | 48.33 | 8.67 | 22.33 | 6.09 | 1100.00 | 253.33 | 23.10 |
| 31. | VC-3092 | // | 48.33 | 8.00 | 17.67 | 6.45 | 900.00 | 233.33 | 26.07 |
| 32. | VC-3301A | // | 50.33 | 8.00 | 23.67 | 5.45 | 1200.00 | 243.33 | 20.30 |
| 33. | VC-3476 | // | 46.00 | 10.00 | 31.33 | 3.32 | 1066.67 | 320.00 | 30.10 |
| 34. | VC-3726 | // | 42.67 | 10.00 | 24.67 | 6.28 | 866.67 | 203.33 | 23.50 |
| 35. | VC-3945A | // | 43.67 | 9.00 | 31.00 | 5.77 | 900.00 | 300.00 | 33.50 |
| 36. | VC-6153B-20G | // | 42.00 | 6.67 | 14.67 | 6.31 | 533.33 | 63.33 | 11.97 |
| 37. | VC-6153B-20P | // | 44.67 | 9.00 | 21.33 | 6.98 | 300.00 | 73.33 | 24.43 |
| 38. | VC-6173B-6 | // | 43.00 | 8.00 | 24.00 | 6.31 | 600.00 | 120.00 | 20.00 |
| 39. | VC-6369 (53-97) | // | 51.67 | 10.33 | 30.67 | 5.07 | 1200.00 | 900.00 | 74.87 |
| 40. | VC-6370A | // | 45.67 | 11.00 | 27.00 | 5.23 | 500.00 | 73.33 | 14.67 |

## Results and Discussion

Highly significant differences among mungbean genotypes were observed for most of the traits (Table 2) that reflects the presence of considerable genetic variability. Metroglyph scatter diagram of 40 mungbean genotypes based on seed weight and seed yield formed 8 distinct groups (Fig. 1) on the basis of relative dispositioning of genotypes on the graph. Groups I and II consisted of only one genotype viz., VC 6369(53-97) (Genotype No. 39) and Mung-88 (Genotype No. 8), respectively (Fig. 1). These represented close genetic relationship in respect of seed yield and seed weight, which was evident in terms of the total index scores of 16 and 17, respectively. Groups III and IV included 3 and 7 genotypes, respectively. Likewise Groups V and VI consisted of four genotypes each and Groups VII and VIII each had 10 genotypes. The inclusion of greater number of genotypes in a group increased group score.

In general, maximum number of genotypes came in the range of 12 to 14 index scores (Table 4) which were mostly distributed among groups IV, VII and VIII. Least index score of 10 was attained by three genotypes viz., KPS-2, NM-94 and VC 2984B (Genotype No. 6, 14 and 29, respectively). First genotype belongs to Group VIII and remaining two genotypes belong to Group V. Genotypes like NM 6368 (46-40-4) (Genotype No. 13) and VC 3945A (Genotype No. 35) of groups VIII and VII attained highest index score of 18, respectively.

**Table 2. Means, mean squares and coefficients of variation for various traits of mungbean genotypes.**

| Traits | Mean | Mean square | F. Value | c.v (%) |
|---|---|---|---|---|
| Plant height (cm) | 48.51 | 159.31** | 60.61 | 3.34 |
| Clusters per plant | 9.95 | 8.05** | 6.62 | 11.06 |
| Pods per plant | 27.46 | 108.49** | 22.48 | 8.00 |
| 100-seed weight (g) | 5.07 | 3.53** | 196.96 | 2.63 |
| Biological yield /plot (g) | 943.33 | 307297.01** | 23.09 | 12.09 |
| Harvest index (%) | 23.57 | 327.88** | 40.48 | 12.07 |
| Seed yield/plot (g) | 225.67 | 66043.06** | 88.82 | 12.01 |

**** = Significant at 0.01 probability level.

**Table 3. Range of means and index scores for various quantitative traits of 40 mungbean genotypes.**

| Traits | Range of means | Score I Value more than | Sign | Score II Value from to | Sign | Score III Value less than | Sign |
|---|---|---|---|---|---|---|---|
| Plant height | 34.0-69.0 | 50.0 | ✦ | 47.0-50.0 | ↘ | 47.0 | ↘ |

| Traits | Range of means | Score I Value less than | Sign | Score II Value from to | Sign | Score III Value more than | Sign |
|---|---|---|---|---|---|---|---|
| Clusters/plant | 6.67-13.67 | 9.0 | ✦ | 9.0-11.0 | ↰ | 11.0 | ↑ |
| Pods/plant | 14.67-40.33 | 26.0 | ✦ | 26.00-28.67 | ✓ | 28.67 | ↗ |
| 100-Seed weight | 3.23-6.98 | 4.98 | ✦ | 4.98-5.11 | ↓ | 5.11 | ↓ |
| Biological yield | 300.00-1766.67 | 866.67 | ✦ | 866.67-1033.33 | → | 1033.33 | — |
| Seed yield/plot (SYLD) | 63.33-900.0 | 200.00 | ✦ | 200.00-243.33 | ⌐ | 243.33 | ⌐ |
| Harvest index (HI) | 11.97-74.87 | 21.10 | ✦ | 21.10-26.07 | ↗ | 26.07 | ↗ |
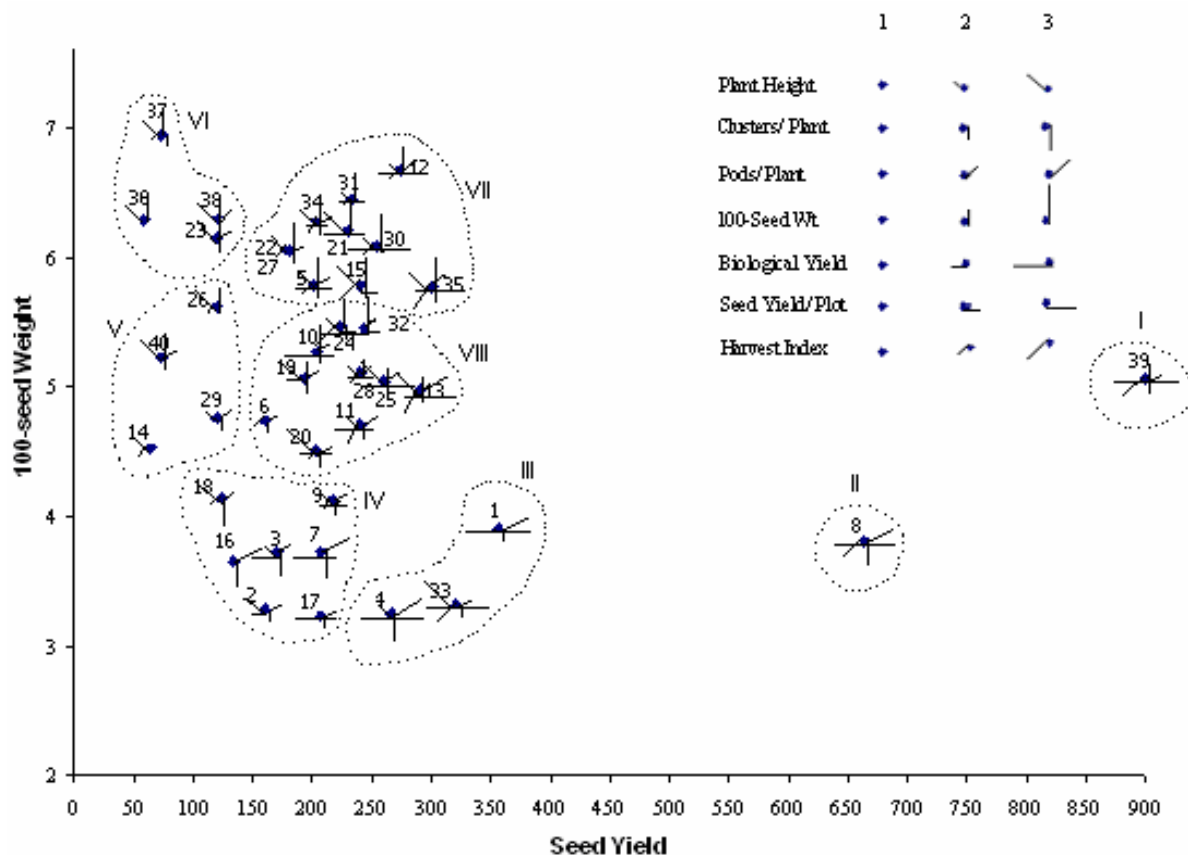
Fig 1. Metroglyph Scatter Diagram showing 8 groups from 40 mungbean genotypes.

Out of 24 genotypes of Thailand, 22 got clustered in low yield groups (Groups V, VI, VII and VIII) (Table 1, Fig. 1). Likewise most of the genotypes from India also got confined to low yield group (Group III), while local germplasm scattered among different complexes, ranged from low to high yielders. Majority of the genotypes of Thailand origin belonging to low yield groups have larger seed size. In contrary, the genotypes originating from India have mostly less seed weight. Generally, the genotypes within a group showed little divergence from each other than from the genotypes of different groups as has been observed by Chandra *et al.*, (1997). Hybridization among the genotypes of same group may not be fruitful. But in contrary, the genotypes within Group III showed maximum divergence from each other. Variation within this group may be due to different genetic make up of the genotypes and different sources of collection. Similar findings had been reported by Bharawadraj *et al.*, (2001); Ibrahim *et al.*, (1990) and Kotaiah *et al.*, (1986).

The mean performance of each group for different plant traits is presented in Table 5. The range of total mean index score varied from 12.6 to 17.0. Maximum index scores were obtained for groups I, II and III. In all the three groups, biological yield and seed yield contributed more to index scores. The traits like clusters per plant and pods per plant contributed more towards mean index scores in group II, thus separating it from groups I and III. The index score allotted to each individual trait is given in Table 4 which indicates the worth of that genotype for that particular trait. Genotypes included in Groups I and II can be characterized by plants with variable height and greater biological and seed yield. However, genotypes of Group III were bold seeded. Hybridization may be attempted between the genotypes of different groups with high index scores to produce new genetic recombinants with desirable traits. In a similar study Bish *et al.*, (1998) demonstrated the patterns of variations at population level in mungbean.

**Table 4. Index scores for different genotypes and individual traits of 40 mungbean genotypes.**

| Sr. No. | Genotypes | Plant height (cm) (X₂) | Clusters/ plant (X₃) | Pods/ plant (X₄) | 100-seed weight (g) (X₅) | Biological yield /plot (g) (X₆) | Seed yield/plot (g) (X₇) | Harvest index (%) (X₈) | Total |
|---|---|---|---|---|---|---|---|---|---|
| 1. | AEM-96 | 1 | 2 | 3 | 1 | 3 | 3 | 1 | 14 |
| 2. | BASANTI | 3 | 2 | 2 | 1 | 2 | 1 | 1 | 12 |
| 3. | BINA MUNG-2 | 2 | 3 | 2 | 1 | 3 | 1 | 1 | 13 |
| 4. | CO-3 | 2 | 3 | 3 | 1 | 3 | 3 | 1 | 16 |
| 5. | KPS-1 | 2 | 2 | 2 | 3 | 2 | 2 | 2 | 15 |
| 6. | KPS-2 | 1 | 2 | 2 | 1 | 1 | 1 | 2 | 10 |
| 7. | ML-613 | 1 | 3 | 3 | 1 | 3 | 2 | 1 | 14 |
| 8. | MUNG-88 | 1 | 3 | 3 | 1 | 3 | 3 | 3 | 17 |
| 9. | NM 42-16-1-1 | 2 | 2 | 2 | 1 | 2 | 2 | 2 | 13 |
| 10. | NM 4320-5 | 1 | 2 | 2 | 3 | 3 | 2 | 1 | 14 |
| 11. | NM 4331-4 | 2 | 2 | 2 | 1 | 3 | 2 | 3 | 15 |
| 12. | NM 4350-2 | 2 | 1 | 2 | 3 | 3 | 3 | 2 | 16 |
| 13. | NM 6368 (46-40-4) | 3 | 2 | 3 | 2 | 2 | 3 | 3 | 18 |
| 14. | NM 94 | 3 | 1 | 1 | 1 | 1 | 1 | 2 | 10 |
| 15. | PAK-17 | 3 | 2 | 1 | 3 | 1 | 2 | 3 | 15 |
| 16. | PDM-11 | 1 | 3 | 3 | 1 | 1 | 1 | 1 | 11 |
| 17. | PUSA-9072 | 1 | 2 | 2 | 1 | 3 | 2 | 1 | 12 |
| 18. | SML-134 | 3 | 3 | 2 | 1 | 1 | 1 | 2 | 13 |
| 19. | VC-1000A | 3 | 2 | 2 | 2 | 2 | 1 | 1 | 13 |
| 20. | VC-2184 | 3 | 2 | 2 | 1 | 2 | 2 | 2 | 14 |

Table 4. (Cont'd).

| Sr. No. | Genotypes | Plant height (cm) $(X_2)$ | Clusters/ plant $(X_3)$ | Pods/ plant $(X_4)$ | 100-seed weight (g) $(X_5)$ | Biological yield /plot (g) $(X_6)$ | Seed yield/plot (g) $(X_7)$ | Harvest index (%) $(X_8)$ | Total |
|---|---|---|---|---|---|---|---|---|---|
| 21. | VC-2307A | 3 | 1 | 1 | 3 | 3 | 2 | 1 | 14 |
| 22. | VC-2523A | 3 | 2 | 2 | 3 | 1 | 1 | 2 | 14 |
| 23. | VC-2528 | 2 | 2 | 1 | 3 | 1 | 1 | 1 | 11 |
| 24. | VC-2719A | 2 | 2 | 1 | 3 | 1 | 2 | 3 | 14 |
| 25. | VC-2754A | 3 | 2 | 2 | 2 | 3 | 3 | 1 | 16 |
| 26. | VC-2768B | 3 | 1 | 1 | 3 | 1 | 1 | 2 | 12 |
| 27. | VC-2771A | 3 | 2 | 2 | 3 | 1 | 1 | 2 | 14 |
| 28. | VC-2984A | 2 | 1 | 2 | 2 | 2 | 2 | 2 | 13 |
| 29. | VC-2984B | 2 | 2 | 2 | 1 | 1 | 1 | 1 | 10 |
| 30. | VC-3061A | 2 | 1 | 1 | 3 | 3 | 3 | 2 | 15 |
| 31. | VC-3092 | 2 | 1 | 1 | 3 | 2 | 2 | 2 | 13 |
| 32. | VC-3301A | 1 | 1 | 2 | 3 | 3 | 2 | 1 | 13 |
| 33. | VC-3476 | 3 | 2 | 2 | 1 | 3 | 3 | 3 | 17 |
| 34. | VC-3726 | 3 | 2 | 2 | 3 | 2 | 2 | 2 | 16 |
| 35. | VC-3945A | 3 | 2 | 2 | 3 | 2 | 3 | 3 | 18 |
| 36. | VC-6153B-20G | 3 | 1 | 1 | 3 | 1 | 1 | 1 | 11 |
| 37. | VC-6153B-20P | 3 | 2 | 1 | 3 | 1 | 1 | 2 | 13 |
| 38. | VC-6173B-6 | 3 | 1 | 2 | 3 | 1 | 1 | 1 | 12 |
| 39. | VC-6369 (53-97) | 1 | 2 | 2 | 2 | 3 | 3 | 3 | 16 |
| 40. | VC-6370A | 3 | 2 | 2 | 3 | 1 | 1 | 1 | 13 |

Table 5. Group means for different traits, their mean index scores (based on seed weight and seed yield) and mungbean genotypes included in each group.

| Group | Genotypes included (numbers) | Plant height (cm) | Clusters/plant | Pods/plant | 100-seed weight (g) | Biological yield /plot (g) | Seed yield/plot (g) | Harvest index (%) | Total mean index score |
|---|---|---|---|---|---|---|---|---|---|
| I | 39 | 51.67 (1.0) | 10.33 (2.0) | 30.67 (2.0) | 5.07 (2.0) | 1200.00 (3.0) | 900.00 (3.0) | 74.87 (3.0) | 16.0 |
| II | 8 | 66.33 (1.0) | 11.67 (3.0) | 39.33 (3.0) | 3.81 (1.0) | 1300.00 (3.0) | 663.33 (3.0) | 44.30 (3.0) | 17.0 |
| III | 1, 4, 33 | 53.67 (2.0) | 11.11 (2.3) | 34.44 (2.7) | 3.49 (1.0) | 1455.56 (3.0) | 314.44 (3.0) | 22.54 (1.7) | 15.7 |
| IV | 2, 3, 7, 9, 16, 17, 18 | 54.00 (1.9) | 11.86 (2.6) | 33.00 (2.3) | 3.70 (1.0) | 1004.76 (2.1) | 173.81 (1.4) | 17.83 (1.3) | 12.6 |
| V | 14, 26, 29, 40 | 44.17 (2.5) | 9.25 (1.8) | 23.67 (1.5) | 5.04 (2.5) | 516.67 (2.0) | 94.17 (2.3) | 18.48 (2.3) | 14.9 |
| VI | 23, 36, 37, 38 | 44.75 (2.3) | 8.50 (1.8) | 20.33 (1.8) | 6.44 (2.0) | 550.00 (2.3) | 94.17 (2.0) | 18.11 (2.0) | 14.2 |
| VII | 5, 12, 15, 21, 22, 27, 30, 31, 34, 35 | 46.27 (1.9) | 9.13 (2.0) | 24.23 (2.0) | 6.12 (2.0) | 946.67 (2.1) | 229.33 (1.8) | 24.90 (1.3) | 13.1 |
| VIII | 6, 10, 11, 13, 19, 20, 24, 25, 28, 32 | 46.50 (2.2) | 9.73 (2.0) | 27.57 (1.9) | 5.04 (1.9) | 1010.00 (1.7) | 225.67 (1.7) | 23.58 (1.9) | 13.3 |

On the basis of present study, it can be concluded that metroglyph technique was useful in identifying groups of genotypes with yield enhancing traits among the collection of diverse genotypes and thus suggesting its potential value in mungbean improvement. An effective hybridization program must include the genotypes of group I (VC-6369(53-97)), Group II (Mung-88), Group VII (KPS-1, NM 4350-2, Pak-17, VC2307A, VC2523A, VC2771A, VC3061A, VC3092, VC3726, VC3945A) and Group VIII (KPS-2, NM4320-5, NM4331-4, NM6368(46-40-4), VC1000A, VC2184, VC2719A, VC2754A, VC2984A   VC3301A) to yield better segregants that may result in the evolution of high yielding mungbean varieties. VC-6369(53-97) (Genotype No. 39, Group I) was identified as the most important genotype of Thailand exhibiting an index score of 16 with maximum seed yield and moderate seed weight. Likewise Mung-88 (Genotype No. 8, Group II) belonging to Pakistan exhibiting an index score of 17 with higher seed yield and less seed weight may also be selected among local germplasm for hybridization programme. VC-6153B-20P (Genotype No. 37, Group VI) originating from Thailand showed maximum seed weight and exhibited moderate index score but its seed yield was lowest.

If a character is to be improved, which is undesirable or otherwise weak in a genotype, the information furnished here will be helpful in identifying the cross (s) that can be attempted to obtain the desired results.

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