***Original Research Article***

**Genetic and Phenotypic Diversity of elite Mung bean (*Vigna radiate* L. Wilczek) Genotypes**

**ABSTRACT**

The present investigation was carried out at Indira Gandhi Krishi Vishwavidyalaya, Raipur with the 19 green gram genotypes to evaluate the genetic variability parameters and phenotypic variation for ten quantitative traits. The genotypes assessed in this study posses significant difference among themselves. Genotypes TRM-251, TRM-230, TRM-250, HUM-12, HUM-16 and IGKM-2021-1 showed best performance for days to flowering, seeds per pod, 100-seed weight, biological yield per plant, seed yield per plant and harvest index, respectively. The high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) found for seed yield per plant, 100-seed weight, number of pods per plant and harvest index. High genetic advance as % of mean coupled with high heritability was observed for plant height, number of branches per plant, number of pods per plant, 100-seed weight and harvest index indicating that the possibility of direct selection. This indicated the role of additive gene effects and less effect of environmental factors on the expression of the traits, implying the potential efficacy of simple selection for trait improvement. Out of 10, four principal components exhibited more than one eigen value and showed about 81.162% variability among the traits studied for each genotypes. First three PCs were predominantly related to yield and yield contributing traits. Based on the PC scores RMO3-71, IGKM-6-27-5 and HUM 16 will be recommended for direct cultivation programme. HUM 12, TRM 146, TRM 251 and TRM 250 were the most distinct from the others and can be used for crossing purpose.

**Keywords:** Genetic advance, Genetic Variability, Heritability, Mung bean, Principal component Analysis

**INTRODUCTION**

“Mung bean (*Vigna radiata* L. Wilczek) is one of the most important grain legumes extensively cultivated in arid, semi-arid and subtropics of the world. Mung bean seed is rich in easily digestible protein which makes it an important component of a balanced diet. Seeds are also a very good source of the minerals calcium, iron, zinc, potassium, phosphorus, and vitamins such as vitamin K and dietary fibers” (Keatinge *et al.,* 2011). It is highly preferred due to its rapid growth, early maturity and its ability to fix nitrogen.

Despite its importance, the area, production and productivity of green gram is still low, which may due to lack of determinate and high yielding varieties. Mung bean is a highly self-pollinated crop lacks natural variability for seed yield and yield-related traits is very narrow in mung bean which makes the selection ineffective. Saeed *et al.* (2007) observed “low genetic variability in mung bean genotypes due to the narrow genetic backgrounds of local collections. Needless to say, there is a need to broaden the genetic base of the released varieties” (Win *et al.,* 2020). “Another, yield, a complex quantitative trait, is the result of multiple morphological and physiological traits are always influenced by environmental factors” (Gupta *et al.,* 2023). “Assessment of genetic diversity in mung bean genotypes would facilitate the development of elite cultivars. Genetic variability is a key for the success of a plant breeding program since it provides an opportunity to breeders to make the selection for desirable superior individuals from a genetically diverse base population” (Partap *et al.,* 2019). “Understanding the level of genetic variability might support plant breeders’ decision on the selection of parental genotypes with a broad genetic base for further genetic improvement and amenities in the development of the breeding strategy” (Omima *et al.,* 2018). “Estimates of genetic parameters indicate the relative importance of the various types of gene effects affecting the total variation of a plant character. Heritability estimate provide the information regarding the amount of transmissible genetic variation to total variation and determine genetic improvement and response to selection. The high heritability value showed that traits is less influenced by environmental effects, the selection of such traits is not beneficial because heritability is the estimate of both fixable and non-fixable variances. The genetic advance as per cent of mean is important in providing an idea of the amount of progress that can be achieved by selection for the concerned traits. Heritability along with genetic gain in per cent of mean is a more useful criterion to predicting the resultant effect for selecting the best individuals. The characters with high genetic advance would response to selection better than those with high heritability and low genetic advance” (Burton and Devane, 1953). “High heritability estimates along with high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone” (Arora, 1991).

“Principal Component Analysis (PCA) is a powerful tool in modern data analysis because this is a well-known multivariate statistical technique which is used to identify the minimum number of components, which can explain maximum variability out of the total variability (Anderson, 1972 and Morrison, 1978) and also to rank genotypes on the basis of PC scores. It also identified the characters that contribute most to the variation within a group of entries” (Ogunbodede, 1997). Therefore, the present study was conducted (1) to assess the genetic variability, heritability and genetic advance of mung bean genotypes and (2) to determine the phenotypic variation of the mung bean genotypes using PCA.

**MATERIALS AND METHODS**

The present investigation was carried at Research-cum-Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) with the 19 green gram genotypes including 3 checks (Table 1). The experiment followed a Completely Randomized Block Design (CRBD), with three replications and line sowing (Rainfed) method during *kharif 2022*. Each genotype was grown in four rows of 3 meter length with row to row and plant to plant spacing of 30 cm and 10 cm, respectively. The plot size for each entry was 3.6 square meter. The observations on days to 50% flowering (DTF) and days to maturity (DM) were recorded on plot basis, whereas, other agronomical traits *viz.,* plant height (PH), number of branches per plant (NB), number of pods per plant (NP), number of seeds per pod (NS), 100-seed weight (HSW), biological yield per plant (BY) and seed yield per plant (SY) were recorded on five randomly selected plants from each replication and harvest index (HI) is derived character.

**Table 1: List of genotypes used in the study**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Genotypes** | **Source** | **S. No.** | **Genotypes** | **Source** |
| 1. | IGKM-5-6-27 | IGKV, Raipur | 11. | TRM-140 | BARC, Trombay |
| 2. | IGKM-6-27-5 | IGKV, Raipur | 12. | TRM-141 | BARC, Trombay |
| 3. | IGKM-6-10-7 | IGKV, Raipur | 13. | TRM-146 | BARC, Trombay |
| 4. | IGKM-6-4-2 | IGKV, Raipur | 14. | TRM-230 | BARC, Trombay |
| 5. | RMO3-71 | IGKV, Raipur | 15. | TRM-250 | BARC, Trombay |
| 6. | RMO3-79 | IGKV, Raipur | 16. | TRM-251 | BARC, Trombay |
| 7. | IGKM-2021-1 | IGKV, Raipur | 17. | HUM-1 | (Check 1) |
| 8. | IGKM-2021-2 | IGKV, Raipur | 18. | HUM-12 | (Check 2) |
| 9. | IGKM-2021-3 | IGKV, Raipur | 19. | HUM-16 | (Check 3) |
| 10. | TRM-117 | BARC, Trombay |  |  |  |

The analysis of variance for each character was carried out as suggested by Fisher (1918). The genetic parameters *viz.,* phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability in the broad sense and genetic advance analyzed as per the standard procedure described by Burton (1952), Johnson et al. (1955); Allard (1960), Burton and DeVane (1953) using the OPSTAT software. In order to identify the patterns of variation, Principal component Analysis (PCA) was conducted to evaluate each character’s contribution to the overall observed phenotypic diversity using the PAST 4.17 software. Those PCs with Eigen values greater than one were selected as proposed by Jeffers (1967).

**RESULTS AND DISCUSSION**

Analysis of variance (ANOVA) for ten quantitative traits in 19 mung bean genotypes including checks revealed highly significant differences between genotypes for all the studied characters, indicated presence of considerable inherent genetic differences among genotypes for all the different characters (Table2).

**Table 2: ANOVA for yield and yield attributing traits in elite mung bean genotypes.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **S. No.** | **Source of Variation** | **Mean sum of squares** | | |
| **Replication** | **Genotypes** | **Error** |
| **Characters** | **df=2** | **df=18** | **df=36** |
| **1** | Days to 50%flowering | 5.895 | 26.456\*\* | 0.117 |
| **2** | Days to Maturity | 1.000 | 16.366\*\* | 0.130 |
| **3** | Plant height (cm) | 9.111 | 146.792\*\* | 3.053 |
| **4** | No. of branches per plant | 0.090 | 0.168\*\* | 0.027 |
| **5** | No. of pods per plant | 0.886 | 13.777\*\* | 0.271 |
| **6** | No. of Seeds per Pod | 0.372 | 1.191\*\* | 0.202 |
| **7** | 100 seed weight (g) | 0.236 | 1.811\*\* | 0.118 |
| **8** | Biological yield (g) | 9.158 | 31.061\*\* | 5.214 |
| **9** | Seed Yield per plant (g) | 0.015 | 3.411\*\* | 0.193 |
| **10** | Harvest index (%) | 28.224 | 60.809\* | 31.701 |

***Level of significance, \* at 5% & \*\* at 1%***

**Mean and genetic variability parameters for quantitative characters**

Execution of the breeding programmes depends largely on the presence of significant genetic variability to permit effective selection. Relative magnitude of variability presence in a crop species helps the breeder to handle the breeding population created by hybridizing the selected donors with high yielding base varieties.

Results revealed that high degree of variability was present in the mung bean genotypes for all the characters under study (Fig 1). The mean performance, range, GCV, PCV, h2(bs) and genetic advance as % of mean (GAM) for different quantitative characters under present study is presented in Table 3. The study observed considerable variability among 19 mung bean genotypes for ten quantitative traits. Traits like days to flowering ranged from 34.67 to 44.67 days, days to maturity 66.67 to 76 days, plant height 52.87 to 77.67 cm, number of branches 1 to 1.82, pods per plant 10.86 to 17.29, seeds per pod 11.04 to 13.47, 100 seed weight 2.30 to 5.64g, biological yield 10 to 22g, seed yield 2.59 to 6.04g and harvest index 16.52 to 33.38%. Genotypes TRM-251, TRM-230, TRM-250, HUM-12 and IGKM-2021-1 showed best performance for days to flowering, seeds per pod, 100-seed weight, biological yield per plant and harvest index respectively, indicating significant genetic variability exists among the genotypes for these yield contributing traits.

“The magnitude of phenotypic and genotypic coefficient of variation depends upon the genetic constitution of the base material used. Generally, the phenotypic coefficients of variability were higher than corresponding genotypic coefficients of variability for the observed traits which indicates the impact of environment upon the traits. The classification of variation was given by Sivasubramanian and Madhavamenon (1973) as low (<10%), moderate (10-20%), and high (>20%). Genotypic and phenotypic coefficient of variation was estimated which showed that values of phenotypic coefficient of variation was slightly greater than the corresponding genotypic coefficient of variation values for most of the traits studied indicating the negligible influence of extraneous factors” (Gogoi *et al.,* 2024).

|  |  |  |
| --- | --- | --- |
|  |  |  |
|  |  |  |
|  |  |  |
|  | **Fig. 1. Graphical representation of variability for different quantitative characters in mung bean genotypes** | |

**Table 3: Estimation of Genetic variability parameters for quantitative traits**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **S. No.** | **Characters** | **Mean** | **Range** | | **GCV %** | **PCV %** | **h² (bs) %** | **GAM** |
| **Minimum** | **Maximum** |
| **1** | Days to 50%flowering | 40.47 | 34.67  (TRM-251) | 44.67  (IGKM-6-4-2\_ | 7.32 | 7.37 | 98.69 | 14.98 |
| **2** | Days to Maturity | 72.63 | 66.67  (TRM-230) | 76.00  (RMO3-71) | 3.20 | 3.24 | 97.66 | 6.52 |
| **3** | Plant height (cm) | 66.64 | 52.87  (TRM-146) | 77.67  (HUM-12) | 10.38 | 10.71 | 94.01 | 20.75 |
| **4** | No. of branches per plant | 1.31 | 1.00  (TRM-250) | 1.82  (HUM-12) | 16.59 | 20.86 | 63.30 | 27.20 |
| **5** | No. of pods per plant | 13.87 | 10.86  (TRM-140) | 17.29  (RMO3-79) | 15.29 | 15.75 | 94.32 | 30.60 |
| **6** | No. of Seeds per Pod | 11.95 | 11.04  (HUM-12) | 13.47  (TRM-230) | 4.80 | 6.10 | 62.04 | 7.80 |
| **7** | 100 seed weight (g) | 3.10 | 2.30  (RMO3-79) | 5.64  (TRM-251) | 24.20 | 26.61 | 82.73 | 45.34 |
| **8** | Biological yield (g) | 15.90 | 10.00  (TRM-117) | 22.00  (HUM-12) | 18.47 | 23.39 | 62.30 | 30.02 |
| **9** | Seed Yield per plant (g) | 4.34 | 2.59  (TRM-250) | 6.04  (HUM-16) | 23.85 | 25.91 | 84.74 | 45.22 |
| **10** | Harvest index (%) | 27.85 | 16.52  (TRM-250) | 33.38  (IGKM-2021-1) | 11.18 | 23.10 | 23.43 | 11.52 |

Phenotypic coefficient of variation was recorded to be high for 100 seed weight (26.61%) followed by seed yield per plant (25.91 %), biological yield(23.39 %), harvest index (23.10 %) and no. of branches per plant(20.86%). Similarly, genotypic coefficient of variation was high for 100-seed weight (24.20%) followed by seed yield per plant (23.85 %), biological yield per plant (18.47 %),no. of branches per plant (16.59%), no. of pods per plant (15.29%) and harvest index (%) (11.18%). High PCV and GCV were recorded for number of pods per plant and number of seed per pod by Ramakrishnan *et al.* (2018) and Nalajala *et al.* (2022); for harvest index by Pulagampalli and Lavanya (2017) and by Kumar *et al.* (2024); for seed yield per plant and primary branch per plant by Nalajala *et al.* (2022).

Days to 50% flowering, days to maturity and number of seeds per pod have low GCV and PCV which indicated the narrow range of variability thereby restricting for further improvement of these characters through simple selection. Similar finding had been earlier reported by Ghimire *et al.* (2018) and Gogoi *et al.* (2024).

An attempt has been made in the present investigation to estimate heritability in broad sense and categorized into three categories low (<30 %), moderate (30-60 %) and high (>60 %) as suggested Johnson et al. (1955). The highest heritability was observed for days to 50% flowering (98.69%) followed by days to maturity (97.66%), no. of pods per plant (94.32%), plant height (94.01%), seed yield per plant (84.74 %), no. of branches per plant (63.30%) and number of seed per pod (62.04%). Similar results for high heritability for plant height were reported earlier by Das and Barua (2015) and Garg *et al.* (2017). In general, traits having high heritability estimates were mainly controlled by additive types of genes while those traits with low heritability indicate those characters are highly influenced by environmental effects and governed by the non-additive types of genes. Characters with high heritability values are less impacted by their environment and have more potential for genetic improvement through selection.

The advanced breeding lines showed genetic advance as a percent of the mean from a low to a high value. Classification of genetic advance as low (<10%), moderate (10-20) and high (>20%) was given by Johnson *et al.,* (1955). This parameter provides more reliable information regarding selection efficiency for improving traits. The success of genetic advance under selection depends on heritability of the character under consideration. In the present investigation the expected genetic advance as per cent of mean varied from 6.52% for days to maturity to 45.34% for 100 seed weight. The highest magnitude of genetic advance as percent of mean was recorded for 100 seed weight (45.34%) followed by seed yield per plant (45.22%), number of pods per plant (30.60%) and biological yield (30.02%). Whereas, it was low for days to maturity (6.52%) and number of seeds per pod (7.80%).The genetic advance as per cent of mean is important in providing an idea of the amount of progress that can be achieved by selection for the concerned traits. High genetic advance as per cent of mean was estimated for Harvest index (%) and Biological yield. Similar result was found by Singh and Bharti, 2022.

High genetic advance coupled with high heritability was observed for plant height (94.01% and 20.75%), the number of primary branches per plant (63.30% and 27.20%), number of pods per plant (94.32% and 30.60%), hundred seed weight (82.73% and 45.34%) and seed yield per plant (84.74% and 45.24%).High heritability values coupled with high genetic advance as a per cent of mean were reported by Ahmad *et al.* (2012) for hundred seed weight, pod length, and pods per plant; by Yusufzai *et al.* (2017) for the number of pods per plant, which coincides with the report by Itefa *et al. (*2014) for seed yield per hectare and pods per plant on mung bean genotypes indicating that the possibility of direct selection. This indicated the predominance of additive gene action, implying the potential efficacy of simple selection for trait improvement.

Characters which showed moderate heritability with moderate genetic advance was number of seeds per pod and biological yield, indicating that these traits might be governed by non- additive gene action and such traits could not be improved through simple or direct selection. Dugassa *et al.* (2015) concluded that even if heritability magnitude provide basis for selection on the phenotypic performance, magnitude of heritability and genetic advance as percent of mean should be considered simultaneously to select method for improvement of traits.

**Principal component analysis**

“Principal component analysis (PCA) of the ten quantitative traits indicated phenotypic differentiations that play a key role in the phenotypic diversity of the studied green gram genotypes. If the eigen value is less than one, it indicates that the explanatory efficacy of the principal components is inferior to the average explanatory efficacy of the original variables” (Jadhav *et. al.,* 2023). “Principal components with eigen values less than one were considered non-significant. Out of 10, four principal components exhibited more than one eigen value and showed about 81.162% variability among the traits studied for each genotypes. So, these four principal components were given due importance for the further explanation. For each principal axis there are numbers of character contributing to the total variation. The PC1 had 41.748%, PC2 showed 17.623%, PC3 exhibited 11.200% and PC4 showed 10.591%variability among the genotypes for the traits under study. Eigen value and variance associated with each principal, decreased gradually and stopped at 0.002 and 0.022%, respectively (Table 4)”. (Bhawana et al. 2020)

**Table 4: Eigen value, % variance and cumulative variances of mungbean genotypes**

|  |  |  |  |
| --- | --- | --- | --- |
| **Principal Components** | **Eigenvalue** | **% variance** | **Cumulative variance %** |
| PC1 | 4.175 | 41.748 | 41.748 |
| PC 2 | 1.762 | 17.623 | 59.371 |
| PC 3 | 1.120 | 11.200 | 70.571 |
| PC 4 | 1.059 | 10.591 | 81.162 |
| PC 5 | 0.601 | 6.012 | 87.174 |
| PC 6 | 0.483 | 4.827 | 92.002 |
| PC 7 | 0.422 | 4.218 | 96.219 |
| PC 8 | 0.278 | 2.775 | 98.994 |
| PC 9 | 0.098 | 0.984 | 99.9785 |
| PC 10 | 0.002 | 0.022 | 100.000 |

The first PC accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible. Within each PC, only highly loaded traits were retained for further explanation (Table 5). The first PC was more related to BY (0.419), SY (0.400), PH (0.399) and NB (0.396) so it must be considered for direct selection. In second principal component HI (0.627), NS (0.433), SY (0.342) and NP (0.310) were the more related traits. The third principal component exhibited positive effects for NS (0.660) and HSW (0.460). It showed maximum variation for these characters. The fourth principal component was positively more related to DM (0.614) and NP (0.588). First three PCs were predominantly related to yield and yield contributing traits.

**Table 5: Principal components for yield and related characters of mungbean genotypes**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Characters** | **Principal Components** | | | |
| **PC 1** | **PC 2** | **PC 3** | **PC 4** |
| Days to 50%flowering | 0.380 | -0.214 | 0.089 | -0.392 |
| Days to Maturity | 0.194 | -0.326 | -0.116 | **0.614** |
| Plant height (cm) | **0.399** | -0.181 | 0.247 | 0.058 |
| No. of branches per plant | **0.396** | -0.134 | -0.193 | -0.049 |
| No. of pods per plant | 0.266 | **0.310** | 0.020 | **0.588** |
| No. of Seeds per Pod | 0.043 | **0.433** | **0.660** | -0.102 |
| 100 seed weight (g) | -0.299 | -0.033 | **0.460** | 0.323 |
| Biological yield (g) | **0.419** | -0.053 | 0.249 | -0.035 |
| Seed Yield per plant (g) | **0.400** | **0.342** | -0.010 | -0.037 |
| Harvest index (%) | 0.071 | **0.627** | -0.414 | 0.006 |

Values in Bold Represent Highly Weighted Factors in Respective PC

“The prominent characters coming together in different principal components and contributing towards explaining the variability have the tendency to remain together which may be kept into consideration during utilization of these characters in breeding programme. Through PCA we could identify the number of plant characters which are responsible for the observed genotypic variation within a group. PCA also helps us to indentify the characters which have great impact of phenotype of different accessions of rice, and this is very much important to the selection procedure of breeding programme”. (Bhawana et al. 2020)

**PC scores of the germplasm selected on the basis of >1.0 each PCs**

Based on the PC scores of each component (PC 1, PC 2, PC3 and PC4) having positive values in each PCs, top five genotypes were selected (Table 6 and 7).

**Table 6: Principal component score of the mung bean genotypes**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **S. No.** | **Genotypes** | **Scores** | | | |
| **PC 1** | **PC 2** | **PC 3** | **PC 4** |
| 1 | IGKM-5-6-27 | 0.987 | -0.297 | -0.417 | 0.136 |
| 2 | IGKM-6-27-5 | **2.595** | -0.237 | -0.249 | **1.196** |
| 3 | IGKM-6-10-7 | -0.140 | -1.300 | 0.464 | 0.109 |
| 4 | IGKM-6-4-2 | **2.240** | -0.246 | 0.179 | -0.904 |
| 5 | RMO3-71 | **1.818** | -0.734 | **1.062** | **1.388** |
| 6 | RMO3-79 | 0.709 | **2.307** | 0.620 | **0.637** |
| 7 | IGKM-2021-1 | **2.283** | **1.066** | -0.583 | 0.129 |
| 8 | IGKM-2021-2 | -1.845 | 0.589 | -1.755 | 0.201 |
| 9 | IGKM-2021-3 | 1.239 | 0.085 | -0.856 | 0.020 |
| 10 | TRM-117 | -1.637 | 0.305 | -1.355 | -0.533 |
| 11 | TRM-140 | -1.095 | -0.866 | -0.415 | -0.140 |
| 12 | TRM-141 | -1.462 | -1.248 | 0.452 | -0.876 |
| 13 | TRM-146 | -3.004 | **1.919** | -1.427 | -0.372 |
| 14 | TRM-230 | -1.215 | **1.653** | **2.567** | -2.161 |
| 15 | TRM-250 | -2.604 | -2.762 | **0.958** | **0.316** |
| 16 | TRM-251 | -3.305 | 0.498 | **0.915** | **2.552** |
| 17 | HUM-1 | -0.317 | -1.545 | -0.661 | -1.328 |
| 18 | HUM-12 | **3.566** | -0.832 | -0.403 | -0.375 |
| 19 | HUM-16 | 1.186 | **1.645** | **0.905** | 0.004 |

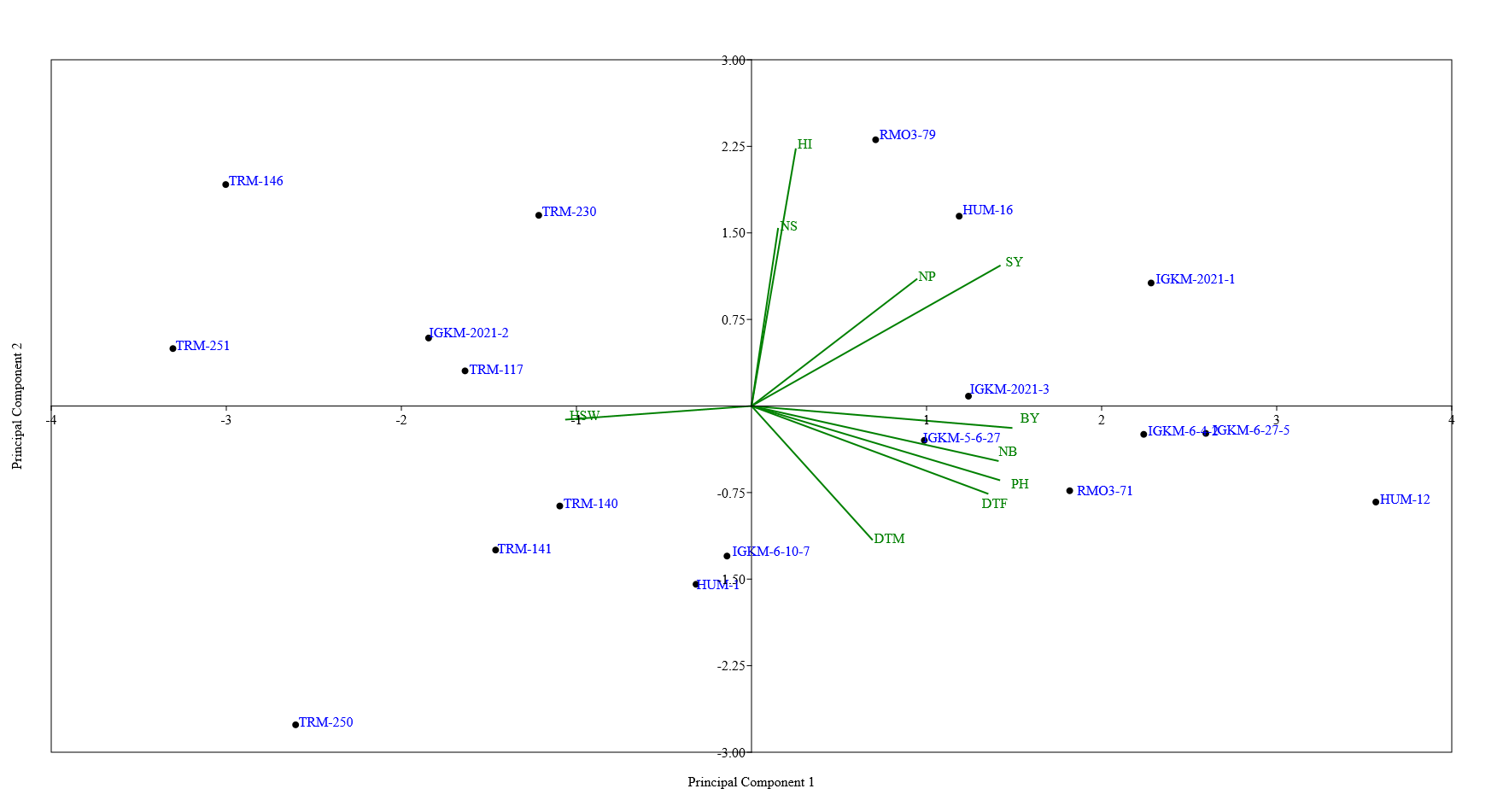
Figures in bold represent top 5 scores in each principal component

**Table 7: List of selected genotypes in each principal component on the basis of top five PC Score**

|  |  |  |  |
| --- | --- | --- | --- |
| **PC 1** | **PC 2** | **PC 3** | **PC 4** |
| HUM-12  (3.566) | RMO3-79  (2.307) | TRM-230  (2.567) | TRM-251  (2.552) |
| IGKM-6-27-5  (2.595) | TRM-146  (1.919) | RMO3-71  (1.062) | RMO3-71  (1.388) |
| IGKM-2021-1  (2.283) | TRM-230  (1.653) | TRM-250  (0.958) | IGKM-6-27-5  (1.196) |
| IGKM-6-4-2  (2.240) | HUM-16  (1.645) | TRM-251  (0.915) | RMO3-79  (0.637) |
| RMO3-71  (1.818) | IGKM-2021-1  (1.066) | HUM-16  (0.905) | TRM-250  (0.316) |

It can be observed that RMO3-71 comes in PC1, PC3 and PC 4 which has relation with BY, SY, PH, HSW and NP. IGKM-6-27-5 comes in PC1 and PC4 both which exhibited better performance in BY, SY, Dm and NP. Likewise HUM 16 comes in PC2 and PC3 has relation with HI, SY, NS, NP and HSW. These genotypes can be recommended directly for cultivation programme.

A further understanding was obtained by plotting the PC scores for individual observations in relation to the axes of PC1 and PC2 (Fig. 2). Principal components 1 and 2 accounted for much of the total variation (59.371%) and hence distinguished among the mung bean genotypes. Two dimensional scaling of the genotypes by the first two PCs showed two distinct groups of genotypes. HUM 12, TRM 146, TRM 251 and TRM 250 were the most distinct from the others and can be used for crossing purpose.

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**Fig 2: Distribution of 19 mung bean genotypes across first two components based on PCA**

**Conclusions**

The genotypes used under present study posses significant difference among themselves. The high GCV and PCV found in character SY (g), HSW (g), NB and HI (%) and high heritability were found in character DTF and DM demonstrated that there was enough variation among the genotypes. High genetic advance coupled with high heritability was observed for PH, NB, NP, HSW and GY indicating that the possibility of direct selection. This indicated the predominance of additive gene action, implying the potential efficacy of simple selection for trait improvement.

Principal component analysis was utilized to examine the variation and to estimate the relative contribution of various traits for total variability. The PC 1 and PC 2 exhibited 59.371% variability. The first PC was more related to BY, SY, PH and NB so it must be considered for direct selection. RMO3-71, IGKM-6-27-5 and HUM 16 will be recommended for direct cultivation programme. Base on the biplot HUM 12, TRM 146, TRM 251 and TRM 250 were the most distinct from the others and can be used for crossing purpose.

**Disclaimer (Artificial intelligence)**

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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