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# Genetic variability, association and principal component analysis for agronomical traits in mungbean (*Vigna radiata* L. Wilczek)

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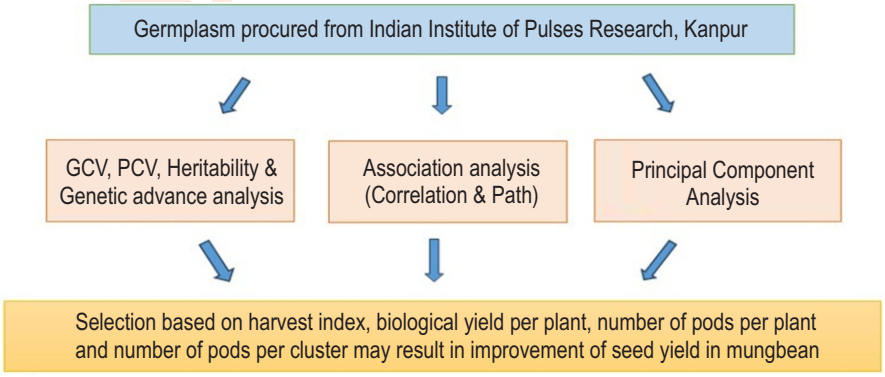
## Abstract

**Aim:** This study aimed to assess the extent of genetic variability in 205 diverse green gram genotypes for agronomical traits and to identify the most effective traits for consideration in development of high yielding cultivars in mungbean.

**Methodology:** The 205 diverse genotype including five checks of mungbean were evaluated in augmented block design-I with eight blocks. In each block, the 30 genotypes (25 genotypes + 5 checks) were grown in paired rows of 4 m length with 45 x 10 cm spacing. The mean data from selected plants across all the genotypes and checks were analyzed for genetic variability parameters (PCV, GCV, $h^2_{bs}$, GAM), Correlation, Path Analysis and Principal Component Analysis (PCA).

**Results:** The high estimates of genotypic coefficient of variation, phenotypic coefficient of variation, heritability ($h^2_{bs}$) along with high genetic advance over mean were observed for number of branches per plant, number of clusters per plant, number of pods per cluster,number of pods per plant and seed yield per plant. The present study indicated that seed yield per plant had significant and positive correlation with harvest index, biological yield per plant, number of pods per plant and number of pods per cluster, and also highly influenced by these traits both directly and indirectly. PCA analysis revealed that out of thirteen principal components, five Pcs (PC1 to PC5) had eigenvalue of >1.0 explaining 19.20%, 16.10%, 11.90%, 10.70% and 8.10%, respectively, accounted for 66% of total variation indicated the strong association of PCs and traits studied. PCA suggested that traits such as vegetative period, number of clusters per plant, number of pods per cluster, number of pods per plant and harvest index were the principal discriminatory traits.




**Interpretation:** It is suggested that selection based on harvest index, biological yield per plant, number of pods per plant and number of pods per cluster may result in improvement of seed yield in mungbean.

**Key words:** Correlation analysis, Genetic variability, Mungbean, Path analysis, Principal component analysis

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## Introduction

Mungbean or greengram (*Vigna radiata* L. Wilczek) is one of the most important pulse crops of sub humid tropics and sub-tropics climate with wider adaptability (Singh *et al.,* 2014a). It is fast growing crop with short life span (75-90 days) and low input requirement (Dahiya *et al.,* 2015). In India, mungbean is cultivated over approximately 4.755 million hectare, producing 2.456 million tons annually (DAC & FW, GOI 2018-19). Because of its short life cycle, mungbean is cultivated as intercropping with sugarcane, maize, pearl millet, cotton, groundnut, sorghum and pigeonpea, and also as a relay crop in rice fallows during winter (Mehandi *et al.,* 2019). Thus, there is great scope for expansion of area and production due to short duration legume that fits well in cropping pattern and low input requirements. The production and productivity is still low due to non-availability of high yielding varieties, adverse climatic condition (drought, high temperature, salinity, water logging), pathogenicity (Yellow mosaic disease, *Cercospora* leaf spot and powdery mildew) and insect-pest (whitefly, pod borer, thrips).

The present study focus to generate the information of major yield attributing traits with prominent genotypes by using diverse primary gene pool, which may provide opportunity to the breeders to develop new generation high yielding mungbean varieties with desirable traits including biotic as well as abiotic tolerance. The evaluation of phenotypic diversity through characterizing agronomical traits plays important role in the selection of appropriate parents for genetic improvement (Abna *et al.,* 2012; Basnet *et al.,* 2014). Nair *et al.* (2013) and Azam *et al.* (2023) also emphasized that the information on estimation of large number of genotypes with agronomic traits may help in breeding of improved mungbean variety in the near future. Therefore, the information regarding genetic variability pattern presents in the existing population of a given crop provides the opportunity for selection to develop a variety with desirable traits. Further knowledge of association between yield and its components accessible both at genotypic and phenotypic levels help to formulate selection criteria. Path analysis is useful in splitting the correlation coefficients of component traits into direct and indirect effects toward contributing to yield. Moreover, yield is a complex trait which depends upon large number of its component traits which are under the influence of environmental factors. These traits are usually correlated, and difficulty may be encountered in interpreting and summarizing analysis of results for germplasm evaluation and characterization.

Principal Component Analysis (PCA) is a multivariate statistical technique that aims to transform a given set of correlated traits in to a new system of non-correlated traits (principal components) and helps in identifying which agronomic traits of the crop contribute most to yield. The phenomenon of compensation among yield components is considered to be the main yield limiting factor. In mungbean, a limited number of genotypes to fewer quantitative traits (Azam *et al.,* 2023) and small number of parents with high degree of relatedness were repeatedly used in crossing programmes (Mehandi *et al.,* 2019). Hence, large and diverse genetic resources must be examined to broaden the genetic variability of yield attributing traits in mungbean. Keeping in view, the 205 mungbean genotypes were evaluated based on the agronomical traits to identify genetic variability among them and to select effective traits for consideration in breeding of new high yielding varieties of mungbean.

## Materials and Methods

**Plant material:** The experiment was conducted at the Agriculture Farm of Banda University of Agriculture and Technology, Banda (25.5$^0$N, 80.3$^0$E and 113 MSL) during *Kharif* 2020. The experimental site fell into semi-arid zone characterized with low humidity and uneven rainfall distribution with average of 900 mm. The soil was characterized as clay loam with pH 8.40, low organic content (0.33%) and low to medium soluble solids (0.79 dS m$^{-1}$). The recommended dose of fertilizer @ 20 kg N, 60 kg $P_2O_5$ and 40 kg $K_2O$ per hectare was applied after final ploughing, followed by making the ridges by ridge maker and seeds were sown after opening the ridges by hand. All the cultural operations were carried out as per the package and practices recommended for raising a good crop. Harvesting of crop was done through first picking when more than 75% pods were mature and final harvesting was done after 10 days of first picking. The study comprised 205 diverse genotype including five checks of mungbean procured from Indian Institute of Pulses Research (IIPR), Kanpur. These genotypes were evaluated in augmented block design-I with eight blocks. In each block, 30 entries (25 genotypes + 5 checks) were allotted to each plot. Each genotype was grown in paired rows of 4 m length with 45 x 10 cm spacing.

**Observations recorded:** The observations were recorded for plant height (PH), number of branches per plant (NBP), number of clusters per plant (NCP), number of pods per cluster (NPC), number of pods per plant (NPP), pod length (PL), number of seeds per pod (NSP), seed weight (SW), biological yield per plant (BYP), harvest index (HI) and yield per plant (YPP). These traits were recorded from five random competitive plants in each entry of every block at harvest and the observations were averaged by dividing each value by five. However, data of vegetative period (VP) was counted from date of sowing to first anthesis and reproductive period (RP) was recorded as days taken from anthesis to days to more than 75% pods maturity on plot basis.

**Statistical analyses:** The analysis of data generated from Augmented Block Design-I was done using Statistical Package for Augmented Design (SPAD) software developed by IASRI, New Delhi. The correlation and path analysis was done by using R-Statistical Programme version 4.0 (package "Metan"). The package of ggbiplot, ggplot and factoextra of R-statistical programme was used for principal component analysis.

## Results and Discussion

The Analysis of variance (ANOVA) revealed significant mean sum of squares for all traits for different sources of variation

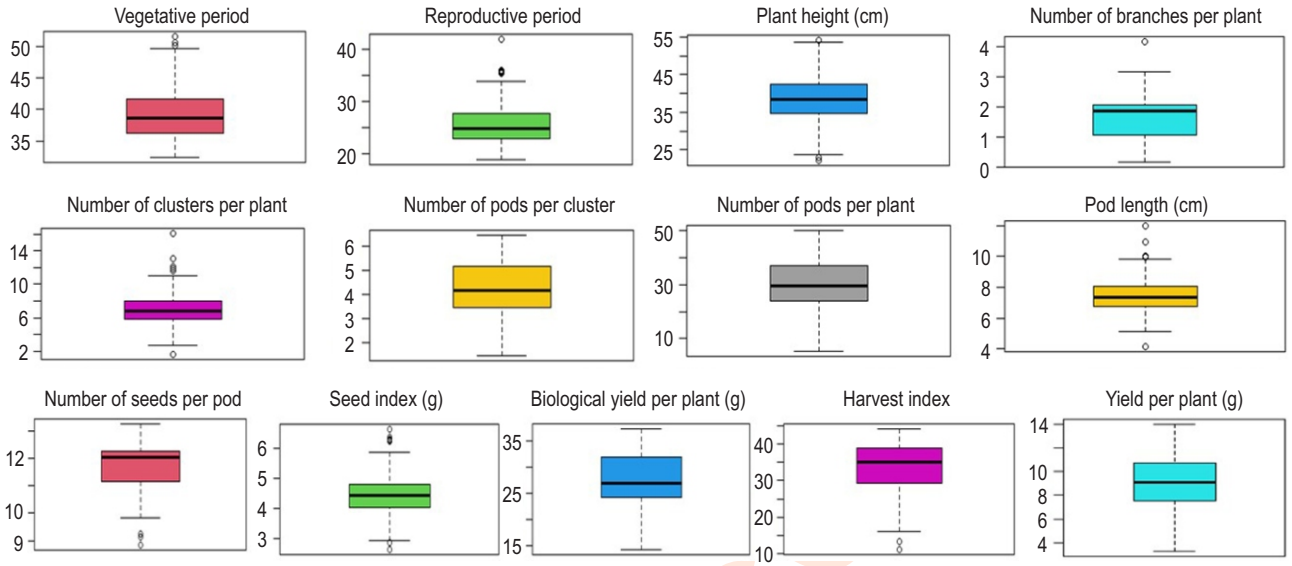


**Fig. 1:** Box plot for performance of genotypes for different traits. Upper and lower line outside box represents maximum and minimum adjacent values, respectively. Dark black line inside box stands for median value. The upper and lower hinge stands for 75% and 25% percentile, respectively. The circle 'o' stands for outliers.

(Table 1). However, the adjusted block, effects were non-significant for all the traits except for RP, PH and NCP indicating homogeneity of evaluation blocks. The analysis of variance for 13 quantitative characters among checks and genotypes revealed the presence of significant variation in the genotypes studied for all the traits, except for NBP and NSP due to non-significant difference among the genotypes, indicating that lesser amount of genetic variability is available for these two traits in primary gene pool of mungbean. The mean sum of squares due to checks vs genotypes showed significant difference for all the traits, except for PH, NPC and NSP. The non-significant differences among genotypes for NBP and between check vs genotypes for NSP were also observed by Divyaramakrishnan and Savithramma (2014) in mungbean. The mean performance of genotypes for all the studied traits indicated considerable variation for all studied traits (Fig.1).

The results of the analysis of genetic parameters namely, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense ($h^2$bs) and genetic advance over mean (GAM) for all thirteen characters are presented in Table 2. In the present study, the lowest estimates of GCV (5.91%) and PCV (7.16%) were observed for NSP while the highest estimates of GCV (36.08%) and PCV (41.12%) were recorded for NBP. Sivasubramanian and Menon (1973) categorized the PCV and GCV values as high (20%), moderate (10% to 20%) and Low (10%). The high (>20%) estimates of GCV and PCV were observed for NBP, NCP, NPC, NPP and YPP. These traits reflect greater genetic variability and preponderance of additive gene action, further improvement could be made through simple plant selection method. The moderate (10-20%) estimates of GCV and PCV were recorded from traits like PH, RP, PL, SW, BYP and HI whereas low GCV and PCV values (<10%) were recorded for NSP and VP indicating very low opportunity of selection to improve the population for these traits directly. Sofia *et al.* (2017) and Mohanlal *et al.* (2018) also reported the low estimates of PCV and GCV for NSP. The high magnitude (>70%) of heritability ($h^2_{bs}$) along with high genetic advance (>20%) over mean (GAM) was exhibited by VP, RP, PH, NBP, NCP, NPC, NPP, PL, HI, SW, BYP and YPP. This clearly indicates preponderance of additive gene action with low environmental influence for determination of these characters and would be effective in phenotypic selection. Comparable findings were also reported by Vadivel *et al.* (2020), Salman *et al.* (2021), Sineka *et al.* (2021), Nalajala *et al.* (2022), Susanthika *et al.* (2024) and Dar *et al.* (2024). The moderate heritability along with low magnitude of genetic advance over mean for NSP suggested that this trait was governed by non-additive genes and direct selection for improvement of this trait may not be rewarding. However, some of the workers gave the emphasized on considering the GCV, PCV, $h^2_{bs}$ and GAM together for selecting the traits and deciding the breeding procedure (Singh *et al.,* 2014b). Traits like RP, PH, NCP, NPP, PL, SW, BYP, HI and YPP showed high GCV, PCV coupled with high heritability, and GAM indicated that simple plant selection for these traits could be rewarding.

The magnitude of genotypic correlation coefficient was non-significantly higher than the corresponding phenotypic correlation coefficient for most of the characters indicating that genetic variance is predominant in expression of characters (Table 3). The YPP showed a significant and positive genotypic and phenotypic correlation with HI, BYP, NPC, SW and NPP, indicating the these characters were strongly and positively

**Table 1:** Analysis of variance (ANOVA) for 13 quantitative traits in mungbean genotypes evaluated using augmented design

| Source of variation | d. f. | Vegetative period (days) | Reproductive period (days) | Plant height (cm) | Number of branches per plant | Number of clusters per plant | Number of pods per cluster | Number of pods per plant | Pod length (cm) | Number of seeds per pod | Seed weight (g) | Biological yield per plant (g) | Harvest index (%) | Yield per plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Block (Adj.) | 7 | 0.80 | 4.49* | 5.28* | 0.20 | 2.72* | 0.65 | 2.36 | 0.13 | 0.21 | 0.01 | 1.96 | 0.97 | 0.13 |
| Treatment (Adj.) | 204 | 18.18* | 19.96* | 35.89* | 0.50* | 4.19* | 1.06* | 75.34* | 1.05* | 0.78* | 0.49* | 26.72* | 40.74* | 4.83* |
| Checks | 4 | 16.94* | 8.84* | 33.23* | 0.50* | 4.19* | 1.05* | 75.71* | 1.04* | 0.79* | 0.45* | 26.93* | 38.89* | 4.83* |
| Genotypes | 199 | 4.10* | 216.08* | 177.06* | 0.21 | 3.05* | 1.74* | 39.35* | 1.3* | 0.48 | 1.84* | 13.26* | 9.97* | 0.86* |
| Checks vs Genotypes | 1 | 321.36* | 1448.70* | 0.72 | 3.91* | 8.75* | 0.84 | 146.30* | 1.77* | 0.01 | 3.65* | 38.82* | 531.32* | 20.76* |
| Error | 28 | 1.37 | 1.46 | 1.12 | 0.11 | 0.73 | 0.28 | 1.42 | 0.09 | 0.22 | 0.01 | 1.23 | 1.01 | 0.14 |

*Significant at 5% probability level

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**Table 2:** Estimates of genetic parameters on 13 quantitative traits in mungbean genotypes

| Characters | Mean±SEm | GCV(%) | PCV (%) | Heritability in broad sense ($h^2_{bs}$) (%) | Genetic advance (GA) | Genetic advance as percent of mean (GAM) |
|---|---|---|---|---|---|---|
| Vegetative period (days) (VP) | 39.26±1.34 | 9.79 | 10.24 | 91.51 | 8.13 | 20.71 |
| Reproductive period (days) (RP) | 25.43±1.38 | 15.86 | 16.56 | 91.75 | 5.68 | 22.35 |
| Plant height (cm) (PH) | 38.11±1.20 | 14.51 | 14.77 | 96.48 | 12.32 | 32.34 |
| Number of branches Per plant (NBP) | 1.65±0.37 | 36.08 | 41.12 | 77.01 | 1.17 | 71.34 |
| Number of clusters Per plant (NCP) | 7.18±0.97 | 24.32 | 27.06 | 80.72 | 3.70 | 51.63 |
| Number of pods per cluster (NPC) | 4.12±0.60 | 20.16 | 23.87 | 71.32 | 1.50 | 36.46 |
| Number of pods per plant (NPP) | 29.60±1.36 | 27.24 | 27.53 | 97.86 | 17.91 | 60.53 |
| Pod length (cm) (PL) | 7.43±0.35 | 12.35 | 13.02 | 89.97 | 1.91 | 25.82 |
| Number of seeds per pod (NSP) | 11.83±0.55 | 5.91 | 7.16 | 68.11 | 1.31 | 11.11 |
| Seed weight (g) )(SW) | 4.46±0.13 | 14.62 | 14.84 | 97.00 | 1.35 | 30.42 |
| Biological yield per plant (g) )(BYP) | 27.33±1.26 | 17.33 | 17.79 | 94.81 | 10.99 | 40.24 |
| Harvest index (%) (HI) | 33.25±2.96 | 17.77 | 18.03 | 97.18 | 13.95 | 41.95 |
| Yield per plant (g) (YPP) | 8.99±4.07 | 22.59 | 22.96 | 96.77 | 4.55 | 50.66 |

**Table 3:** Genotypic (rg) and Phenotypic (rp) correlation coefficients among 13 quantitative traits in mungbean genotypes

| Characters | R | VP | RP | PH | NBP | NCP | NPC | NPP | PL | NSP | SW | BYP | HI | YPP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Vegetative | rg | 1.0000 | -0.1090 | -0.0021 | 0.0350 | -0.0099 | -0.2168* | -0.0779 | -0.0020 | -0.1271 | 0.0900 | -0.3264** | -0.3646** | -0.5496** |
| period | rp | 1.0000 | -0.1254 | 0.0015 | -0.0167 | -0.0423 | -0.1815** | -0.0757 | -0.0111 | -0.1264 | -0.0930 | -0.3142** | -0.3370** | -0.5207** |
| (days) (VP) | | | | | | | | | | | | | | |
| Reproductive | rg | | 1.0000 | 0.1067 | 0.0584 | -0.1442* | -0.1597* | -0.1340 | -0.0669 | 0.0097 | 0.3212** | -0.1406 | 0.0254 | -0.0667 |
| period | rp | | 1.0000 | 0.1115 | 0.0672 | -0.0846 | -0.0981 | -0.1162* | -0.0542 | 0.0273 | 0.3069** | -0.1177 | -0.1177 | -0.0366 |
| (days) (RP) | | | | | | | | | | | | | | |
| Plant height | rg | | | 1.0000 | 0.1689* | 0.0356 | 0.0402 | 0.0281 | 0.0171 | -0.1061 | -0.1184 | 0.1894** | -0.1396* | 0.0136 |
| (cm) (PH) | rp | | | 1.0000 | 0.1401* | 0.0411 | 0.0255 | 0.0343 | 0.0168 | -0.1069 | -0.1184* | 0.1771* | -0.1248 | 0.0173 |
| Number of | rg | | | | 1.0000 | 0.2226** | -0.0004 | 0.1624* | -0.1295 | -0.0503 | 0.0381 | 0.1238 | 0.0187 | 0.0978 |
| branches per | rp | | | | 1.0000 | 0.1629* | 0.0575 | 0.1427* | -0.0809 | -0.0711 | 0.0620 | 0.0992 | 0.0298 | 0.0889 |
| Plant (NBP) | | | | | | | | | | | | | | |
| Number of | rg | | | | | 1.0000 | 0.2979** | 0.7828** | -0.0446 | -0.0232 | -0.1409* | 0.1470* | 0.0139 | 0.1285 |
| clusters per | rp | | | | | 1.0000 | 0.2590** | 0.7119** | -0.0618 | -0.1032 | -0.1280 | 0.1269 | 0.0104 | 0.1094 |
| Plant (NCP) | | | | | | | | | | | | | | |
| Number of | rg | | | | | | 1.0000 | 0.8264** | -0.0982 | -0.1563* | -0.2468** | 0.1050 | 0.1942** | 0.2351** |
| pods per | rp | | | | | | 1.0000 | 0.6970** | -0.0741 | -0.0833 | -0.1891** | 0.0942 | 0.1418 | 0.1877** |
| cluster (NPC) | | | | | | | | | | | | | | |
| Number | rg | | | | | | | 1.0000 | -0.0482 | -0.1247 | -0.1472* | 0.1201 | 0.0877 | 0.1580* |
| of pods per | rp | | | | | | | 1.0000 | -0.0502 | -0.1097 | -0.1451* | 0.1215 | 0.0906 | 0.1629* |
| plant (NPP) | | | | | | | | | | | | | | |
| Pod length | rg | | | | | | | | 1.0000 | 0.1256 | 0.3606** | 0.0492 | -0.0058 | 0.0566 |
| (cm) (PL) | rp | | | | | | | | 1.0000 | 0.1570* | 0.3419** | 0.0360 | -0.0063 | 0.0438 |
| Number of | rg | | | | | | | | | 1.0000 | 0.2256** | -0.0515 | 0.1196 | 0.0629 |
| seeds per | rp | | | | | | | | | 1.0000 | 0.1788* | 0.0150 | 0.0693 | 0.0813 |
| pod (NSP) | | | | | | | | | | | | | | |
| Seed | rg | | | | | | | | | | 1.0000 | 0.0422 | 0.2000** | 0.2126** |
| weight (g) | rp | | | | | | | | | | 1.0000 | 0.0319 | 0.1968** | 0.1998** |
| (SW) | | | | | | | | | | | | | | |
| Biological yield | rg | | | | | | | | | | | 1.0000 | -0.2053** | 0.5559** |
| per plant | rp | | | | | | | | | | | 1.0000 | -0.2160** | 0.5643** |
| (g) (BYP) | | | | | | | | | | | | | | |
| Harvest index | rg | | | | | | | | | | | | 1.0000 | 0.6806** |
| (%) (HI) | rp | | | | | | | | | | | | 1.0000 | 0.6647** |
| Yield per | rg | | | | | | | | | | | | | 1.0000 |
| plant (g) | rp | | | | | | | | | | | | | 1.0000 |
| (YPP) | | | | | | | | | | | | | | |

*,**Significant at 5% and 1% probability level, respectively

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**Table 4:** Direct (diagonal and bold) and indirect (above and below diagonal) effects of twelve quantitative traits on yield per plant at genotypic (G) and phenotypic (P) levels in mungbean

| Characters | Level | VP | RP | PH | NBP | NCP | NPC | NPP | PL | NSP | SW | BYP | HI | Correlation with yield |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Vegetative | G | **-0.0240** | -0.0004 | 0.0000 | -0.0008 | 0.0022 | 0.0634 | -0.0319 | 0.0001 | -0.0001 | -0.0035 | -0.2425 | -0.3122 | -0.5496** |
| period (days) (VP) | P | **0.0560** | -0.0259 | -0.0001 | 0.0003 | -0.0012 | -0.0030 | 0.0018 | -0.0007 | -0.0013 | 0.0077 | -0.2534 | -0.3007 | -0.5207** |
| Reproductive | G | 0.0026 | **0.0040** | -0.0001 | -0.0013 | 0.0325 | 0.0467 | -0.0549 | -0.0011 | 0.0000 | -0.0124 | -0.1045 | 0.0218 | -0.0667 |
| period (days) (RP) | P | -0.0070 | **0.2060** | -0.0051 | -0.0011 | -0.0024 | -0.0016 | 0.0028 | -0.0033 | 0.0003 | -0.0255 | -0.0949 | -0.1050 | -0.0366 |
| Plant height | G | 0.0001 | 0.0004 | **-0.0010** | -0.0038 | -0.0080 | -0.0118 | 0.0115 | 0.0003 | -0.0001 | 0.0046 | 0.1407 | -0.1195 | 0.0136 |
| (cm) (PH) | P | 0.0001 | 0.0230 | **-0.0460** | -0.0022 | 0.0012 | 0.0004 | -0.0008 | 0.0010 | -0.0011 | 0.0099 | 0.1428 | -0.1114 | 0.0173 |
| Number of | G | -0.0008 | 0.0002 | -0.0001 | **-0.0220** | -0.0501 | 0.0001 | 0.0665 | -0.0022 | -0.0001 | -0.0015 | 0.0920 | 0.0160 | 0.0978 |
| branches per plant (NBP) | P | -0.0009 | 0.0139 | -0.0064 | **-0.0160** | 0.0047 | 0.0009 | -0.0034 | -0.0049 | -0.0007 | -0.0052 | 0.0800 | 0.0266 | 0.0889 |
| Number of | G | 0.0002 | -0.0006 | 0.0000 | -0.0049 | **-0.2250** | -0.0872 | 0.3204 | -0.0008 | 0.0000 | 0.0054 | 0.1092 | 0.0119 | 0.1285 |
| clusters per plant (NCP) | P | -0.0024 | -0.0175 | -0.0019 | -0.0026 | **0.0290** | 0.0042 | -0.0169 | -0.0037 | -0.0010 | 0.0107 | 0.1023 | 0.0093 | 0.1094 |
| Number of | G | 0.0052 | -0.0006 | 0.0000 | 0.0000 | -0.0671 | **-0.2930** | 0.3383 | -0.0017 | -0.0002 | 0.0095 | 0.0780 | 0.1663 | 0.2351** |
| pods per cluster (NPC) | P | -0.0101 | -0.0202 | -0.0012 | -0.0009 | 0.0075 | **0.0160** | -0.0165 | -0.0045 | -0.0008 | 0.0157 | 0.0760 | 0.1265 | 0.1877** |
| Number of | G | 0.0019 | -0.0005 | 0.0000 | -0.0036 | -0.1763 | -0.2418 | **0.4090** | -0.0008 | -0.0001 | 0.0057 | 0.0892 | 0.0751 | 0.1580* |
| pods per plant (NPP) | P | -0.0042 | -0.0240 | -0.0016 | -0.0022 | 0.0205 | 0.0113 | **-0.0240** | -0.0030 | -0.0011 | 0.0121 | 0.0980 | 0.0808 | 0.1629* |
| Pod length | G | 0.0001 | -0.0003 | 0.0000 | 0.0029 | 0.0100 | 0.0287 | -0.0197 | **0.0170** | 0.0001 | -0.0139 | 0.0366 | -0.0050 | 0.0566 |
| (cm) (PL) | P | -0.0006 | -0.0112 | -0.0008 | 0.0013 | -0.0018 | -0.0012 | 0.0012 | **0.0600** | 0.0016 | -0.0284 | 0.0290 | -0.0056 | 0.0438 |
| Number of | G | 0.0030 | 0.0000 | 0.0001 | 0.0011 | 0.0052 | 0.0457 | -0.0510 | 0.0021 | **0.0010** | -0.0087 | -0.0383 | 0.1024 | 0.0629 |
| seeds per pod (NSP) | P | -0.0070 | 0.0056 | 0.0049 | 0.0011 | -0.0030 | -0.0014 | 0.0026 | 0.0095 | **0.0100** | -0.0149 | 0.0121 | 0.0618 | 0.0813 |
| Seed weight | G | -0.0022 | 0.0013 | 0.0001 | -0.0009 | 0.0317 | 0.0722 | -0.0603 | 0.0062 | 0.0003 | **-0.0380** | 0.0314 | 0.1713 | 0.2126** |
| (g) (SW) | P | -0.0052 | 0.0633 | 0.0054 | -0.0010 | -0.0037 | -0.0031 | 0.0034 | 0.0206 | 0.0018 | **-0.0830** | 0.0257 | 0.1756 | 0.1998** |
| Biological | G | 0.0078 | -0.0006 | -0.0001 | -0.0028 | -0.0331 | -0.0307 | 0.0492 | 0.0008 | -0.0001 | -0.0016 | **0.7430** | -0.1758 | 0.5559** |
| yield per plant (g) (BYP) | P | -0.0175 | -0.0243 | -0.0081 | -0.0016 | 0.0037 | 0.0015 | -0.0029 | 0.0022 | 0.0002 | -0.0027 | **0.8060** | -0.1927 | 0.5643** |
| Harvest | G | 0.0087 | 0.0001 | 0.0001 | -0.0004 | -0.0031 | -0.0568 | 0.0359 | -0.0001 | 0.0001 | -0.0077 | -0.1525 | **0.8560** | 0.6806** |
| index (%) (HI) | P | -0.0188 | -0.0243 | 0.0057 | -0.0005 | 0.0003 | 0.0023 | -0.0022 | -0.0004 | 0.0007 | -0.0164 | -0.1742 | **0.8920** | 0.6647** |

Residual effect=0.0337 and 0.0013 at genotypic and phenotypic level, respectively

associated due to linkages of genes controlling the characters at coupling phase. These results corroborates with the findings of Asari *et al.* (2019) for NPC, Manivelan *et al.* (2019) for NPP, Kumar *et al.* (2018) for SW, BYP and HI, Azam *et al.* (2023) and Mukesh *et al.* (2024) for NPP and SW, Dar *et al.* (2024) for NPP and BYP. However, YPP had significant and negative correlation with VP both at genotypic and phenotypic levels suggested that increasing VP may decrease yield per plant and vice-versa as reported by earlier workers also (Bhutia *et al.* 2016 and Parihar *et al.* 2018). Thus optimum days of VP should be emphasized while direct selection of high yielding genotype in mungbean. The negative correlation may be due to dispersed variability formed through different kinds of genetic materials such as varieties, germplasm, advanced lines in the present study.

The phenotypic and genotypic correlations of various characters were subjected to path analysis for partitioning the values into direct and indirect effects (Table 4). Path coefficient analysis revealed that HI made high direct and positive contribution and also exerted low and positive indirect influence towards YPP via SW and NPC. Similarly, BYP is next important trait which had high direct effects and also contributed indirectly to YPP through PH and NCP at both genotypic and phenotypic level The results of maximum positive direct effects are accordance with the findings of Prasanna *et al.* (2013) for HI and Nalajala *et al.* (2022) for HI and BYP. It was noted that NPP contributed directly in moderate and positive direction towards YPP, and also contributed indirectly towards yield through NCP and NPC at genotypic level. Similar results with direct contribution of HI, BYP and NPP towards yield were also observed by Abbas *et al.* (2018). The NCP and NPC showed moderate and negative direct effect on yield per plant. The present study indicated that YPP had not only significant and positive correlation with HI, BYP, NPP and NPC but was also highly influenced by these traits both directly and

**Table 5:** Eigen values, proportion of contribution by first five PCs and component loading of quantitative traits in mungbean

| Characters | PC1 | PC2 | PC3 | PC4 | PC5 |
|---|---|---|---|---|---|
| Eigenvalues | 2.498 | 2.087 | 1.552 | 1.394 | 1.051 |
| Proportion explained (%) | 19.20 | 16.10 | 11.90 | 10.7 | 8.10 |
| Cumulative proportion explained (%) | 19.20 | 35.30 | 47.20 | 57.90 | 66.00 |
| Vegetative period (days) (VP) | 0.539 | 0.498 | 0.106 | 0.178 | 0.309 |
| Reproductive period (days) (RP) | 0.266 | -0.081 | -0.172 | 0.358 | -0.518 |
| Plant height (cm) (PH) | -0.108 | 0.133 | -0.477 | -0.389 | 0.126 |
| Number of branches per plant (NBP) | -0.201 | 0.229 | -0.245 | -0.015 | 0.608 |
| Number of clusters per plant (NCP) | -0.501 | 0.447 | -0.169 | 0.457 | 0.005 |
| Number of pods per cluster (NPC) | -0.666 | 0.324 | 0.182 | 0.077 | -0.172 |
| Number of podsper plant (NPP) | -0.715 | 0.491 | 0.055 | 0.414 | -0.038 |
| Podlength (cm) (PL) | 0.059 | -0.384 | -0.251 | 0.428 | 0.395 |
| Number of seeds per pod (NSP) | 0.060 | -0.354 | -0.299 | 0.348 | -0.200 |
| Seed weight (g) (SW) | 0.098 | -0.574 | -0.060 | 0.553 | 0.198 |
| Biological yield per plant (g) (BYP) | -0.472 | -0.245 | -0.692 | -0.234 | -0.083 |
| Harvest index (%) (HI) | -0.378 | -0.443 | 0.719 | -0.014 | 0.153 |
| Yield per plant (g) (YPP) | -0.705 | -0.598 | 0.075 | -0.176 | 0.064 |

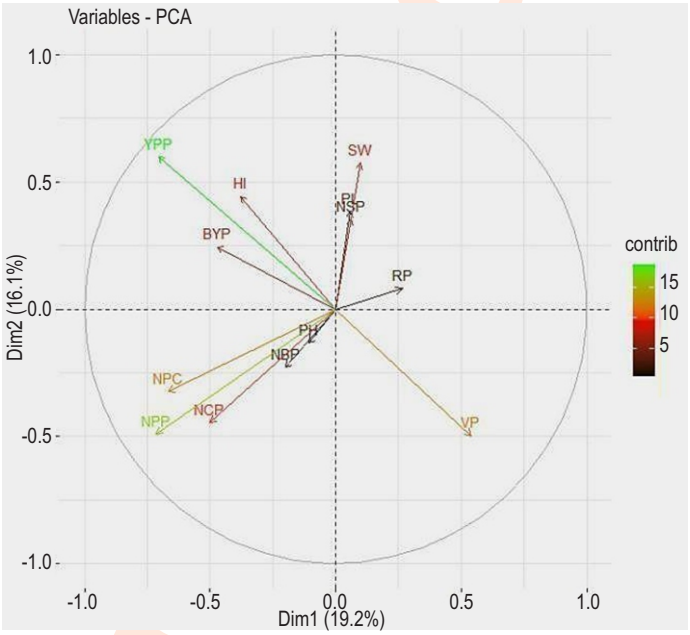


**Fig. 2:** GT biplot showing interrelationship among measured traits. VP-Vegetative period (days); RP- Reproductive period (days); PH- Plant height (cm); NBP- Number of branches per plant; NCP- Number of clusters per plant; NPC- Number of pods per cluster; NPP- Number of pods per plant; PL- Pod length (cm); NSP- Number of seeds per pod; SW- Seed weight (g); BYP- Biological yield per plant (g); HI- Harvest index (%) and YPP-Yield per plant (g).

indirectly. It is, therefore suggested that selection based on HI, BYP, NPP and NPC may result in improvement of seed yield in mungbean. PCA is a method of data reduction to clarify the relationships between two or more characters and to divide the total variance of the original characters into a limited number of uncorrelated new variables (Wiley, 1981).

Among 13 principal components (PC1 to PC13) explaining the 100% of diversity, the five PCs (PC1 to PC5) approximately accounted for 66% of the total variation having eigenvalues greater than unity, indicating that the identified traits within the axes exhibited greater influence on the phenotype. Out of these, 5 principal components, the PC1 accounted for 19.20%; PC2 for 16.10%; PC3 for 11.90%; PC4 for 10.70% and PC5 for 8.10% of the variation (Table 5). Pathak *et al*. (2014) also reported 79.18% of the total variability among

51 genotypes for ten characters from four principal components in mungbean.

Further, according to Pathak *et al.* (2014), the traits having coefficient value greater than 0.3 are considered to be significant on the overall variation. The correlation between principle components with yield and its component traits are presented in Table 5. The first principal component had high positive component loading from VP (0.539). The second principal component (PC2) had high positive loadings for VP (0.498), NCP (0.447), NPC (0.324) and NPP (0.491) whereas the third principal component (PC3) had the highest positive loading for HI (0.719). In the fourth principal component (PC4), the characters that contributed to the component include SW (0.553), NCP (0.457), PL (0.428), NPP (0.414), RP (0.358) and NSP (0.348). The fifth component (PC5) was positively associated with high contribution through NBP (0.608), PL (0.395) and VP (0.309). These results suggest that VP, NCP, NPC, NPP and HI were the principal discriminatory characteristics. The similar observations of Divyaramakrishnan and Savithramma (2014) for NPP and NCP, Priya *et al.* (2019) for NPP and NPC were also reported while evaluation of germplasm in mungbean. Singh *et al.* (2015) identified the harvest index as selection criteria for screening the genotypes for high yield based on principal component analysis.

The first two principal components were plotted to observe relationship among measured traits of greengram (Fig. 2). The correlation coefficient between any two traits is estimated from cosine of the angle between their vectors (Yan and Rajcan, 2002; Dehghani *et al.,* 2008). An angle lower than 90° imply a positive correlation and an angle near to 90° indicates that traits are not correlated whereas an angle greater than 90° and close to 180° represents negative relationship. According to biplot, there are high positive association between NPC, NPP, NCP, NBP and PH; between YPP, BYP and HI in left section of biplot whereas in right section of biplot, there were high and strong association between SW, NSP, PL and RP. The component traits positively correlated with yield per plant were PL, NSP, SW, NPC, NPP and NCP because of small angle (<90°) between their vectors. The traits include PH, NBP and RP which were not correlated or independent of yield as indicated by their near right angle with yield. The YPP was negatively correlated with VP as indicated by its near angle of approximately 180°. Some differences between the biplot predictions and original data is projected because the biplot is explained less than 100% of the total variation (Sharifi and Ebadi, 2018).

Yield is the most complex traits and strongly influenced by numerous environmental factors. Yield improvement remains the top priority of crop breeding with the changing climate and increasing food demand. Yield related traits play a significant role in increasing grain yield due to having higher heritability than grain yield. The present findings demonstrate the existence of sufficient genetic variability within and among genotypes for yield related traits. Identification of genotypes with desirable yield attributing traits can be readily used in regular breeding programme for developing of high yielding mungbean varieties. Based on estimation of genetic parameters, correlation and principal component analysis, it is concluded that NPC, NCP, NPP and HI are important traits and governed by additive genes, hence, weightage should be given to these traits while selecting genotypes in mungbean breeding programme. In the present findings, IPM 2-19, AKM/NP/8/9, PAU 911, ML 1299, IC 296672, Taram 18 and SML 1815 were identified as prominent genotypes and can be used in hybridization programme for yield improvement in mungbean. The information of these important yield-related traits may also be dissect further in identifying candidate genes and quantitative trait loci (QTL) that are strongly associated with yield attributing traits with the help of advance genomic techniques.

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