Original Research Article

**Character Association Analysis of Yield and Yield-Contributing Traits in Local Landraces and Released Varieties of Mungbean (*Vigna radiata* L. Wilczek) for Eastern Plain Zones of Uttar Pradesh.**



**ABSTRACT**

Eighteen genotypes of mungbean were systematically evaluated to elucidate the character associations between yield and its component traits. The experiment was conducted between March to May of the year 2021 at Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, employing a Randomized Block Design (RBD) with three replications. The analysis of variance revealed significant differences among the genotypes for all traits studied, indicating the presence of substantial genetic variability within the population. In general, genotypic correlations were observed to be higher than their phenotypic counterparts, reflecting a stronger intrinsic association between traits at the genetic level. Correlation coefficient analysis demonstrated that seed yield per plant exhibited a significant and positive association with most traits, except for days to 50% flowering, days to 50% pod setting, days to maturity, and biological yield, where associations were non-significant at both genotypic and phenotypic levels. Path coefficient analysis identified that traits such as days to maturity, number of primary branches per plant, number of seeds per pod, biological yield, and harvest index exerted a direct positive effect on seed yield at both genotypic and phenotypic levels. These findings underscore the pivotal role of these traits in determining seed yield. The results highlight that seed yield is predominantly influenced by the direct and indirect effects of these attributing characters. Consequently, these traits should be accorded priority during selection programs aimed at genetic enhancement of mungbean for yield improvement.

Keywords: Correlation coefficient, Genotypes, Mungbean, Path Coefficient.

**INTRODUCTION**

Pulse crops, often referred to as "grain legumes," hold a pivotal position as staple food sources after cereals, contributing significantly to nutritional security. Enriched with 20–30% protein content, they serve as an essential dietary protein source in India, second only to cereals, which contribute 55% of dietary protein intake (Saran *et al.*, 2021). Additionally, pulses are rich in calcium and phosphorus, earning the epithet "poor man’s meat" due to their affordability, accessibility, and high protein content. Their ability to fix atmospheric nitrogen, coupled with deep-root systems, enhances soil health by improving aeration, water-holding capacity, microbial activity, and nutrient cycling. These attributes enable pulses to function effectively as catch crops, cover crops, intercrops, and crop rotations. The Indian Council of Medical Research (ICMR) recommends a per capita daily pulse intake of 150 g, yet current consumption trends reveal a decline, contributing to protein deficiency and malnutrition (Deekshith *et al.*, 2022). Mungbean (*Vigna radiata* L. Wilczek), a diploid (2n=22) self-pollinating species of the Leguminosae family, originated in the Indo-Burma region (Vavilov, 1935). This vital legume, cultivated primarily in South-East Asia, serves as a protein-rich food for vegetarians, offering superior digestibility and a nutrient-dense profile with 22–28% protein, 59–65% carbohydrates, and abundant iron and folate (Keatinge *et al.*, 2011). Landraces, dynamic populations with genetic diversity and local adaptations, are invaluable genetic reservoirs for breeding programs addressing abiotic stress and nutrient efficiency (Camacho-Villa *et al.*, 2005; Dwivedi *et al.*, 2016). Correlation forms the basis for the selection index there by helping the plant breeder with crop improvement. Measurement of the correlation coefficient helps identify the relative contribution of component characters towards yield (Panse, 1957). Moreover, the correlation between grain yield and a component character may sometimes be misleading due to an over estimation or underestimation of its association with other characters. Thus, yield components influence ultimate yield both directly and indirectly (Tukey, 1954). Splitting of total correlation into direct and indirect effects, therefore, would provide a more meaningful interpretation of such association. Path coefficient, which is a standard partial regression coefficient, specifies the cause-and-effect relationship and measures the relative importance of each variable (Wright, 1921). Therefore, correlation in combination with path coefficient analysis will be an important tool to find out the association and quantify the direct and indirect influence of one character upon another (Dewey and Lu, 1959). Holding the above focuses viable the current experiment was attempted to isolate the reasonable attributing traits for genetic improvement program through manipulation of genotypes.

**MATERIAL AND METHODS**

The experiment was executed following a Randomized Block Design (RBD) with 18 genotypes replicated three times between March to May of year 2021 at the Central Research Farm, Department of Genetics and Plant Breeding, Naini Agricultural Institute, SHUATS, Prayagraj. Geographically, Naini is situated between 20°33'40'' to 21°50' N latitude and 73°27'58'' to 73°56'36'' E longitude. The region experiences a tropical climate marked by hot summers, moderately cold winters, and a humid monsoon season with significant rainfall, primarily between June and September. Observations were taken from five randomly selected and tagged plants per plot, excluding border plants to eliminate edge effects. For traits such as days to 50% flowering and days to maturity, measurements were recorded across the entire plot. The parameters assessed included 14 agronomic and yield-contributing traits: days to 50% flowering, days to 50% pod setting, days to maturity, plant height (cm), number of primary branches, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, seed index (g), biological yield (g), harvest index, and seed yield per plant (g). Weights were measured in grams using a precision balance. The data were analyzed for variance using the RBD method described by Panse and Sukhatme (1985) and Singh and Chaudhary (1985). Phenotypic and genotypic correlations were computed following the approach of Al-Jibouri *et al.* (1958), while path coefficient analysis was carried out as per Dewey and Lu (1959). These analyses aimed to unravel the relationships among traits and quantify their direct and indirect contributions to yield, providing insights for genetic improvement in mungbean.

**RESULTS AND DISCUSSION**

The mean sum of squares for the various traits evaluated is presented in Table 1. The analysis of variance revealed highly significant differences among the 18 genotypes for all traits studied, including days to 50% flowering, days to 50% pod setting, days to maturity, plant height (cm), number of primary branches, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, seed index (g), biological yield (g), harvest index, and seed yield per plant (g). This underscores the existence of a substantial degree of genetic variability within the mungbean germplasm under investigation. These findings are consistent with earlier studies conducted by Pathak *et al.* (2014), Pulagampalli and Lavanya (2017), and Abdus *et al.* (2021). The discernible presence of significant genetic variability highlights the potential of the mungbean genotypes under study for further exploration and breeding programs. Such variability serves as a critical foundation for selection, enabling the identification and utilization of superior genotypes to enhance yield and other agronomic traits. Consequently, the germplasm under evaluation demonstrates considerable promise for advancing genetic improvement efforts in mungbean.

**Correlation Coefficient Analysis**

The potential productivity of any crop is fundamentally evaluated based on grain yield per unit area. Enhancing yield through direct selection is inherently challenging due to its polygenic nature and dependence on various contributing traits as well as environmental factors. Consequently, it becomes imperative to assess the association of seed yield with its attributing characters and the interrelationships among these traits. Understanding such associations enables the determination of their relative importance in yield improvement. The magnitude and direction of correlation provide insights into how changes in one trait influence others simultaneously. For effective indirect selection for grain yield, a strong and positive genotypic correlation between attributing traits and yield is crucial. Given the absence of a suitable significance test for genotypic correlations, the "t-test" has predominantly been used to evaluate phenotypic correlations. In the present study, higher genotypic correlation coefficients compared to their phenotypic counterparts across most traits indicate stronger inherent associations, with environmental influences diminishing phenotypic correlations. These findings corroborate the observations of Dhunde *et al.* (2021). Phenotypic and genotypic correlation coefficient analysis (Table 2) revealed that seed yield per plant exhibited positive and significant correlations with all characters except days to 50% flowering, days to 50% pod setting, and days to maturity. Seed yield per plant showed a non-significant positive correlation with biological yield. Significant positive correlations between seed yield per plant and plant height were reported by Garg *et al.* (2017) and Ahmad and Belwal (2020). Positive and significant correlations with the number of primary branches, clusters per plant, and pods per cluster were similarly reported by Garg *et al.* (2017), Ahmad and Belwal (2020), and Dhunde *et al.* (2021). Previous studies, including those by Das and Barua (2015) and Choudhary *et al.* (2017) also confirmed positive and significant correlations with the number of pods per plant, pod length, and seeds per pod. Positive associations with seed index and harvest index were earlier highlighted by Tabasum *et al.* (2010) and Garg *et al.* (2017). Conversely, negative and significant correlations of seed yield per plant with days to 50% flowering, days to 50% pod setting, and days to maturity were consistent with findings from Raturi *et al.* (2015) and Choudhary *et al.* (2017).

**Path Coefficient Analysis**

In the present investigation, at the phenotypic level (Table 3), the highest positive direct effect on seed yield per plant was exhibited by harvest index (0.4564), followed by the number of seeds per pod (0.2145), pod length (cm) (0.0883), number of primary branches per plant (0.0875), biological yield (g) (0.0693), number of clusters per plant (0.0522), plant height (cm) (0.0464), and days to maturity (0.0270). Conversely, negative direct effects on seed yield were observed for days to 50% flowering (-0.0512), seed index (g) (-0.0807), number of pods per plant (-0.0967), number of pods per cluster (-0.1450), and days to 50% pod setting (-0.2164). The residual component of the phenotypic path analysis indicated that 73% of the variability in seed yield was explained by these fourteen traits. At the genotypic level (Table 4), the maximum positive direct effects were noted for the number of seeds per pod (0.8282), followed by the number of pods per cluster (0.7009), days to maturity (0.6479), harvest index (0.3408), biological yield (0.1215), and the number of primary branches per plant (0.1191). Negative direct effects were attributed to plant height (-0.0133), number of pods per plant (-0.1381), number of clusters per plant (-0.2217), days to 50% pod setting (-0.4014), seed index (-0.4289), days to 50% flowering (-0.4345), and pod length (-0.5659). The residual component of the genotypic path analysis indicated that 83% of the variability in seed yield was accounted for by these fourteen characters. Similar findings have been reported in earlier studies. Das and Barua (2015), and Garg *et al.* (2017) highlighted the substantial positive direct effect of harvest index on seed yield per plant. Additionally, Das and Barua (2015) and Hemavanthy *et al.* (2015) emphasized the positive direct influence of the number of seeds per pod on seed yield. The positive contributions of pod length and the number of primary branches per plant were corroborated by Garg *et al.* (2017) and Ahmad and Belwal (2020). Biological yield also displayed a positive direct impact on seed yield, as previously reported by Tabasum *et al.* (2010) and Garg *et al.* (2017). Similar results regarding the positive influence of the number of clusters per plant were supported by Hemavanthy *et al.* (2015) and Ahmad and Belwal (2020). Plant height and days to maturity exhibited positive direct effects on seed yield, aligning with earlier findings by Vinay *et al.* (2010) and Itefa *et al.* (2014). Negative direct effects of days to 50% flowering and seed index on seed yield, as observed in this study, were previously reported by Vinay *et al.* (2010) and Ghimire *et al.* (2018). Positive direct effects of the number of pods per cluster at the genotypic level were also noted by Dhunde *et al.* (2021). Path analysis further revealed that the strong positive association of other traits with seed yield per plant resulted from high indirect effects mediated through harvest index and biological yield per plant. The negative association of days to 50% flowering and days to 50% pod setting with seed yield was attributed to their negative direct effects. Interestingly, traits such as plant height, number of pods per cluster, number of pods per plant, pod length, and seed index, despite having negative direct effects at the genotypic level, demonstrated positive associations with seed yield due to indirect effects via biological yield per plant and harvest index. Thus, path analysis underscored the substantial direct and indirect contributions of the number of seeds per pod, pod length, number of primary branches, biological yield, number of clusters per plant, plant height, days to maturity, and harvest index to seed yield. These findings suggest that selection for these traits would be effective in improving seed yield in mungbean. The low residual effect observed in the path analysis indicates that the traits examined in this study sufficiently explained the majority of the variability in seed yield for mungbean.

**CONCLUSION**

The correlation coefficient analysis demonstrated that seed yield per plant exhibited a significant and positive association with traits such as harvest index, seed index, number of seeds per pod, pod length, plant height, number of primary branches per plant, number of pods per plant, number of clusters per plant, and number of pods per cluster at both genotypic and phenotypic levels. These associations highlight the potential importance of these traits in influencing seed yield directly or indirectly. Path coefficient analysis further revealed that days to maturity, number of primary branches per plant, number of seeds per pod, biological yield, and harvest index exhibited a direct positive effect on seed yield at both genotypic and phenotypic levels. These findings suggest that these traits play a critical role in determining seed yield in mungbean and should be prioritized during selection programs aimed at genetic improvement. Emphasis on these traits during breeding efforts could effectively enhance seed yield in mungbean.

**Declaration of Competing Interest**

The corresponding author is in charge of making sure that all authors agree on the descriptions and that they are correct. And all authors have no competing interests

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**Table 1. Analysis of Variance for various traits in mungbean**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Source** | ***df*** | **DF50** | **DPS50** | **DM** | **PH** | **NPB** | **NCPP** | **NPPC** | **NPPP** | **NSPP** | **PL** | **BY** | **SI** | **HI** | **SYPP** |
| **Replication** | 2 | 9.85 | 21.94 | 1.76 | 0.79 | 1.29 | 0.03 | 0.01 | 0.13 | 0.30 | 0.21 | 2.44 | 0.15 | 0.62 | 0.61 |
| **Treatment** | 17 | 21.63\* | 27.76\* | 51.12\*\* | 307.66\*\* | 5.45\*\* | 2.14\*\* | 1.12\*\* | 4.28\*\* | 2.52\*\* | 1.04\*\* | 45.22\*\* | 1.21\*\* | 205.89\*\* | 2.27\*\* |
| **Error** | 34 | 8.53 | 10.95 | 3.25 | 1.63 | 0.43 | 0.07 | 0.02 | 0.31 | 0.23 | 0.18 | 2.65 | 0.11 | 2.40 | 0.54 |

\*\*Significant at 1%. DF50-Days to flowering (50%), DPS50-Days to pod setting (50%) DM-Days to maturity, PH-Plant height (cm), NPB-Number of branches/plant, NCPP-Number of clusters/plant, NPPC-Number of pods/cluster, NPPP-Number of pods/plant, PL-Pod length (cm), NSPP-Number of seeds/pod, SI-100-seed weight (g), SYPP-Seed yield/plant (g), BY-Biological yield/plant (g) and HI-Harvest index (%).

**Table 2. Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among various characters in mungbean**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **DF50** | **DPS50** | **DM** | **PH** | **NPB** | **NCPP** | **NPPC** | **NPPP** | **NSPP** | **PL** | **BY** | **SI** | **HI** | **SYPP** |
| **DF50** | **1.000** | 0.738\*\* | 0.719\*\* | -0.364\*\* | -0.329\*\* | -0.452\*\* | -0.413\*\* | -0.489\*\* | -0.384\*\* | -0.286\*\* | -0.0714 | -0.337\* | -0.380\*\* | -0.413\*\* |
| **DPS50** | 0.922\*\* | **1.000** | 0.709\*\* | -0.363\*\* | -0.2650 | -0.387\*\* | -0.373\*\* | -0.406\*\* | -0.369\*\* | -0.292\* | -0.0481 | -0.305\* | -0.337\* | -0.439\*\* |
| **DM** | 0.897\*\* | 0.857\*\* | **1.000** | 0.633\*\* | -0.524\*\* | -0.494\*\* | -0.517\*\* | -0.601\*\* | -0.460\*\* | -0.411\*\* | -0.0446 | -0.420\*\* | -0.430\*\* | -0.431\*\* |
| **PH** | -0.653\*\* | -0.636\*\* | -0.698\*\* | **1.000** | 0.822\*\* | 0.581\*\* | 0.684\*\* | 0.721\*\* | 0.618\*\* | 0.535\*\* | 0.0567 | 0.400\*\* | 0.556\*\* | 0.465\*\* |
| **NPB** | -0.670\*\* | -0.608\*\* | -0.652\*\* | 0.926\*\* | **1.000** | 0.644\*\* | 0.749\*\* | 0.639\*\* | 0.666\*\* | 0.529\*\* | 0.2285 | 0.487\*\* | 0.640\*\* | 0.507\*\* |
| **NCPP** | -0.838\*\* | -0.712\*\* | -0.581\*\* | 0.614\*\* | 0.765\*\* | **1.000** | 0.791\*\* | 0.797\*\* | 0.684\*\* | 0.514\*\* | 0.0365 | 0.814\*\* | 0.828\*\* | 0.544\*\* |
| **NPPC** | -0.689\*\* | -0.635\*\* | -0.599\*\* | 0.718\*\* | 0.880\*\* | 0.835\*\* | **1.000** | 0.738\*\* | 0.710\*\* | 0.707\*\* | 0.1495 | 0.650\*\* | 0.807\*\* | 0.551\*\* |
| **NPPP** | -0.920\*\* | -0.876\*\* | -0.736\*\* | 0.798\*\* | 0.760\*\* | 0.859\*\* | 0.827\*\* | **1.000** | 0.650\*\* | 0.580\*\* | 0.0857 | 0.617\*\* | 0.679\*\* | 0.481\*\* |
| **NSPP** | -0.782\*\* | -0.635\*\* | -0.561\*\* | 0.703\*\* | 0.859\*\* | 0.839\*\* | 0.831\*\* | 0.800\*\* | **1.000** | 0.447\*\* | 0.0891 | 0.445\*\* | 0.771\*\* | 0.620\*\* |
| **PL** | -0.868\*\* | -0.876\*\* | -0.683\*\* | 0.644\*\* | 0.768\*\* | 0.676\*\* | 0.921\*\* | 0.781\*\* | 0.697\*\* | **1.000** | 0.1001 | 0.384\*\* | 0.540\*\* | 0.412\*\* |
| **BY** | -0.0433 | 0.0119 | -0.0342 | 0.0701 | 0.2393 | 0.0818 | 0.1753 | 0.0938 | 0.0276 | 0.2643 | **1.000** | 0.0681 | -0.724\* | 0.0205 |
| **SI** | -0.836\*\* | -0.728\*\* | -0.486\*\* | 0.459\*\* | 0.569\*\* | 0.955\*\* | 0.809\*\* | 0.808\*\* | 0.594\*\* | 0.646\*\* | 0.1149 | **1.000** | 0.702\*\* | 0.395\*\* |
| **HI** | -0.678\*\* | -0.634\*\* | -0.490\*\* | 0.570\*\* | 0.749\*\* | 0.868\*\* | 0.840\*\* | 0.744\*\* | 0.874\*\* | 0.684\*\* | -0.1576 | 0.799\*\* | **1.000** | 0.624\*\* |
| **SYPP** | -0.573\*\* | -0.427\*\* | -0.520\*\* | 0.665\*\* | 0.879\*\* | 0.810\*\* | 0.792\*\* | 0.744\*\* | 0.824\*\* | 0.756\*\* | 0.0030 | 0.630\*\* | 0.923\*\* | **1.000** |

**\*** Significant at 5 per cent, **\*\*** Significant at 1 per cent. DF50-Days to flowering (50%), DPS50-Days to pod setting (50%) DM-Days to maturity, PH-Plant height (cm), NPB-Number of branches/plant, NCPP-Number of clusters/plant, NPPC-Number of pods/cluster, NPPP-Number of pods/plant, PL-Pod length (cm), NSPP-Number of seeds/pod, SI-100-seed weight (g), SYPP-Seed yield/plant (g), BY-Biological yield/plant (g) and HI-Harvest index (%).

**Table 3. Direct (diagonal) and indirect path effects of different characters on seed yield per plant in mungbean at phenotypic level.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **DF50** | **DPS50** | **DM** | **PH** | **NPB** | **NCPP** | **NPPC** | **NPPP** | **NSPP** | **PL** | **BY** | **SI** | **HI** |
| **DF50** | **-0.0512** | -0.0378 | -0.0368 | 0.0187 | 0.0168 | 0.0231 | 0.0211 | 0.0250 | 0.0197 | 0.0147 | 0.0037 | 0.0172 | 0.0195 |
| **DPS50** | -0.1596 | **-0.2164** | -0.1533 | 0.0785 | 0.0573 | 0.0836 | 0.0806 | 0.0879 | 0.0798 | 0.0631 | 0.0104 | 0.0660 | 0.0729 |
| **DM** | -0.0194 | 0.0192 | **0.0270** | -0.0171 | -0.0142 | -0.0133 | -0.0140 | -0.0162 | -0.0124 | -0.0111 | -0.0012 | -0.0114 | -0.0116 |
| **PH** | -0.0169 | -0.0169 | -0.0294 | **0.0464** | 0.0382 | 0.0270 | 0.0318 | 0.0335 | 0.0287 | 0.0248 | 0.0026 | 0.0186 | 0.0258 |
| **NPB** | -0.0288 | -0.0232 | -0.0458 | 0.0720 | **0.0875** | 0.0563 | 0.0655 | 0.0559 | 0.0583 | 0.0463 | 0.0200 | 0.0427 | 0.0560 |
| **NCPP** | -0.0236 | -0.0202 | -0.0258 | 0.0303 | 0.0336 | **0.0522** | 0.0412 | 0.0416 | 0.0357 | 0.0268 | 0.0019 | 0.0425 | 0.0432 |
| **NPPC** | 0.0598 | 0.0541 | 0.0750 | -0.0992 | -0.1086 | -0.1147 | **-0.1450** | -0.1071 | -0.1030 | -0.1025 | -0.0217 | -0.0943 | -0.1170 |
| **NPPP** | 0.0473 | 0.0393 | 0.0581 | -0.0697 | -0.0618 | -0.0771 | -0.0714 | **-0.0967** | -0.0628 | -0.0561 | -0.0083 | -0.0597 | -0.0657 |
| **NSPP** | -0.0825 | -0.0791 | -0.0986 | 0.1325 | 0.1429 | 0.1467 | 0.1524 | 0.1394 | **0.2145** | 0.0959 | 0.0191 | 0.0955 | 0.1655 |
| **PL** | -0.0253 | -0.0258 | -0.0363 | 0.0472 | 0.0467 | 0.0454 | 0.0624 | 0.0512 | 0.0395 | **0.0883** | 0.0088 | 0.0339 | 0.0477 |
| **BY** | -0.0049 | -0.0033 | -0.0031 | 0.0039 | 0.0158 | 0.0025 | 0.0104 | 0.0059 | 0.0062 | 0.0069 | **0.0693** | 0.0047 | -0.0119 |
| **SI** | 0.0272 | 0.0246 | 0.0339 | -0.0323 | -0.0393 | -0.0657 | -0.0525 | -0.0498 | -0.0359 | -0.0310 | -0.0055 | **-0.0807** | -0.0567 |
| **HI** | -0.1733 | -0.1538 | -0.1961 | 0.2539 | 0.2922 | 0.3777 | 0.3682 | 0.3100 | 0.3520 | 0.2463 | -0.0787 | 0.3204 | **0.4564** |
| **SYPP** | -0.413\*\* | -0.439\*\* | -0.0117 | 0.465\*\* | 0.507\*\* | 0.544\*\* | 0.551\*\* | 0.481\*\* | 0.620\*\* | 0.412\*\* | 0.0205 | 0.395\*\* | 0.624\*\* |

Residual: 0.271

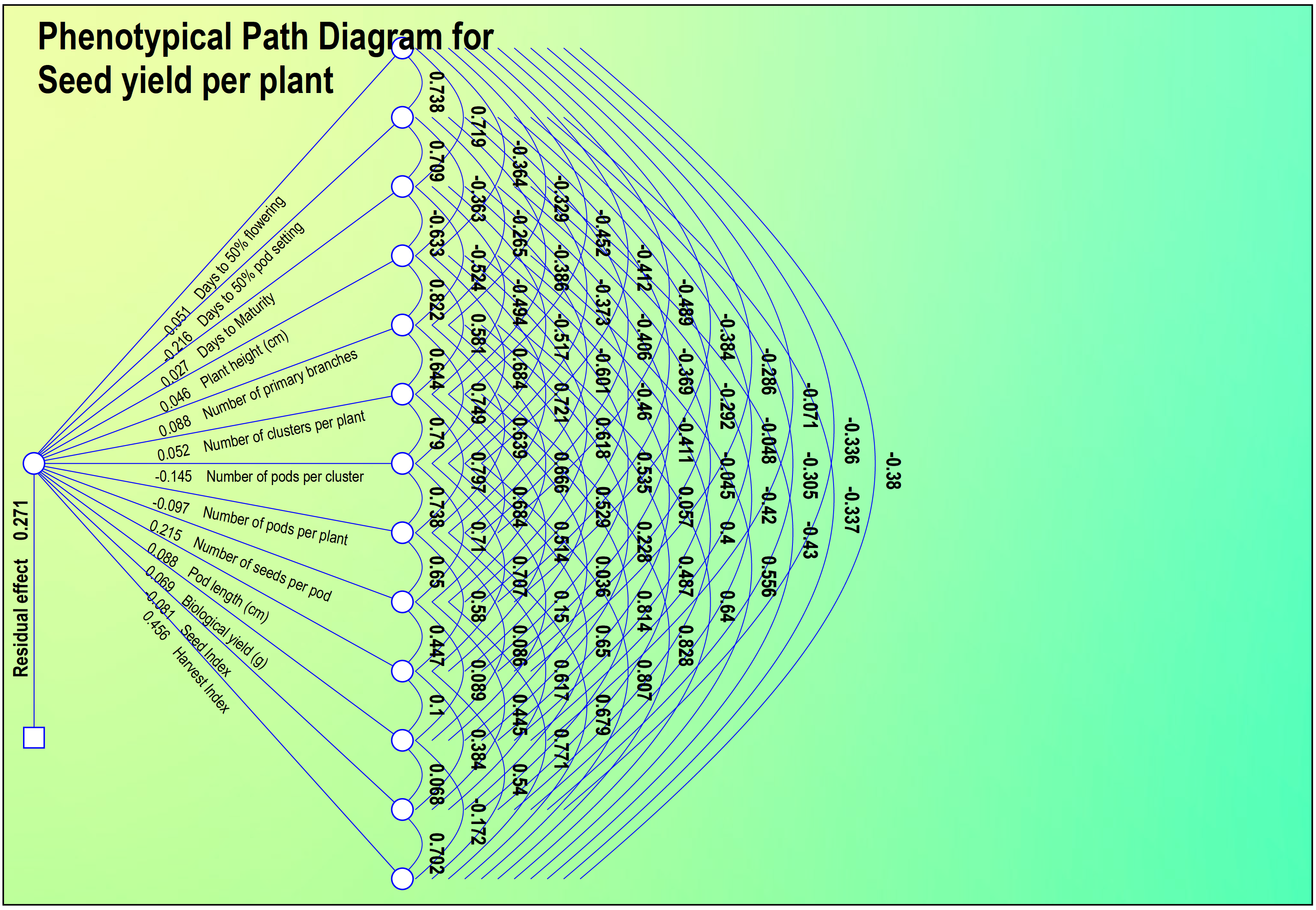
DF50-Days to flowering (50%), DPS50-Days to pod setting (50%) DM-Days to maturity, PH-Plant height (cm), NPB-Number of branches/plant, NCPP-Number of clusters/plant, NPPC-Number of pods/cluster, NPPP-Number of pods/plant, PL-Pod length (cm), NSPP-Number of seeds/pod, SI-100-seed weight (g), SYPP-Seed yield/plant (g), BY-Biological yield/plant (g) and HI-Harvest index (%).

**Table 4. Direct (diagonal) and indirect path effects of different characters on seed yield per plant in mungbean at genotypic level**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **DF50** | **DPS50** | **DM** | **PH** | **NPB** | **NCPP** | **NPPC** | **NPPP** | **NSPP** | **PL** | **BY** | **SI** | **HI** |
| **DF50** | **-0.4345** | -0.5582 | -0.4377 | 0.2835 | 0.2911 | 0.3640 | 0.2995 | 0.3998 | 0.3397 | 0.3771 | 0.0188 | 0.3633 | 0.2947 |
| **DPS50** | -0.5156 | **-0.4014** | -0.4311 | 0.2554 | 0.2438 | 0.2857 | 0.2550 | 0.3515 | 0.2547 | 0.3514 | -0.0048 | 0.2923 | 0.2546 |
| **DM** | 0.6527 | 0.6958 | **0.6479** | -0.4520 | -0.4226 | -0.3761 | -0.3878 | -0.4767 | -0.3636 | -0.4422 | -0.0222 | -0.3149 | -0.3176 |
| **PH** | 0.0086 | 0.0084 | 0.0092 | **-0.0133** | -0.0123 | -0.0081 | -0.0095 | -0.0106 | -0.0093 | -0.0085 | -0.0009 | -0.0061 | -0.0075 |
| **NPB** | -0.0798 | -0.0723 | -0.0777 | 0.1103 | **0.1191** | 0.0911 | 0.1047 | 0.0904 | 0.1023 | 0.0914 | 0.0285 | 0.0677 | 0.0891 |
| **NCPP** | 0.1857 | 0.1578 | 0.1287 | -0.1361 | -0.1697 | **-0.2217** | -0.1851 | -0.1904 | -0.1859 | -0.1499 | -0.0181 | -0.2116 | -0.1923 |
| **NPPC** | -0.4832 | -0.4452 | -0.4195 | 0.5036 | 0.6166 | 0.5854 | **0.7009** | 0.5795 | 0.5825 | 0.6452 | 0.1228 | 0.5667 | 0.5887 |
| **NPPP** | 0.1271 | 0.1209 | 0.1016 | -0.1101 | -0.1049 | -0.1186 | -0.1142 | **-0.1381** | -0.1104 | -0.1078 | -0.0129 | -0.1116 | -0.1028 |
| **NSPP** | -0.6474 | -0.5255 | -0.4619 | 0.5824 | 0.7116 | 0.6947 | 0.6883 | 0.6623 | **0.8282** | 0.5771 | 0.0228 | 0.4920 | 0.7235 |
| **PL** | 0.4911 | 0.4955 | 0.3863 | -0.3644 | -0.0434 | -0.3826 | -0.5209 | -0.4420 | -0.3944 | **-0.5659** | -0.1496 | -0.3653 | -0.3870 |
| **BY** | -0.0053 | 0.0014 | -0.0042 | 0.0085 | 0.0291 | 0.0099 | 0.0213 | 0.0114 | 0.0033 | 0.0321 | **0.1215** | 0.0140 | -0.0192 |
| **SI** | 0.3586 | 0.3123 | 0.2085 | -0.1966 | -0.2440 | -0.4094 | -0.3468 | -0.3465 | -0.2548 | -0.2769 | -0.0493 | **-0.4289** | -0.3425 |
| **HI** | -0.2311 | -0.2162 | -0.1670 | 0.1941 | 0.2551 | 0.2957 | 0.2862 | 0.2536 | 0.2977 | 0.2330 | -0.0537 | 0.2721 | **0.3408** |
| **SYPP** | -0.573\*\* | -0.427\*\* | -0.520\*\* | 0.665\*\* | 0.879\*\* | 0.810\*\* | 0.792\*\* | 0.744\*\* | 1.0899 | 0.756\*\* | 0.0030 | 0.630\*\* | 0.923\*\* |

Residual: 0.170

DF50-Days to flowering (50%), DPS50-Days to pod setting (50%) DM-Days to maturity, PH-Plant height (cm), NPB-Number of branches/plant, NCPP-Number of clusters/plant, NPPC-Number of pods/cluster, NPPP-Number of pods/plant, PL-Pod length (cm), NSPP-Number of seeds/pod, SI-100-seed weight (g), SYPP-Seed yield/plant (g), BY-Biological yield/plant (g) and HI-Harvest index (%).



**Figure 1. Genotypic path diagram for seed yield per plant in mungbean at phenotypic level**

**Figure 2. Genotypic path diagram for seed yield per plant in mungbean at genotypic level**