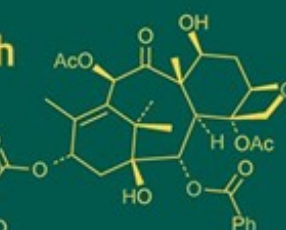
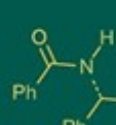


## International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693  
 ISSN Online: 2617-4707  
 NAAS Rating (2026): 5.29  
 Indexing: Embase  
 IJABR 2026; SP-10(9): 2041-2052  
[www.biochemjournal.com](http://www.biochemjournal.com)  
 Received: 17-06-2026  
 Accepted: 14-08-2026  
 Published: 22-09-2026

The names and affiliations of all authors are provided below, following the references.

## Assessment of genetic variability, heritability, genetic advance and trait associations for yield improvement in lentil (*Lens culinaris* Medik.)

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DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i9Sz.10105>

### ABSTRACT

The present investigation was undertaken to assess genetic variability, heritability, genetic advance, character associations and path coefficient analysis among fifteen lentil (*Lens culinaris* Medik.) genotypes (12 lines and 3 testers) and their  $F_1$  and  $F_2$  generations for fifteen quantitative and quality traits. The experiment was conducted in a randomized complete block design during Rabi 2025–26 at the Student Instructional Farm, C.S. Azad University of Agriculture and Technology, Kanpur. Substantial genetic variability was observed among parents,  $F_1$ s and  $F_2$ s. Phenotypic coefficient of variation (PCV) was generally higher than genotypic coefficient of variation (GCV) for most traits. High GCV coupled with high heritability and high genetic advance as per cent of mean was recorded for number of secondary branches (GCV = 22.29%,  $h^2$  = 98.70%, GA = 45.60%), number of primary branches (GCV = 18.00%,  $h^2$  = 82.80%, GA = 33.74%), seed yield per plant (GCV = 14.72%,  $h^2$  = 97.30%, GA = 29.90%), total pods per plant, biological yield and methionine content in parents, indicating predominance of additive gene action. Seed yield per plant exhibited strong positive genotypic correlations with biological yield (0.813\*\*), harvest index (0.723\*\*), 100-seed weight (0.774\*\*), plant height (0.629\*\*) and seeds per pod (0.498) in parents; similar trends persisted in  $F_1$  (BY = 0.887\*\*, HI = 0.591\*\*, HSW = 0.679\*\*) and  $F_2$  (BY = 0.763\*\*, HI = 0.667\*\*, SPD = 0.814\*\*). Negative associations of seed yield with days to 50% flowering (–0.517\*\* parents; –0.496\*\*  $F_1$ ; –0.458\*\*  $F_2$ ) and days to maturity indicated scope for simultaneous improvement of earliness and yield. Path coefficient analysis revealed that biological yield exerted the highest positive direct effect on seed yield in parents (2.130),  $F_1$  (0.736) and  $F_2$  (0.711), followed by harvest index (0.755, 0.426 and 0.525, respectively). Strong negative direct effects were observed for seeds per pod (–1.953), total pods per plant (–0.752), 100-seed weight (–0.718) and days to 50% flowering (–0.951) in parents. Protein content showed a very strong positive association with methionine content (0.974\*\*). Selection based on biological yield, harvest index, 100-seed weight, number of pods per plant and secondary branches, together with earliness, would be effective for developing high-yielding lentil genotypes with improved nutritional quality.

**Keywords:** Lentil, Genetic variability, Heritability, Genetic advance, Correlation, *Lens culinaris*

### Research Article

### Introduction

Lentil (*Lens culinaris* Medikus) is an important grain legume belonging to the family Fabaceae and genus *Lens*. It is one of the oldest domesticated food legumes and is considered one of the founder crops associated with the origin of agriculture in Southwest Asia (Zohary *et al.*, 1973) [1]. Lentil is a predominantly self-pollinated, diploid crop ( $2n = 2x = 14$ ) and is cultivated across diverse agro-ecological conditions, particularly in Mediterranean, subtropical, arid and semi-arid regions. Its adaptation to diverse production environments has resulted in considerable variation among genotypes for phenological, morphological, agronomic and quality attributes (Erskine *et al.*, 2011; Erskine *et al.*, 2016) [2, 3].

The cultivated species, *L. culinaris subsp. culinaris*, is closely related to its wild progenitor, *L. culinaris subsp. orientalis*, and both possess substantial morphological and genetic similarity. The diploid nature and predominantly self-pollinated reproductive system of lentil are important considerations in the conservation, evaluation and utilization of its genetic variability for breeding purposes (Erskine *et al.*, 2011; Erskine *et al.*, 2016) [2, 3]. The genus *Lens* contains considerable diversity, and cultivated lentil represents an important component of this genetic resource. Molecular studies have further contributed to the understanding of genetic structure and relationships within the genus *Lens* (Liber *et al.*, 2021) [4].

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In India, lentil is an important rabi pulse crop and is predominantly cultivated under rainfed conditions, frequently utilizing residual soil moisture. It is grown in several agro-climatic regions and forms an important component of cereal–pulse and other cropping systems. According to Agricultural Statistics at a Glance 2024–25, lentil occupied approximately 1.70 million hectares, with a production of 1.65 million tonnes and an average productivity of 973 kg ha<sup>-1</sup> during 2024–25 (DA&FW, 2025) [5]. Uttar Pradesh is one of the major lentil-producing states in India. During 2024–25, the crop was cultivated on approximately 0.60 million hectares in the state, producing about 0.63 million tonnes with an average productivity of 1,035 kg ha<sup>-1</sup>. The state contributed approximately 37.8 per cent of India’s total lentil production and recorded productivity higher than the national average (DA&FW, 2025) [5].

Assessment of genetic variability provides the first step towards effective selection. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) help quantify the magnitude of genetic and phenotypic variation for quantitative traits. Comparison of GCV and PCV provides an indication of the relative influence of environmental variation on trait expression. Significant genetic variation for growth, yield and yield-related traits has been reported in lentil, although the magnitude of variation differs among traits and genetic materials (Poudel *et al.*, 2022; Tadesse *et al.*, 2022) [6, 7]. Heritability provides information about the proportion of phenotypic variation attributable to genetic differences. Broad-sense heritability includes additive, dominance and epistatic components. However, heritability alone does not indicate the expected magnitude of improvement through selection. Genetic advance, when considered together with heritability, provides additional information regarding the probable response to selection. High heritability associated with high

genetic advance is generally indicative of a greater contribution of additive genetic effects (Johnson *et al.*, 1955) [8]. In lentil, substantial heritability and genetic advance have been reported for several yield and yield-related traits, although their magnitude varies with genetic material and environment (Poudel *et al.*, 2022; Anant *et al.*, 2025) [6, 9].

Correlation analysis is useful for determining the direction and magnitude of association among quantitative characters. Genotypic correlation provides information regarding the genetic association between traits, whereas phenotypic correlation represents the combined influence of genetic and environmental factors. Since seed yield is a complex character, understanding its association with component traits can help identify suitable secondary characters for indirect selection. However, correlation alone does not distinguish whether an association results from a direct influence or from an indirect relationship through other traits (Tadesse *et al.*, 2022) [7]. Keeping the above facts in view, the present study was undertaken to estimate genetic variability, heritability, genetic advance and character associations among parents and segregating generations of lentil.

Materials and methods

The experimental material comprised fifteen lentil genotypes (12 lines and 3 testers). The genotypes were selected on the basis of their origin, adaptability and morpho-physiological characters viz., earliness, higher yield potential, disease resistance etc. These genotypes were obtained from the Legume Section, Department of Genetics and Plant Breeding, C. S. Azad University of Agriculture and Technology, Kanpur. Details of the genotypes used as parents are presented in Table 1.

Table 1. Details of genotypes used as parents in the experiment

| S. No. | Name of Lines | Pedigree  | Source             | Key Features                                                   |
|--------|---------------|-----------|--------------------|----------------------------------------------------------------|
| 1      | KLS 1445      | Germplasm | CSAUA&T, Kanpur    | High biomass, early maturity with higher yield                 |
| 2      | KLS 1447      | Germplasm | CSAUA&T, Kanpur    | Small seed, early maturity in late sown condition              |
| 3      | KLS 1449      | Germplasm | CSAUA&T, Kanpur    | High biomass with multiple disease resistance (wilt)           |
| 4      | KLS 1451      | Germplasm | CSAUA&T, Kanpur    | Small seed with early maturity, resistant to wilt & rust       |
| 5      | KLS 1453      | Germplasm | CSAUA&T, Kanpur    | Early maturity with higher yield                               |
| 6      | PL 318        | Germplasm | GBPUA&T, Pantnagar | Small seed with more clusters, higher yield                    |
| 7      | PL 342        | Germplasm | GBPUA&T, Pantnagar | Medium bold, high biomass, more clusters                       |
| 8      | IPL 24-3      | Germplasm | ICAR-IIPR, Kanpur  | Medium bold, early with more clusters & multiple resistance    |
| 9      | IPL 244       | Germplasm | ICAR-IIPR, Kanpur  | Small seed with early maturity, high biomass                   |
| 10     | VL 161        | Germplasm | ICAR-VPKAS Almora  | Medium bold with high biomass, resistant to wilt & rust        |
| 11     | NDL 2018      | Germplasm | ANDUA&T, Ayodhya   | Large seed, higher yield, resistant to rust                    |
| 12     | VL 162        | Germplasm | ICAR-VPKAS Almora  | Large seed, high biomass with more clusters, resistant to rust |

Crossing was performed in a line × tester fashion to generate 36 F<sub>1</sub> hybrids. The F<sub>1</sub> s were advanced to F<sub>2</sub> generation. The final trial comprising 87 treatments (15 parents + 36 F<sub>1</sub> s + 36 F<sub>2</sub> s) was conducted in a randomized complete block design during Rabi season 2025-26 at the Student Instructional Farm (SIF), C. S. Azad University of

Agriculture and Technology, Kanpur-208002 (U.P.). Each parent and F<sub>1</sub> was grown in a single-row plot, while F<sub>2</sub>s were grown in double-row plots. Recommended package of practices was followed to raise a healthy crop.

**Table 1.** (contd.). Testers used in the experiment

| S. No. | Name of Testers | Pedigree       | Source             | Key Features                        |
|--------|-----------------|----------------|--------------------|-------------------------------------|
| 13     | KLS 218         | KLS 5133/L9362 | CSAUA&T, Kanpur    | Resistant to rust and wilt          |
| 14     | KL 320          | PL 406/P237    | CSAUA&T, Kanpur    | Moderately resistant to wilt & rust |
| 15     | PL 639          | L-9/TYPE 8     | GBPUA&T, Pantnagar | Small seeded, susceptible to wilt   |

### Observations recorded

Observations were recorded on five randomly selected competitive plants for the following traits: days to 50% flowering (DFF), days to maturity (DM), plant height (PH, cm), number of primary branches per plant (NPB), number of secondary branches per plant (NSB), number of clusters per plant (NCP), number of pods per cluster (NPC), total number of pods per plant (TPP), seeds per pod (SPD), 100-seed weight (HSW, g), biological yield per plant (BY, g), seed yield per plant (SYP, g), harvest index (HI, %), protein content (PC, %) and methionine content (MC, %). Protein and methionine contents were estimated in the laboratory using standard biochemical assays.

### Statistical analyses

Analysis of variance was performed as per standard procedure. Genotypic and phenotypic coefficients of variation were calculated according to Burton (1952) [10]. Broad-sense heritability was estimated following Hanson *et al.* (1956) [11]. Genetic advance as per cent of mean was computed as suggested by Johnson *et al.* (1955) [8]. Genotypic and phenotypic correlation coefficients were calculated according to the method of Al-Jibouri *et al.* (1958) [12]. Significance of correlation coefficients was tested against tabulated 'r' values at 5% and 1% levels of significance.

## Results and discussion

### Genetic variability, heritability and genetic advance

Estimates of genetic variability parameters for parents, F<sub>1</sub> and F<sub>2</sub> generations are presented in Table 2. The analysis revealed considerable range of variation for all the traits studied across generations. In general, phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for most of the traits, indicating the influence of environment on the expression of these characters. However, the difference between PCV and GCV was relatively small for several traits, suggesting that the traits were less influenced by environmental factors and selection based on phenotypic performance would be effective.

Among parents, high GCV (> 20%) was recorded for number of secondary branches per plant (22.29%), while moderate GCV (10–20%) was observed for number of primary branches per plant (18.00%), number of pods per cluster (16.66%), seeds per pod (15.36%), total pods per plant (14.50%), seed yield per plant (14.72%), number of clusters per plant (12.30%), methionine content (11.82%) and biological yield (10.41%). Low GCV (< 10%) was noted for days to 50% flowering, days to maturity, plant height, 100-seed weight, harvest index and protein content. Similar trends of high variability for yield-attributing traits have been reported by Poudel *et al.* (2022) [6] and Tadesse *et al.* (2022) [7].

High broad-sense heritability (> 80%) coupled with high genetic advance as per cent of mean (> 20%) was observed in parents for number of secondary branches per plant ( $h^2 = 98.70\%$ , GA = 45.60%), number of primary branches per plant ( $h^2 = 82.80\%$ , GA = 33.74%), number of pods per cluster ( $h^2 = 86.80\%$ , GA = 31.97%), seed yield per plant ( $h^2 = 97.30\%$ , GA = 29.90%), total pods per plant ( $h^2 = 77.50\%$ , GA = 26.29%), seeds per pod ( $h^2 = 71.10\%$ , GA = 26.67%), methionine content ( $h^2 = 97.32\%$ , GA = 24.34%), number of clusters per plant ( $h^2 = 93.70\%$ , GA = 24.52%) and biological yield ( $h^2 = 90.40\%$ , GA = 20.39%). High heritability with moderate genetic advance was recorded for 100-seed weight, plant height, days to 50% flowering, harvest index and protein content. The combination of high heritability and high genetic advance indicates predominance of additive gene action and offers good scope for selection (Johnson *et al.*, 1955) [8]. These findings are in agreement with Anant *et al.* (2025) [9] and Poudel *et al.* (2022) [6].

In F<sub>1</sub> generation, high heritability with high to moderate genetic advance was observed for number of primary branches, number of secondary branches, total pods per plant, biological yield and seed yield per plant. In F<sub>2</sub> generation, high heritability (> 80%) with moderate to high genetic advance was recorded for number of primary branches, number of secondary branches, total pods per plant, 100-seed weight, biological yield, harvest index and seed yield per plant. The persistence of high heritability and genetic advance in segregating generations for these traits indicates their reliable transmission and usefulness for selection in early generations.

**Table 2.** Genetic variability parameters in parents, F<sub>1</sub> and F<sub>2</sub> generations for different traits

| Trait | Gen.           | Mean   | GCV%  | PCV%  | $h^2$ (bs)% | GA% Mean |
|-------|----------------|--------|-------|-------|-------------|----------|
| DFF   | Parents        | 52.38  | 7.25  | 7.54  | 92.40       | 14.36    |
|       | F <sub>1</sub> | 50.69  | 5.11  | 5.39  | 46.40       | 7.57     |
|       | F <sub>2</sub> | 52.88  | 7.92  | 6.82  | 48.30       | 6.79     |
| DM    | Parents        | 122.18 | 2.27  | 2.48  | 83.70       | 4.28     |
|       | F <sub>1</sub> | 119.95 | 2.19  | 2.41  | 82.60       | 4.10     |
|       | F <sub>2</sub> | 120.48 | 1.58  | 1.91  | 68.10       | 2.69     |
| PH    | Parents        | 42.81  | 6.71  | 7.12  | 88.90       | 13.04    |
|       | F <sub>1</sub> | 45.74  | 6.84  | 8.79  | 60.70       | 10.98    |
|       | F <sub>2</sub> | 43.68  | 5.11  | 7.76  | 43.40       | 6.93     |
| NPB   | Parents        | 3.47   | 18.00 | 19.78 | 82.80       | 33.74    |
|       | F <sub>1</sub> | 3.84   | 15.27 | 16.19 | 89.00       | 29.68    |
|       | F <sub>2</sub> | 3.71   | 13.58 | 14.50 | 87.70       | 26.19    |
| NSB   | Parents        | 17.74  | 22.29 | 22.44 | 98.70       | 45.60    |
|       | F <sub>1</sub> | 20.01  | 17.23 | 18.19 | 89.80       | 33.63    |
|       | F <sub>2</sub> | 19.52  | 12.68 | 13.76 | 84.90       | 24.07    |
| TPP   | Parents        | 65.34  | 14.50 | 16.47 | 77.50       | 26.29    |

(continued on next page)

| Trait | Gen.           | Mean  | GCV%  | PCV%  | h <sup>2</sup> (bs)% | GA% Mean |
|-------|----------------|-------|-------|-------|----------------------|----------|
| HSW   | F <sub>1</sub> | 71.50 | 11.89 | 12.98 | 83.90                | 22.44    |
|       | F <sub>2</sub> | 69.61 | 8.95  | 9.59  | 87.10                | 17.19    |
|       | Parents        | 3.10  | 9.07  | 9.14  | 98.60                | 18.56    |
|       | F <sub>1</sub> | 3.18  | 5.77  | 8.48  | 46.40                | 8.10     |
| BY    | F <sub>2</sub> | 3.19  | 5.55  | 5.66  | 96.00                | 11.20    |
|       | Parents        | 8.84  | 10.41 | 10.95 | 90.40                | 20.39    |
|       | F <sub>1</sub> | 9.72  | 9.94  | 10.15 | 95.90                | 20.05    |
|       | F <sub>2</sub> | 9.35  | 6.96  | 7.12  | 95.40                | 14.01    |
| SYP   | Parents        | 3.37  | 14.72 | 14.92 | 97.30                | 29.90    |
|       | F <sub>1</sub> | 3.73  | 11.85 | 13.13 | 81.40                | 22.02    |
|       | F <sub>2</sub> | 3.70  | 9.21  | 9.43  | 95.40                | 18.53    |
|       | Parents        | 25.06 | 7.01  | 7.10  | 97.40                | 14.26    |
| PC    | F <sub>1</sub> | 25.91 | 5.38  | 7.02  | 58.70                | 8.49     |
|       | F <sub>2</sub> | 25.73 | 2.99  | 7.24  | 17.10                | 2.55     |
|       | Parents        | 0.267 | 11.82 | 11.82 | 97.32                | 24.34    |
|       | F <sub>1</sub> | 0.28  | 8.83  | 10.20 | 75.00                | 15.76    |
| MC    | F <sub>2</sub> | 0.27  | 7.36  | 9.74  | 57.10                | 11.45    |

DFE = Days to 50% flowering; DM = Days to maturity; PH = Plant height; NPB = Primary branches/plant; NSB = Secondary branches/plant; TPP = Total pods/plant; HSW = 100-seed weight; BY = Biological yield/plant; SYP = Seed yield/plant; PC = Protein content; MC = Methionine content.

### Character associations

Genotypic and phenotypic correlation coefficients among different traits in parents, F<sub>1</sub> and F<sub>2</sub> generations are presented in **Tables 3–6**. In general, genotypic correlation coefficients were higher in magnitude

than the corresponding phenotypic correlation coefficients, indicating strong inherent association among the characters.

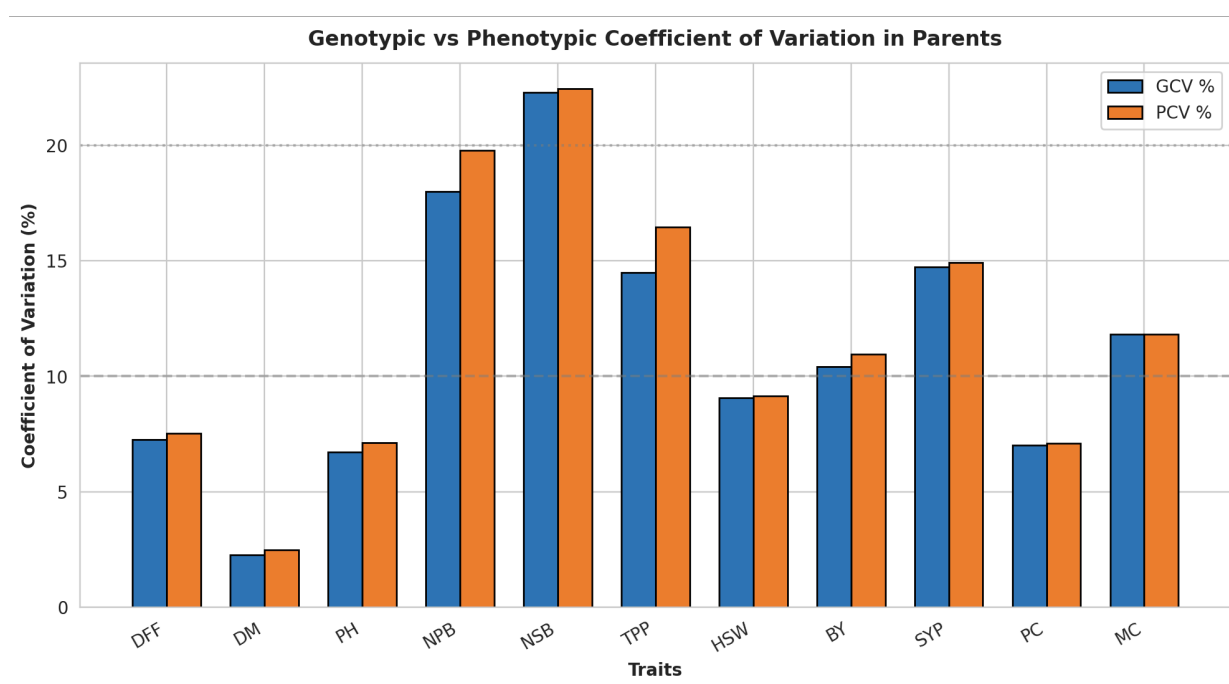


**Figure 1.** Comparison of genotypic (GCV) and phenotypic (PCV) coefficients of variation for key traits in parents

In parents, seed yield per plant showed significant positive genotypic correlation with biological yield (0.813\*\*), harvest index (0.723\*\*), 100-seed weight (0.774\*\*), plant height (0.629\*\*), seeds per pod (0.498) and protein content (0.475\*\*). Significant negative correlations of seed yield were observed with days to 50% flowering (−0.517\*\*) and days to maturity (−0.373\*\*). Similar trends were ob-

served at the phenotypic level. These results suggest that selection for higher biological yield, harvest index and 100-seed weight coupled with earliness would be effective for improving seed yield. Strong positive association between protein content and methionine content (0.974\*\*) indicates the possibility of simultaneous improvement of both quality traits.

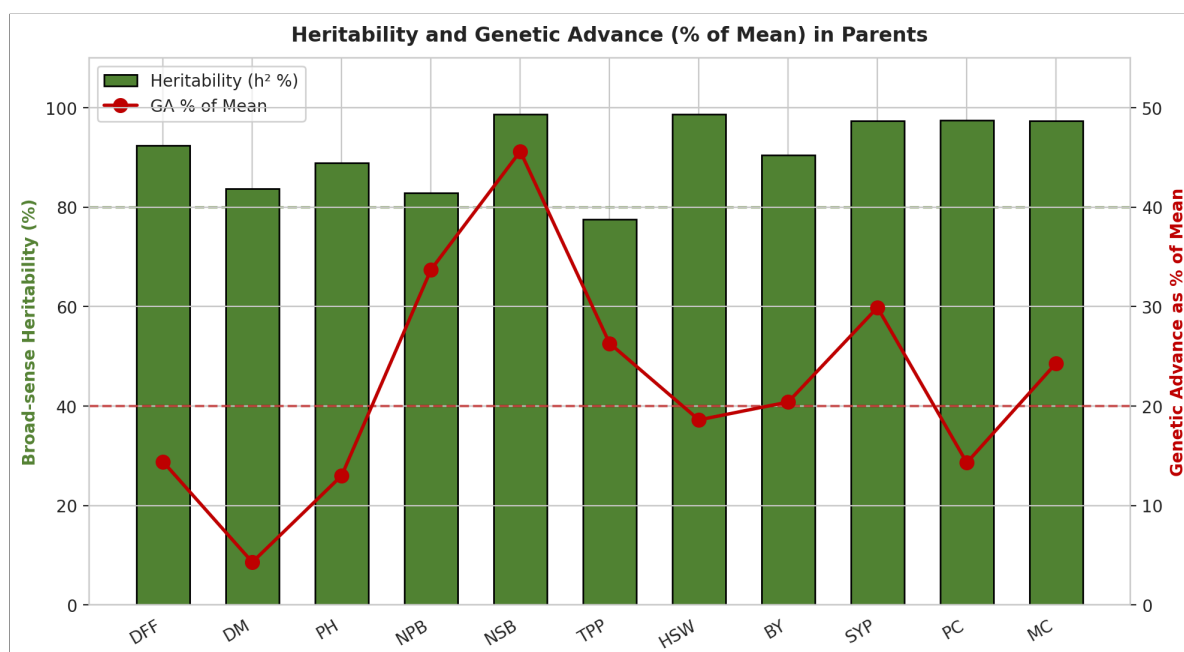


**Figure 2.** Broad-sense heritability and genetic advance as per cent of mean for key traits in parents.

In  $F_1$  generation, seed yield per plant exhibited highly significant positive genotypic correlations with biological yield (0.887\*\*), harvest index (0.591\*\*), 100-seed weight (0.679\*\*), seeds per pod (0.597\*\*), plant height (0.551\*\*) and number of primary branches (0.546\*\*). Negative associations were recorded with days to maturity ( $-0.634^{**}$ ) and days to 50% flowering ( $-0.496^{**}$ ). In  $F_2$  generation, seed yield showed significant positive associations with biological yield (0.763\*\*), harvest index (0.667\*\*), seeds per pod (0.814\*\*) and plant height (0.391\*), while negative associations persisted with days to flowering and maturity. The consistency of these associations across generations strengthens their reliability for use in selection pro-

grammes. Similar positive associations of seed yield with biological yield, harvest index and seed weight have been reported by Tadesse *et al.* (2022) [7] and Poudel *et al.* (2022) [6].

Number of secondary branches showed positive association with total pods per plant and number of pods per cluster, while number of clusters per plant was positively associated with seed yield in parents. Plant height was positively correlated with number of primary branches and seeds per pod across generations. These interrelationships among component traits provide useful guidelines for simultaneous improvement of multiple yield attributes through correlated response to selection.

**Table 3.** Genotypic Correlation Coefficients in Parents among Different Traits

| Traits | DFF  | DM      | PH     | NPB     | NSB    | NCP    | NPC     | TPP     | SPD      | HSW    | BY     | HI     | PC      | MC      | SYP      |
|--------|------|---------|--------|---------|--------|--------|---------|---------|----------|--------|--------|--------|---------|---------|----------|
| DFF    | 1 ** | 0.929** | -0.124 | -0.092  | -0.381 | 0.432  | -0.263  | 0.124   | -0.321   | -0.028 | 0.085  | -0.452 | -0.182  | -0.176  | -0.517** |
| DM     |      | 1 **    | -0.071 | -0.010  | -0.241 | 0.064  | -0.128  | -0.022  | -0.284   | -0.144 | -0.102 | -0.484 | -0.192  | -0.175  | -0.373** |
| PH     |      |         | 1 **   | 0.783** | -0.012 | -0.074 | -0.101  | -0.274  | 0.643**  | -0.173 | 0.198  | 0.012  | 0.063   | -0.008  | 0.629**  |
| NPB    |      |         |        | 1 **    | 0.020  | -0.323 | 0.142   | -0.175  | 0.611*   | 0.018  | 0.372  | 0.008  | -0.041  | -0.150  | 0.260    |
| NSB    |      |         |        |         | 1 **   | -0.338 | 0.636*  | 0.428   | -0.397   | -0.184 | -0.023 | -0.343 | 0.196   | 0.180   | -0.206   |
| NCP    |      |         |        |         |        | 1 **   | -0.561* | 0.272   | -0.069   | 0.087  | 0.464  | -0.049 | -0.095  | -0.065  | 0.302**  |
| NPC    |      |         |        |         |        |        | 1 **    | 0.722** | -0.466   | -0.099 | -0.219 | 0.057  | 0.642** | 0.627*  | -0.103   |
| TPP    |      |         |        |         |        |        |         | 1 **    | -0.642** | 0.019  | 0.154  | 0.041  | 0.666** | 0.694** | 0.162    |
| SPD    |      |         |        |         |        |        |         |         | 1 **     | 0.225  | 0.399  | 0.411  | -0.236  | -0.255  | 0.498    |
| HSW    |      |         |        |         |        |        |         |         |          | 1 **   | 0.634* | 0.570* | -0.003  | 0.087   | 0.774**  |
| BY     |      |         |        |         |        |        |         |         |          |        | 1 **   | 0.189  | -0.170  | -0.118  | 0.813**  |
| HI     |      |         |        |         |        |        |         |         |          |        |        | 1 **   | 0.475   | 0.508   | 0.723**  |
| PC     |      |         |        |         |        |        |         |         |          |        |        |        | 1 **    | 0.974** | 0.475**  |
| MC     |      |         |        |         |        |        |         |         |          |        |        |        |         | 1 **    | 0.232*   |
| SYP    |      |         |        |         |        |        |         |         |          |        |        |        |         |         | 1 **     |

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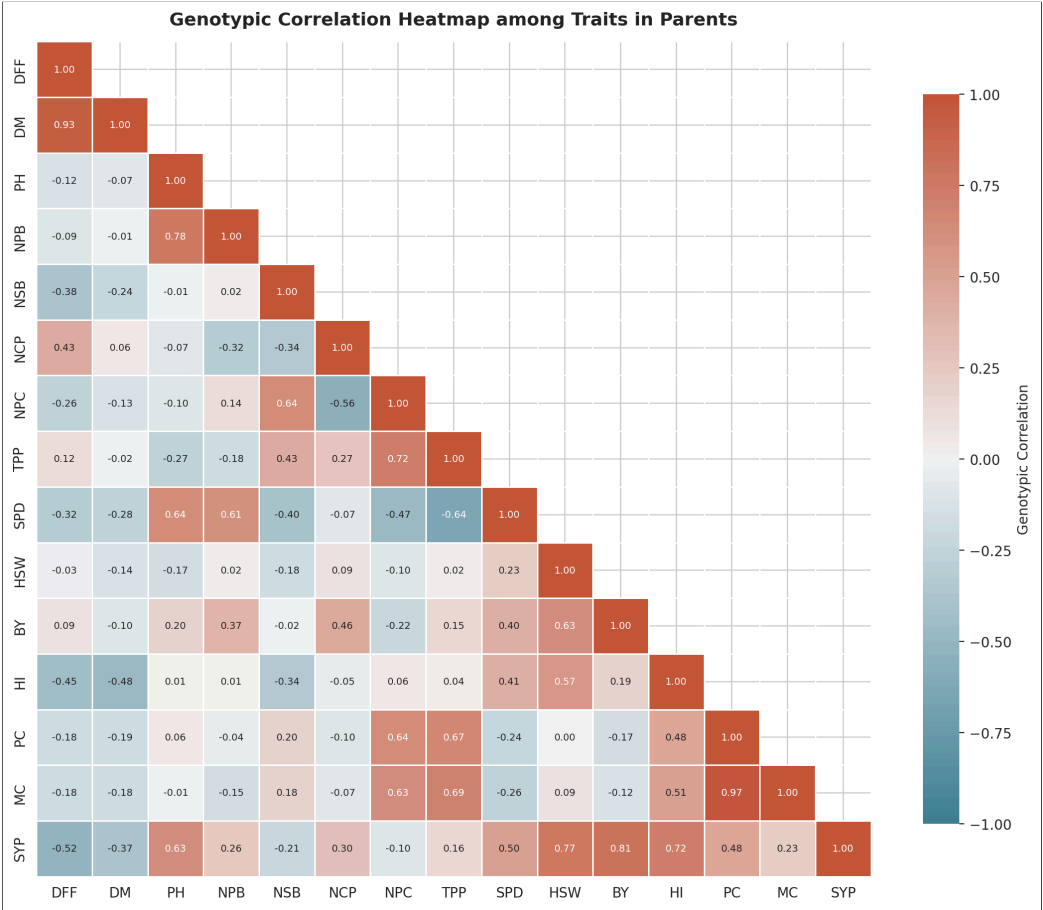


Figure 3. Genotypic correlation heatmap among 15 traits in parents (lower triangle shown).

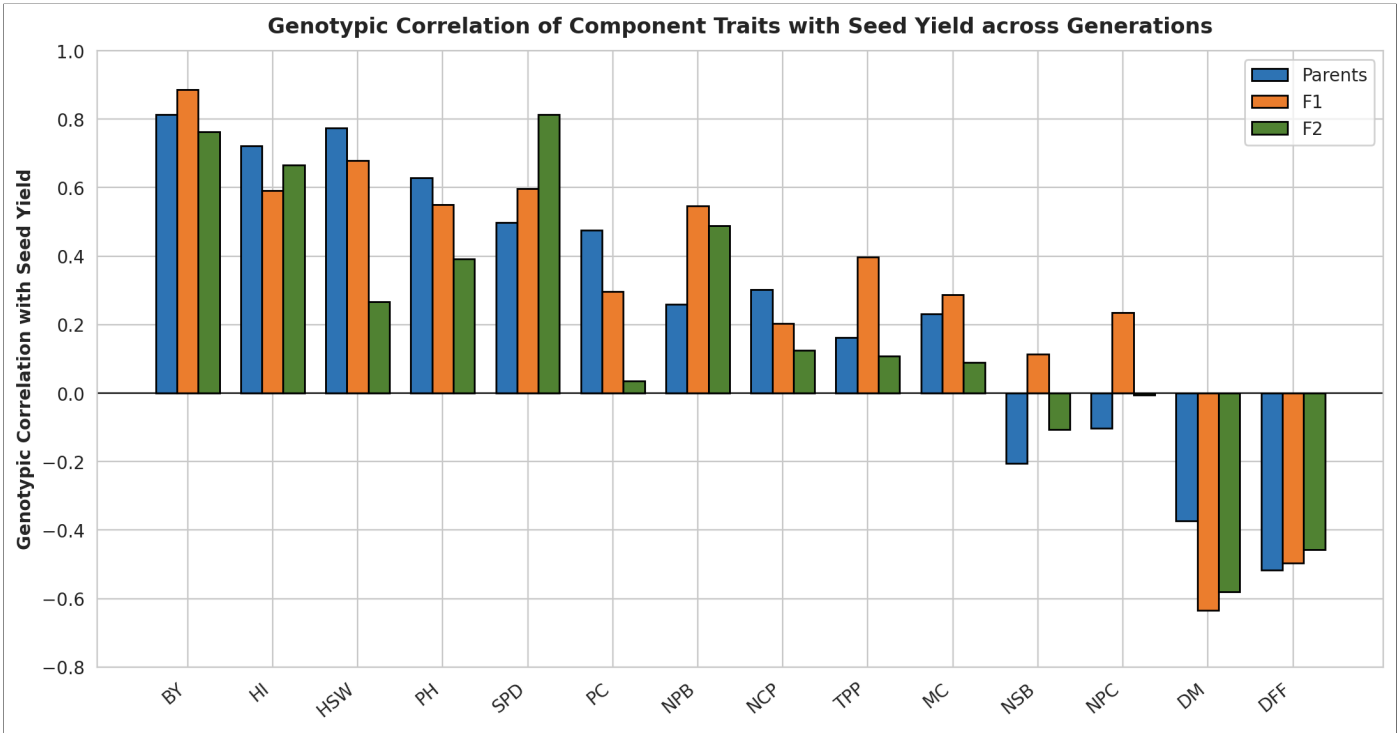


Figure 4. Genotypic correlation of component traits with seed yield per plant across parents, F<sub>1</sub> and F<sub>2</sub> generations.

Table 4. Genotypic Correlation Coefficients in F<sub>1</sub> and F<sub>2</sub> among Different Traits

| Traits | DFF            | DM      | PH      | NPB      | NSB      | NCP      | NPC      | TPP      | SPD      | HSW      | BY       | HI       | PC       | MC       | SYP      |
|--------|----------------|---------|---------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| DFF    | F <sub>1</sub> | 1.000** | 0.958** | -0.482** | -0.404** | -0.657** | 0.350*   | -0.312*  | -0.361** | -0.041   | -0.349*  | -0.407** | -0.438** | -0.377** | -0.496** |
|        | F <sub>2</sub> | 1.000** | 0.987** | -0.39*   | -0.283   | -0.65**  | -0.172   | -0.485** | -0.272   | 0.233    | -0.089   | -0.606** | -0.721** | -0.402*  | -0.458** |
| DM     | F <sub>1</sub> | 1.000** | 1.000** | -0.524** | -0.344*  | -0.582** | 0.055    | -0.520** | -0.293*  | -0.162   | -0.488** | -0.420** | -0.471** | -0.390** | -0.634** |
|        | F <sub>2</sub> | 1.000** | 1.000** | -0.389*  | -0.281   | -0.573** | -0.124   | -0.576** | -0.302   | 0.172    | -0.247   | -0.627** | -0.521** | -0.392*  | -0.581** |
| PH     | F <sub>1</sub> |         | 1.000** | 0.880**  | 0.281*   | -0.103   | 0.194    | 0.156    | 0.681**  | -0.207   | 0.637**  | 0.050    | 0.265    | 0.070    | 0.551**  |
|        | F <sub>2</sub> |         | 1.000** | 0.845**  | 0.164    | -0.255   | -0.355*  | -0.189   | 0.776**  | -0.442** | 0.480**  | 0.055    | -0.530** | -0.175   | 0.391*   |
| NPB    | F <sub>1</sub> |         |         | 1.000**  | 0.056    | -0.242   | 0.174    | 0.048    | 0.666**  | 0.080    | 0.639**  | 0.023    | 0.016    | -0.102   | 0.546**  |
|        | F <sub>2</sub> |         |         | 1.000**  | -0.182   | -0.138   | -0.329   | -0.320   | 0.828**  | -0.128   | 0.543**  | 0.154    | -0.324   | -0.371*  | 0.489**  |
| NSB    | F <sub>1</sub> |         |         |          | 1.000**  | -0.167   | 0.712**  | 0.606**  | -0.271   | -0.175   | 0.225    | -0.171   | 0.514**  | 0.401**  | 0.113    |
|        | F <sub>2</sub> |         |         |          | 1.000**  | -0.152   | 0.645**  | 0.595**  | -0.287   | -0.495** | -0.189   | 0.060    | 0.842**  | 0.472**  | -0.106   |
| NCP    | F <sub>1</sub> |         |         |          |          | 1.000**  | -0.477** | 0.202    | -0.041   | 0.058    | 0.296*   | -0.079   | -0.086   | -0.056   | 0.204    |
|        | F <sub>2</sub> |         |         |          |          | 1.000**  | -0.417*  | 0.113    | -0.103   | 0.305    | 0.187    | -0.011   | -0.165   | -0.075   | 0.125    |
| NPC    | F <sub>1</sub> |         |         |          |          |          | 1.000**  | 0.858**  | -0.316*  | 0.036    | 0.136    | 0.206    | 0.789**  | 0.728**  | 0.236    |
|        | F <sub>2</sub> |         |         |          |          |          | 1.000**  | 0.916**  | -0.264   | -0.188   | -0.353*  | 0.383*   | 0.986**  | 0.881**  | -0.005   |
| TPP    | F <sub>1</sub> |         |         |          |          |          |          | 1.000**  | -0.429** | 0.150    | 0.319*   | 0.221    | 0.797**  | 0.745**  | 0.398**  |
|        | F <sub>2</sub> |         |         |          |          |          |          | 1.000**  | -0.342*  | -0.133   | -0.148   | 0.333*   | 0.895**  | 0.879**  | 0.109    |
| SPD    | F <sub>1</sub> |         |         |          |          |          |          |          | 1.000**  | 0.146    | 0.534**  | 0.331*   | -0.264   | -0.260   | 0.597**  |
|        | F <sub>2</sub> |         |         |          |          |          |          |          | 1.000**  | -0.015   | 0.723**  | 0.435**  | -0.461** | -0.276   | 0.814**  |
| HSW    | F <sub>1</sub> |         |         |          |          |          |          |          |          | 1.000**  | 0.450**  | 0.610**  | 0.036    | 0.085    | 0.679**  |
|        | F <sub>2</sub> |         |         |          |          |          |          |          |          | 1.000**  | 0.141    | 0.244    | -0.373*  | -0.112   | 0.266    |
| BY     | F <sub>1</sub> |         |         |          |          |          |          |          |          |          | 1.000**  | 0.099    | 0.031    | -0.027   | 0.887**  |
|        | F <sub>2</sub> |         |         |          |          |          |          |          |          |          | 1.000**  | 0.028    | -0.432** | -0.322   | 0.763**  |
| HI     | F <sub>1</sub> |         |         |          |          |          |          |          |          |          |          | 1.000**  | 0.575**  | 0.593**  | 0.591**  |
|        | F <sub>2</sub> |         |         |          |          |          |          |          |          |          |          | 1.000**  | 0.518**  | 0.486**  | 0.667**  |
| PC     | F <sub>1</sub> |         |         |          |          |          |          |          |          |          |          |          | 1.000**  | 0.968**  | 0.296*   |
|        | F <sub>2</sub> |         |         |          |          |          |          |          |          |          |          |          | 1.000**  | 1.674**  | 0.035    |
| MC     | F <sub>1</sub> |         |         |          |          |          |          |          |          |          |          |          |          | 0.998**  | 0.287*   |
|        | F <sub>2</sub> |         |         |          |          |          |          |          |          |          |          |          |          | 1.000**  | 0.089    |
| SYP    | F <sub>1</sub> |         |         |          |          |          |          |          |          |          |          |          |          |          | 1.000**  |
|        | F <sub>2</sub> |         |         |          |          |          |          |          |          |          |          |          |          |          | 1.000**  |

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[illegible]

**Table 6.** Phenotypic Correlation Coefficients in  $F_1$  and  $F_2$  among Different Traits

| Traits | DFE            | DM      | PH      | NPB      | NSB      | NCP      | NPC      | TPP      | SPD      | HSW      | BY       | HI       | PC       | MC       | SYP      |
|--------|----------------|---------|---------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| DFE    | F <sub>1</sub> | 1.000** | 0.643** | -0.362** | -0.277** | -0.414** | 0.142    | -0.319** | -0.246** | -0.224** | -0.217** | -0.372** | -0.237** | -0.207*  | -0.405** |
|        | F <sub>2</sub> | 1.000** | 0.658** | -0.191*  | -0.218*  | -0.401** | -0.057   | -0.143   | -0.310** | -0.074   | -0.026   | -0.442** | -0.212*  | -0.236*  | -0.322** |
| DM     | F <sub>1</sub> | 1.000** | 1.000** | -0.347** | -0.303** | -0.497** | -0.003   | -0.418** | -0.426** | -0.225** | -0.444** | -0.312** | -0.304** | -0.285** | -0.519** |
|        | F <sub>2</sub> | 1.000** | 1.000** | -0.164   | -0.217*  | -0.421** | -0.076   | -0.223*  | -0.407** | -0.217*  | -0.180   | -0.475** | -0.144   | -0.180   | -0.468** |
| PH     | F <sub>1</sub> | 1.000** | 1.000** | 1.000**  | 0.639**  | 0.214**  | -0.037   | 0.143    | 0.099    | 0.357**  | 0.480**  | 0.025    | 0.150    | 0.056    | 0.373**  |
|        | F <sub>2</sub> | 1.000** | 1.000** | 1.000**  | 0.480**  | 0.060    | -0.075   | -0.099   | -0.159   | 0.285**  | 0.307**  | 0.067    | 0.298**  | -0.084   | 0.277**  |
| NPB    | F <sub>1</sub> | 1.000** | 1.000** | 1.000**  | 1.000**  | 0.074    | -0.226** | 0.139    | 0.023    | 0.522**  | 0.575**  | 0.063    | 0.015    | -0.067   | 0.477**  |
|        | F <sub>2</sub> | 1.000** | 1.000** | 1.000**  | 1.000**  | -0.187   | -0.135   | -0.281** | -0.280** | 0.491**  | 0.513**  | 0.106    | -0.152   | -0.266** | 0.451**  |
| NSB    | F <sub>1</sub> | 1.000** | 1.000** | 1.000**  | 1.000**  | 1.000**  | -0.173*  | 0.609**  | 0.530**  | -0.151   | 0.201*   | -0.123   | 0.379**  | 0.340**  | 0.090    |
|        | F <sub>2</sub> | 1.000** | 1.000** | 1.000**  | 1.000**  | -0.139   | -0.139   | 0.451**  | 0.513**  | -0.144   | -0.170   | 0.058    | 0.243*   | 0.349**  | -0.092   |
| NCP    | F <sub>1</sub> | 1.000** | 1.000** | 1.000**  | 1.000**  | 1.000**  | 1.000**  | -0.305** | 0.150    | -0.056   | 0.235**  | -0.046   | -0.016   | -0.043   | 0.157    |
|        | F <sub>2</sub> | 1.000** | 1.000** | 1.000**  | 1.000**  | 1.000**  | 1.000**  | -0.281** | 0.109    | -0.123   | 0.141    | 0.027    | -0.001   | -0.059   | 0.124    |
| NPC    | F <sub>1</sub> | 1.000** | 1.000** | 1.000**  | 1.000**  | 1.000**  | 1.000**  | 1.000**  | 0.718**  | 0.264**  | 0.118    | 0.133    | 0.506**  | 0.594**  | 0.174*   |
|        | F <sub>2</sub> | 1.000** | 1.000** | 1.000**  | 1.000**  | 1.000**  | 1.000**  | 1.000**  | -0.281** | 0.109    | 0.264**  | 0.141    | 0.027    | -0.001   | -0.059   |
| TPP    | F <sub>1</sub> | 1.000** | 1.000** | 1.000**  | 1.000**  | 1.000**  | 1.000**  | 1.000**  | 1.000**  | 0.067    | 0.300**  | 0.137    | 0.555**  | 0.657**  | 0.316**  |
|        | F <sub>2</sub> | 1.000** | 1.000** | 1.000**  | 1.000**  | 1.000**  | 1.000**  | 1.000**  | 1.000**  | -0.129   | -0.143   | 0.295**  | 0.435**  | 0.597**  | 0.101    |
| SPD    | F <sub>1</sub> | 1.000** | 1.000** | 1.000**  | 1.000**  | 1.000**  | 1.000**  | 1.000**  | 1.000**  | 0.047    | 0.429**  | 0.178*   | -0.127   | -0.207*  | 0.427**  |

|     |                |         |         |         |         |         |         |         |
|-----|----------------|---------|---------|---------|---------|---------|---------|---------|
| HSW | F <sub>2</sub> | 1.000** | -0.005  | 0.491** | 0.220*  | -0.134  | -0.192* | 0.510** |
|     | F <sub>1</sub> |         | 1.000** | 0.284** | 0.363** | -0.016  | 0.063   | 0.423** |
| BY  | F <sub>2</sub> |         | 1.000** | 0.128   | 0.219*  | -0.191* | -0.083  | 0.252** |
|     | F <sub>1</sub> |         |         | 1.000** | 0.013   | 0.028   | -0.020  | 0.777** |
| HI  | F <sub>2</sub> |         |         | 1.000** | -0.037  | -0.169  | -0.231* | 0.719** |
|     | F <sub>1</sub> |         |         |         | 1.000** | 0.238** | 0.392** | 0.577** |
| PC  | F <sub>2</sub> |         |         |         | 1.000** | 0.234*  | 0.336** | 0.661** |
|     | F <sub>1</sub> |         |         |         |         | 1.000** | 0.718** | 0.202*  |
| MC  | F <sub>2</sub> |         |         |         |         | 1.000** | 0.528** | 0.045   |
|     | F <sub>1</sub> |         |         |         |         |         | 0.999** | 0.215** |
| SYP | F <sub>2</sub> |         |         |         |         |         | 1.000** | 0.064   |
|     | F <sub>1</sub> |         |         |         |         |         |         | 1.000** |
|     | F <sub>2</sub> |         |         |         |         |         |         | 1.000** |

Path coefficient analysis

Path coefficient analysis was performed to partition the genotypic and phenotypic correlations of component traits with seed yield into direct and indirect effects (Tables 7 and 3; Figs. 5–7). In parents, biological yield exerted the highest positive direct effect on seed yield (2.130), followed by harvest index (0.755), methionine content (0.643) and number of primary branches (0.424). Seeds per pod (−1.953), total pods (−0.752), 100-seed weight (−0.718), pods per cluster (−0.694) and secondary branches (−0.632) showed strong negative direct effects, although some of these traits exhibited positive total correlations through favourable indirect effects via biological yield and harvest index. In the F<sub>1</sub> generation, biological yield again had the highest positive direct effect (0.736), followed by harvest index (0.426) and seeds per pod (0.144). In F<sub>2</sub>, biological yield (0.711) and harvest index (0.525) continued to show the strongest positive direct effects. The residual effects were relatively low, indicating that the traits included in the

path model accounted for a substantial proportion of the variation in seed yield. These results confirm that biological yield and harvest index are the most reliable traits for direct selection to improve seed yield in lentil.

Table 7. Summary of genotypic direct effects of component traits on seed yield (Parents)

| Trait | Direct Effect | Trait | Direct Effect |
|-------|---------------|-------|---------------|
| BY    | 2.130         | SPD   | −1.953        |
| HI    | 0.755         | TPP   | −0.752        |
| MC    | 0.643         | HSW   | −0.718        |
| NPB   | 0.424         | NPC   | −0.694        |
| DM    | 0.338         | NSB   | −0.632        |
| PH    | 0.083         | NCP   | −0.544        |
| PC    | 0.013         | DFF   | −0.951        |

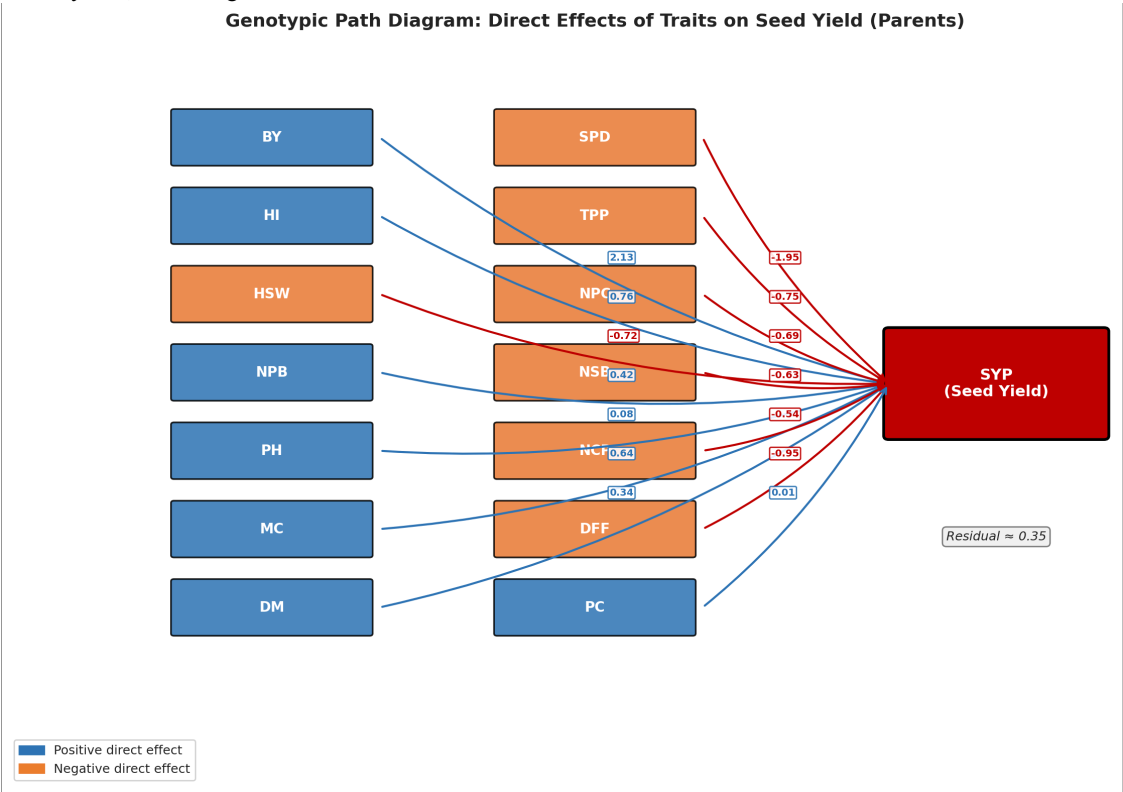


Figure 5. Genotypic path diagram showing direct effects of component traits on seed yield in parents. Blue = positive; orange = negative.

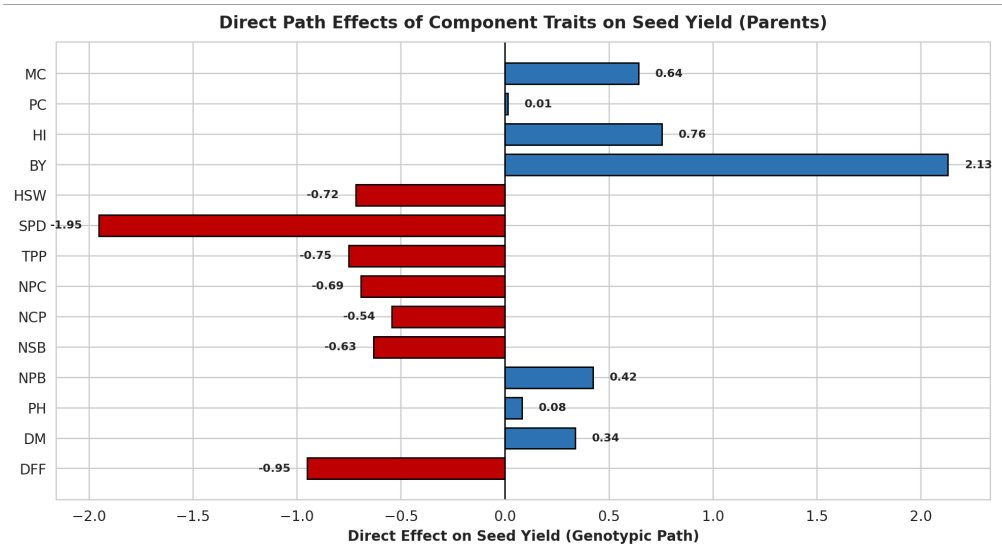


Figure 6. Magnitude and direction of genotypic direct path effects of component traits on seed yield (Parents).

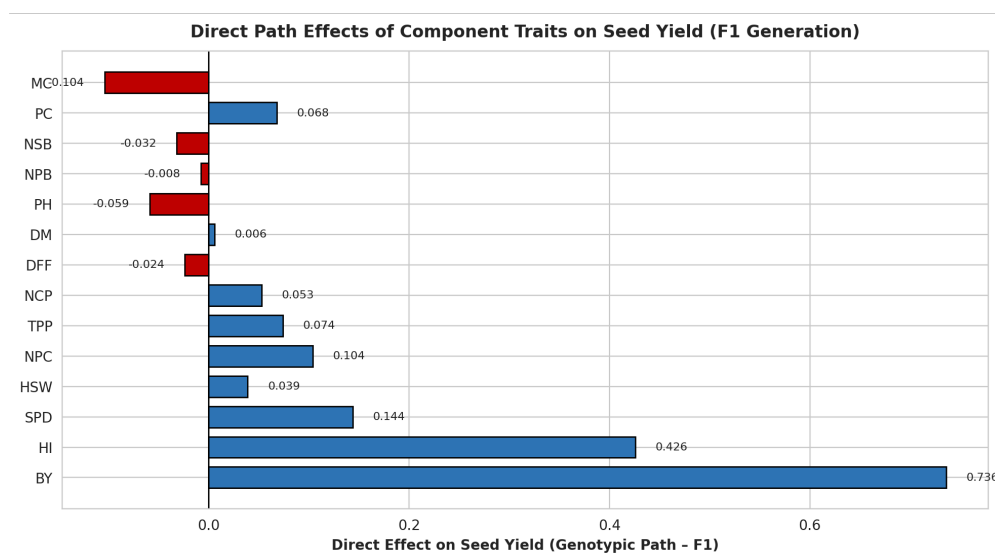


**Figure 7.** Magnitude and direction of genotypic direct path effects of component traits on seed yield ( $F_1$  generation).

The complete path coefficient matrices (genotypic and phenotypic) for parents,  $F_1$  and  $F_2$  are presented in the supplementary tables. Key indirect effects of note include the large positive indirect effect of 100-seed weight on seed yield via biological yield (1.352) and the substantial positive indirect effects of several traits through harvest index. These findings underscore the importance of considering both direct and indirect pathways when formulating selection indices.

## Conclusion

The present study revealed substantial genetic variability among the lentil parents and their  $F_1$  and  $F_2$  generations for most of the quantitative and quality traits. High heritability coupled with high genetic advance as per cent of mean for number of secondary branches, number of primary branches, number of pods per cluster, total pods per plant, biological yield, seed yield per plant and methionine content indicated predominance of additive gene action and offered good scope for improvement through direct selection. Seed yield per plant was positively and significantly correlated with biological yield, harvest index, 100-seed weight, plant height and seeds per pod, while it was negatively associated with days to flowering and maturity. Protein content showed very strong positive association with methionine content. Therefore, selection based on biological yield, harvest index, 100-seed weight, number of pods per plant and secondary branches, along with earliness, would be effective for developing high-yielding lentil genotypes with improved nutritional quality. The promising recombinants identified in  $F_2$  generation may be advanced further for isolation of superior pure lines.

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**How to cite this article:** Singh K, Yadav RK, Kumar S, Shweta, Singh L, Maurya CL, et al. Assessment of genetic variability, heritability, genetic advance and trait associations for yield improvement in lentil (*Lens culinaris* Medik.). *International Journal of Advanced Biochemistry Research*. 2026;SP-10(9):2041-2052. doi: <https://www.doi.org/10.33545/26174693.2026.v10.i9Sz.10105>

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