***Original Research Article***

**Dissecting Yield Determinants Through Genetic Parameters Analysis in Diverse Restorer Lines of Pearl Millet**

**Abstract**

*Pennisetum glaucum* (L.) R. Br. is a nutritionally rich, drought-tolerant cereal crop widely cultivated in arid and semi-arid regions, particularly in India and sub-Saharan Africa. Despite its adaptability to harsh environments, the crop’s productivity remains suboptimal due to complex genetic control of yield and its component traits. Limited characterization of genetic variability and inter-trait relationships hampers the efficiency of selection in breeding programmes. The present investigation aimed to evaluate 77 diverse restorer lines of pearl millet, acquired from ICRISAT, Hyderabad, to assess genetic variability, correlation and path coefficient analyses for yield and related traits. The field experiment was conducted during the *Kharif*, 2023 at the Experimental Farm, RVSKVV, Gwalior, employing a Randomized Complete Block Design (RCBD) with two replications. Substantial genetic variability was observed across all the ten quantitative traits. High heritability (>95%) and genetic advance were recorded for seed yield per plant, harvest index and 1000-seed weight, indicating additive gene action. Furthermore, correlation and path coefficient analysis revealed that harvest index, biological yield, and seed weight exhibited strong positive direct effects on seed yield, making them reliable indicators for selection. In contrast, numbers of productive tillers had a high indirect contribution *via* seed weight and biological yield. The findings underscore the significance of selecting genotypes with superior harvest index, seed weight and biomass to improve grain yield in pearl millet. These traits can serve as key selection criteria for genetic enhancement in future breeding programmes.

**Keywords:** Correlation, Genetic variability, Heritability, Path coefficient analysis, Pearl millet (*Pennisetum glaucum*), Yield-contributing traits.

**Introduction**

Pearl millet (*Pennisetum glaucum* (L.) R. Br.), a diploid species (2n = 2x = 14) belonging to the Poaceae family, is one of the most important staple cereal crops cultivated extensively in the arid and semi-arid regions of the world (Acharya et al., 2017; Choudhary et al., 2021a; Reddy et al., 2021 Riahi et al., 2024). It is recognized for its exceptional adaptability to a wide range of abiotic stresses, including extreme temperatures, erratic and low rainfall, prolonged drought, and nutrient-deficient soils (Yadav & Rai, 2013; Choudhary et al., 2021b; Satyavathi et al., 2021; Khandelwal et al., 2024; Ausiku et al., 2025). These characteristics have earned pearl millet the reputation of being one of the most climate-resilient millets, making it a vital crop for ensuring food and livelihood security in regions prone to climate variability and resource constraints (Serba et al., 2020; Makwana et al., 2022; Agarwal, 2024; Daduwal et al., 2024). Globally, it is a critical component of subsistence agriculture, particularly in sub-Saharan Africa and South Asia, where marginal land and minimal agricultural inputs dominate production systems (Parmar et al., 2022; Parihar et al., 2022; Kheya et al., 2023; Deevi et al., 2024). In India, the crop is primarily grown during the *kharif* (monsoon) season under rainfed conditions. Major pearl millet-growing states include Rajasthan, Maharashtra, Gujarat, Uttar Pradesh and Haryana, where it occupies a significant share of the cropped area (Yadav et al., 2015; Parihar et al., 2023; Panjala et al., 2023). The crop not only contributes to household food security but also provides essential nutrition, as its grains are rich in energy, high-quality proteins, and important micronutrients such as iron and zinc (Hassan et al., 2021; Patel et al., 2023a; Rajpoot et al., 2023a; Meena et al., 2024). These nutritional attributes make pearl millet an excellent option for addressing hidden hunger and micronutrient malnutrition in vulnerable populations (Patel et al., 2023b; Rajpoot et al., 2023b; Vidhya et al., 2023; Aavula et al., 2024). In addition to its nutritional value, pearl millet has considerable economic importance (Verma et al., 2021). It is used as a multipurpose crop, providing grain for human consumption, stover for animal fodder, and biomass for industrial applications (Jukanti et al., 2016; Patel et al., 2024a; Rajpoot et al., 2024; Riahi et al., 2024). Its hardy nature, short duration, and low input requirements make it ideally suited for sustainable agriculture in dryland farming systems (Patel et al., 2024b). Consequently, it plays a pivotal role in enhancing the resilience of smallholder farming communities, especially in agro-ecological zones threatened by climate change and declining soil fertility (Makwana et al., 2023; Akinseye et al., 2024; Mehta et al., 2024; Joshi, 2025).

Despite its agronomic potential and stress tolerance, the average grain yield of pearl millet remains suboptimal, largely due to an array of biotic and abiotic stress factors, poor input management, and limited adoption of improved cultivars (Kumar & Kumar 2021; Okumu et al., 2023; Harish et al., 2024). Moreover, the complex polygenic inheritance of yield and its component traits poses a major challenge to breeders aiming to develop high-yielding varieties (Michel et al., 2019; Raina & Khan 2023). Therefore, a comprehensive understanding of genetic variability, trait associations, and their direct and indirect contributions to grain yield is essential for devising efficient breeding strategies (Jain et al., 2024a; Jain et al., 2024b; Mishra et al., 2024a; Mishra et al., 2025a; Mishra et al., 2025b; Jharia et al., 2025; Rao et al., 2024; Mitiku et al., 2025).

An advanced statistical tool for instance correlation (Miller et al., 1958) and path coefficient analysis (Wright, 1921) are instrumental in dissecting the interrelationships among yield-related traits and identifying those with the most significant impact on seed yield (Sharma et al., 2023; Yadav et al., 2023; Paliwal et al., 2024; Puri et al., 2024; Rajput et al., 2024; Gautam et al., 2025). These methods enable the formulation of selection indices and aid in the identification of elite genotypes with desirable trait combinations (Shrivastav et al., 2023; Mishra et al., 2024b). In this context, the present study aims to evaluate a diverse set of pearl millet restorer lines for different yield-contributing traits, with the objective of identifying superior line (s) and trait-based selection criteria for improving productivity.

**2. Material & Methods**

**2.1 Experimental Site**

The field experiment was conducted during the *Kharif*, 2023 at the Experimental Farm, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya, Gwalior, Madhya Pradesh, India. The geographical region experiences a hot and dry climate, with June being the hottest month. The temperature in the region fluctuates between a minimum of 4°C during the winter to a maximum of approximately 48°C in the peak summer. The annual rainfall ranges from 750 mm to 800 mm, with the majority received between the end of June and the end of September. During the crop growing period (July to October 2023), a total rainfall of 907.7 mm was recorded; however, the rainfall was short and unequally distributed. The average maximum and minimum temperatures during the crop growth period were 35.2°C and 24.5°C, correspondingly. According to the meteorological data recorded during the crop season, during the growing period, the weather conditions remained largely within normal ranges, however, variations in temperature, humidity, rainfall and evaporation were observed on a weekly basis. Additionally, the site is characterized by alluvial soil with moderate fertility and good drainage, suitable for pearl millet cultivation. The soil pH arrayed between 6.8 and 7.5.

**2.2 Experimental Details**

The experimental material comprised 77 restorer lines of *Pennisetum glaucum*, obtained from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, Telangana, India (Table 1). The experiment was laid out in a Randomized Complete Block Design (RCBD) with two replications to minimize experimental error and enhance the precision of results. Each genotype was sown in a single row plot, with a row length of 4.0 meters. Inter-row and intra-row spacing were maintained at 50 cm and 10 cm, respectively, to ensure optimal plant density and facilitate intercultural operations. Standard agronomic practices recommended for pearl millet were followed uniformly across all plots. Land preparation included ploughing, harrowing, and levelling to acquire a fine tilth. Fertilizers were applied as per local recommendations, and timely irrigations were provided as and whenever required. Weed control was carried out manually at regular intervals, and plant protection measures were implemented to safeguard the crop from major pests and diseases. Observations were recorded on ten yield-related traits on five arbitrarily chosen plants from each plot. Data were collected at proper growth stages following standard descriptors, and the average values were utilized for statistical computation.

**Table 1 List of pearl millet restorer lines employed in the present investigation**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **S. No.** | **Restorer line** | **S. No.** | **Restorer line** | **S. No.** | **Restorer line** | **S. No.** | **Restorer line** | **S. No.** | **Restorer line** | **S. No.** | **Restorer line** |
| 1 | R-20002 | 14 | R-20206 | 27 | R-20846 | 40 | R-24657 | 53 | R-25511 | 66 | R-21283 |
| 2 | R-20012 | 15 | R-20208 | 28 | R-20871 | 41 | R-24658 | 54 | R-25850 | 67 | R-21355 |
| 3 | R-20057 | 16 | R-20212 | 29 | R-23906 | 42 | R-24659 | 55 | R-25865 | 68 | R-21370 |
| 4 | R-20079 | 17 | R-20218 | 30 | R-23956 | 43 | R-24661 | 56 | R-25910 | 69 | R-21930 |
| 5 | R-20090 | 18 | R-20443 | 31 | R-23565 | 44 | R-24662 | 57 | R-26462 | 70 | R-21970 |
| 6 | R-20103 | 19 | R-20444 | 32 | R-24610 | 45 | R-24663 | 58 | R-26482 | 71 | R-22013 |
| 7 | R-20105 | 20 | R-20671 | 33 | R-24650 | 46 | R-24664 | 59 | R-26492 | 72 | R-22713 |
| 8 | R-20108 | 21 | R-20706 | 34 | R-24651 | 47 | R-24665 | 60 | R-26607 | 73 | R-22768 |
| 9 | R-20111 | 22 | R-20710 | 35 | R-24652 | 48 | R-24666 | 61 | R-27738 | 74 | R-22908 |
| 10 | R-20113 | 23 | R-20810 | 36 | R-24653 | 49 | R-24667 | 62 | R-20876 | 75 | R-22918 |
| 11 | R-20115 | 24 | R-20822 | 37 | R-24654 | 50 | R-25046 | 63 | R-21111 | 76 | R-22968 |
| 12 | R-20204 | 25 | R-20823 | 38 | R-24655 | 51 | R-25056 | 64 | R-21121 | 77 | R-23774 |
| 13 | R-20205 | 26 | R-20826 | 39 | R-24656 | 52 | R-25086 | 65 | R-21136 |  |  |

**2.3 Statistical analysis**

The recorded data were analysed using OPSTAT for ANOVA to assess the significance of genotypic differences under RCBD. Genetic parameters such as GCV, PCV, heritability and genetic advance were also estimated. AgriAnalyzer software was used to compute genotypic and phenotypic correlations and perform path coefficient analysis to identify traits influencing yield.

**3. Results & Discussion**

**3.1 Coefficient of Variation, Heritability and Genetic Advance**

The analysis of genetic parameters among the 77restorer lines of pearl millet revealed substantial variability for all the recorded traits (Table 2). The range, mean values, coefficients of variation, heritability estimates and genetic advance collectively indicated the presence of significant genetic diversity in the experimental material. The magnitude of both genotypic and phenotypic coefficients of variation (GCV and PCV) was investigated moderate to high for most of the traits, suggesting the influence of genetic factors in the expression of these characters (Kumar et al., 2024; Angel et al., 2024). High heritability estimates, coupled with higher genetic advance as a percentage of the mean, were recorded for traits such as seed yield per plant (100%), harvest index (100%), biological weight (100%), 1000-seed weight (100%), panicle length (100%), plant height (100%), and panicle diameter (98.4%). This designates that these traits are primarily governed by additive gene action and may be effectually improved through selection as earlier described by Pallavi et al. (2020) and Kalagare et al. (2021). Seed yield per plant exhibited the highest genetic advance as percent of mean (80.21%) tracked by harvest index (76.12%) and numbers of productive tillers (70.74%), highlighting their potential as selection criteria for yield enhancement. Traits such as days to 50% flowering (95.6%) and days to maturity (98.4%) displayed high heritability with moderate genetic advance, indicating a moderate scope for improvement through selection. Remarkably, high values of GCV and PCV were experimented for seed weight (56.54%), seed yield per plant (38.93%), harvest index (36.95%), and numbers of productive tillers (36.57%), confirming the presence of considerable variability and potential for genetic gain. The close correspondence between GCV and PCV for most oof the traits suggest minimal environmental influence, thereby reinforcing the reliability of these characters for selection in breeding programmes as previously demonstrated by Govindaraj et al. (2011), Singh et al. (2018), Basavraj et al. (2017), Kumar et al. (2020), Saikumar et al. (2020), Angel et al. (2024) and Reddy et al. (2024). Overall, the findings underline the significance of traits such as seed yield, harvest index, and numbers of productive tillers as key contributors for yield enhancement and their suitability for further genetic improvement in pearl millet.

**Table 2 Estimation of range, mean and different genetic parameters for different characters of 77 restorer lines of pearl millet**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **S.No.** | **Traits** | **Range** | | | **Coefficient of variation** | | **h2 (bs)**  **%** | **Genetic advance** | **Genetic advance as % of mean** |
| **Min.** | **Max** | **Grand Mean** | **GCV**  **%** | **PCV**  **%** |
| **1** | **DTF** | 39.33 | 48.66 | 42.9091 | 3.9507 | 4.0398 | 95.6 | 3.415 | 7.959 |
| **2** | **DTM** | 82.33 | 95.66 | 86.8571 | 2.563 | 2.583 | 98.4 | 4.549 | 5.237 |
| **3** | **PH** | 90.33 | 214.66 | 170.1429 | 12.129 | 12.131 | 100 | 42.504 | 24.981 |
| **4** | **NPTC** | 1.00 | 5.33 | 2.5455 | 36.566 | 38.934 | 88.2 | 1.801 | 70.742 |
| **5** | **PL** | 14.43 | 29.50 | 22.4667 | 16.305 | 16.306 | 100 | 7.546 | 33.586 |
| **6** | **PD** | 1.33 | 3.06 | 2.0580 | 16.182 | 16.315 | 98.4 | 0.680 | 33.065 |
| **7** | **SW** | 1.04 | 16.16 | 7.0204 | 56.543 | 56.543 | 100 | 8.177 | 16.478 |
| **8** | **BW** | 96.76 | 342.94 | 174.4646 | 26.979 | 26.979 | 100 | 96.961 | 55.576 |
| **9** | **HI** | 9.11 | 47.53 | 24.8368 | 36.952 | 36.952 | 100 | 18.906 | 76.121 |
| **10** | **SYPP** | 15.12 | 73.81 | 42.3559 | 38.934 | 38.934 | 100 | 33.972 | 80.205 |

**Abbreviations:** **DTF:** Days to 50% flowering; **DTM:** Days to maturity; **PH:** Plant height; **NPTC:** Numbers of productive tillers; **PL:** Panicle length; **PD:** Panicle diameter; **SW:** 1000-seed weight; **BW:** Biological weight; **HI:** Harvest index; **SYPP:** Seed yield per plant.

**3.2 Correlation Coefficient**

The genotypic and phenotypic correlation coefficients among the different quantitative traits of 77 pearl millet restorer lines revealed several significant associations, providing insights into the interrelationships between traits and their contribution to yield and presented in Table 3 Table 4 and Fig. 1).

At the genotypic level, seed yield per plant (SYPP) exhibited a highly significant positive correlation with harvest index (HI; *r* = 0.7346), numbers of productive tillers (NPTC; *r* = 0.6693), and 1000-seed weight (SW; *r* = 0.5548), indicating these traits are important contributors to yield enhancement and may be prioritized in selection. Kumar et al. (2016), Patil et al. (2021) also found similar results. A moderate positive correlation was also recorded with plant height (PH; *r* = 0.1581) and biological yield (BY; *r* = 0.4587). Remarkably, NPTC showed a strong and highly significant correlation with SW (*r* = 0.9761) and BY (*r* = 0.7262), signifying their close genetic association and combined influence on productivity enhancement. Kumari et al., (2013) and Ezeaku et al. (2015) also addressed similar results.

At the phenotypic level, comparable trends were also observed, although the magnitude of the correlations was generally lower than the genotypic values, indicating environmental influence. SYPP displayed significant positive correlations with HI (*r* = 0.7346), NPTC (*r* = 0.6286), SW (*r* = 0.5548) and BY (*r* = 0.4587), reaffirming their direct role in yield determination. The strong genotypic correlation between SW and NPTC was also reflected at the phenotypic level (*r* = 0.9167), indicating a robust association that can be exploited in selection strategies as advocated by Rakesh et al. (2015), Dehinwal et al. (2017) and Mishra et al. (2024).

Negative correlations were observed between days to 50% flowering (DTF) and main yield attributing traits such as SYPP, SW, NPTC and PL, signifying that early flowering genotypes tend to have higher yield potential. This implies that early flowering could be beneficial in short-duration environments or under terminal stress conditions as investigated by Srivastava et al. (2022) and Ausiku et al. (2025). The stronger genotypic correlations compared to their phenotypic counterparts indicated that most of these associations are genetically controlled and less influenced by the environment as suggested by Dadarwal et al. (2020) and Patil et al. (2021). These findings underscore the importance of traits like NPTC, SW, HI and BY as effective selection criteria in pearl millet breeding programmes aimed to enhance seed yield. Similar studies have also been reported by Patil et al. (2022), Narasimhulu et al. (2021), Kaushik & Vart (2022) and Rajpoot et al. (2023a).

**Table 3 Genotypic correlation coefficient for different quantitative traits among 77 pearl millet restorer lines**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **DTF** | **DTM** | **PH** | **NPTC** | **PL** | **PD** | **SW** | **BY** | **HI** | **SYPP** |
| **DTF** | **1.0000** | 0.0906 | -0.2001 | -0.3439 | -0.1708 | -0.2391 | -0.4136 | -0.2206 | 0.0614 | -0.1328 |
| **DTM** |  | **1.0000** | -0.0273 | 0.1849 | -0.0117 | 0.0092 | 0.1179 | 0.1009 | -0.0911 | 0.0155 |
| **PH** |  |  | **1.0000** | 0.3448 | 0.2831 | 0.3725 | 0.3523 | 0.0764 | 0.1360 | 0.1581 |
| **NPTC** |  |  |  | **1.0000** | 0.1485 | 0.2365 | 0.9761\*\* | 0.7262\*\* | 0.1826 | 0.6693\*\* |
| **PL** |  |  |  |  | **1.0000** | 0.4422 | 0.1079 | -0.0954 | 0.2153 | 0.1165 |
| **PD** |  |  |  |  |  | **1.0000** | 0.2397 | -0.0485 | 0.1421 | 0.0888 |
| **SW** |  |  |  |  |  |  | **1.0000** | 0.6194\* | 0.1310 | 0.5548\* |
| **BY** |  |  |  |  |  |  |  | **1.0000** | -0.2287 | 0.4587 |
| **HI** |  |  |  |  |  |  |  |  | **1.0000** | 0.7346\*\* |
| **SYPP** |  |  |  |  |  |  |  |  |  | **1.0000** |

Significance levels: 0.10 .05 .02 .01

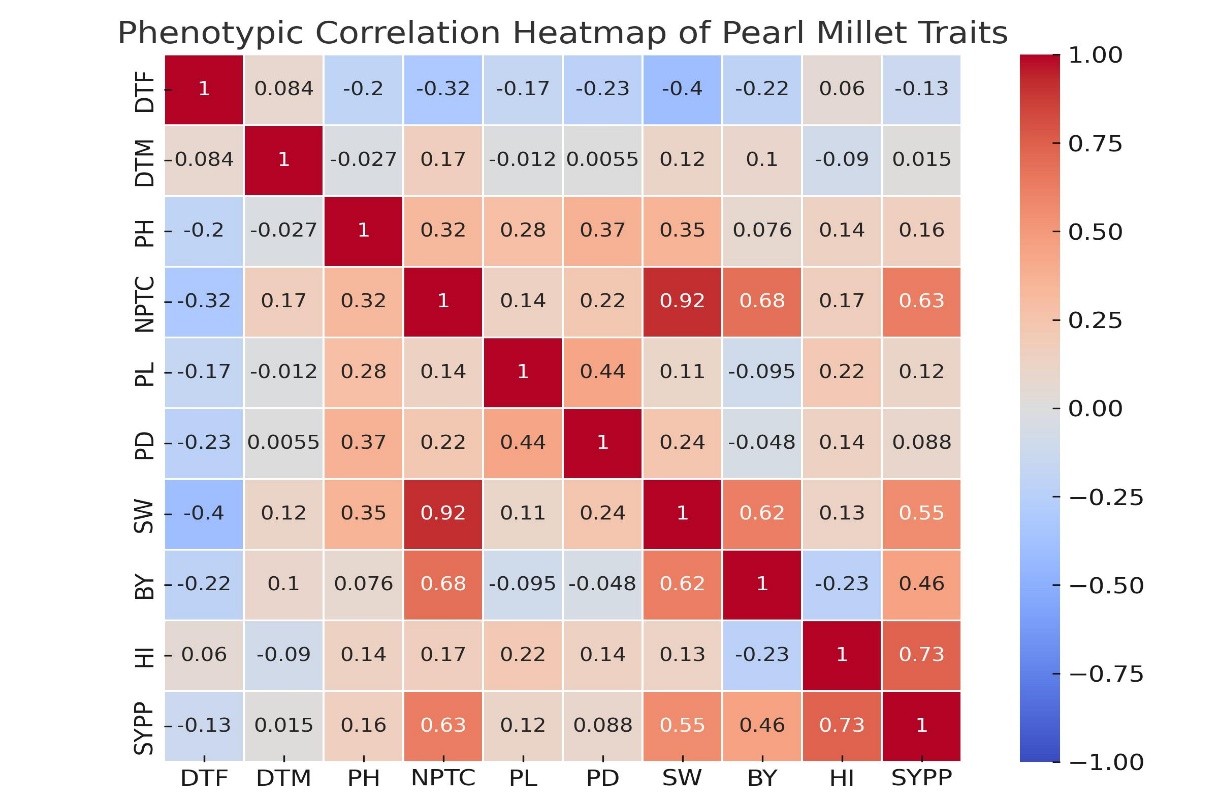
If correlation r => 0.549, 0.632, 0.716, 0.765

**Table 4 Phenotypic correlation coefficient of different quantitative traits among 77 pearl millet restorer lines**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **DTF** | **DTM** | **PH** | **NPTC** | **PL** | **PD** | **SW** | **BY** | **HI** | **SYPP** |
| **DTF** | **1.0000** | 0.0838 | -0.1964 | -0.3171 | -0.1669 | -0.2295 | -0.4045 | -0.2158 | 0.0601 | -0.1299 |
| **DTM** |  | **1.0000** | -0.0267 | 0.1716 | -0.0116 | 0.0055 | 0.1169 | 0.1001 | -0.0904 | 0.0154 |
| **PH** |  |  | **1.0000** | 0.3241 | 0.2830 | 0.3692 | 0.3522 | 0.0764 | 0.1359 | 0.1580 |
| **NPTC** |  |  |  | **1.0000** | 0.1394 | 0.2222 | 0.9167\*\*\*\* | 0.6821\* | 0.1715 | 0.6286\* |
| **PL** |  |  |  |  | **1.0000** | 0.4386 | 0.1079 | -0.0954 | 0.2153 | 0.1165 |
| **PD** |  |  |  |  |  | **1.0000** | 0.2378 | -0.0481 | 0.1409 | 0.0880 |
| **SW** |  |  |  |  |  |  | **1.0000** | 0.6194\* | 0.1310 | 0.5548\* |
| **BY** |  |  |  |  |  |  |  | **1.0000** | -0.2287 | 0.4587 |
| **HI** |  |  |  |  |  |  |  |  | **1.0000** | 0.7346\*\*\* |
| **SYPP** |  |  |  |  |  |  |  |  |  | **1.0000** |

Significance levels: 0.10, .05 .02, .01

If correlation r => 0.549, 0.632, 0.716, 0.765



**Fig. 1: Phenotypic correlation heatmap for yield and its attributing traits of pearl millet**

**3.3 Path Coefficient Analysis**

Path coefficient analysis was carried out at both genotypic and phenotypic levels to assess the direct and indirect effects of yield-contributing traits on seed yield per plant (SYPP) in pearl millet (Tables 5; Table 6; Fig. 2; Fig. 3). This method aids in identifying main traits that may be targeted directly in selection to improve yield.

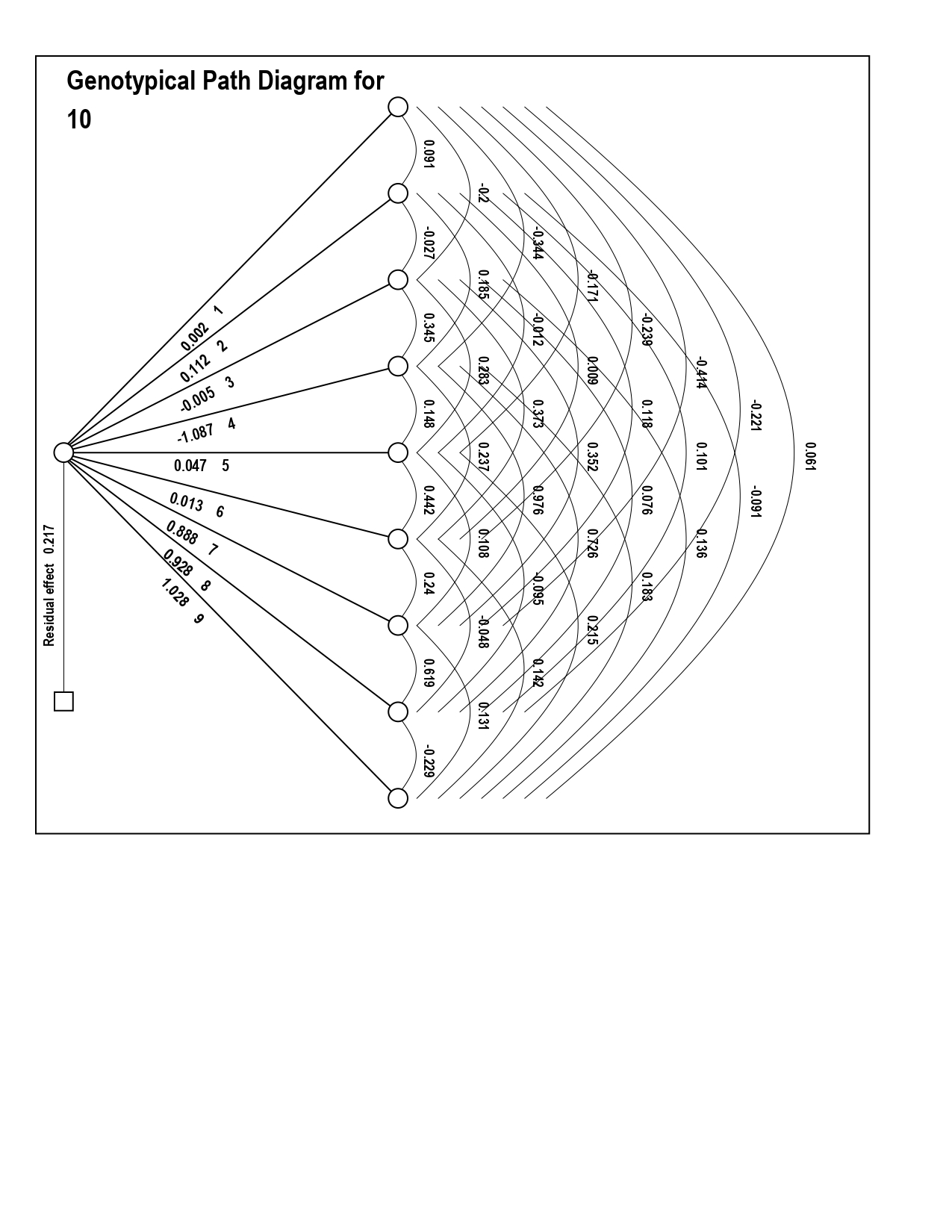
At the genotypic level, harvest index (HI) exerted the highest positive direct effect on SYPP (1.0280), tracked by biological yield (BY; 0.9281) and 1000-seed weight (SW; 0.8877). These traits also demonstrated strong positive genotypic correlations with seed yield, indicating their true association and importance in determining grain yield. Nehra et al. (2017) and Dadarwal et al. (2020) also addressed similar results. In contrast, numbers of productive tillers (NPTC) exhibited the highest negative direct effect (-1.0872), despite showing a strong positive genotypic correlation (r = 0.6693) with SYPP, signifying that its contribution is largely indirect and may be confounded by its association with other characters such as SW and BY. Talawar et al. (2017) and Kumar et al. (2020) also found similar results. Remarkably, DTF and PH exhibited negligible direct effects on yield, implying limited direct contribution. Indirect effects through SW and BY were substantial for most of the traits. For instance, the strong positive indirect effect of NPTC on SYPP through SW (0.8664) and BY (0.6740) indicates the compensatory nature of these traits. The residual effect (0.2169) was found to be low, signifying that the majority of variation in SYPP was explained by the traits included in the path analysis (Dhakar et al., 2014; Rani et al., 2019; Kaushik & Vart, 2022).

At the phenotypic level, similar trends were also observed. HI (0.8777), BY (0.6063), and SW (0.0173) had distinguished positive direct effects on SYPP. These traits also displayed strong and significant positive phenotypic correlations with yield, further validating their importance in yield improvement, as suggested by Latha et al. (2019) and Jain et al. (2023). In contrast, panicle length (PL) and plant height (PH) had negative direct effects, though their overall influence on yield was less prominent owing to lower correlation values. The indirect effects observed phenotypically were consistent with genotypic trends. For example, NPTC, despite having a moderate direct effect (0.0437), contributed positively to SYPP through indirect paths *via* SW (0.0401) and BY (0.0298). The phenotypic residual effect was also investigated low (0.2029), confirming that the traits studied sufficiently accounted for the variation in seed yield. Similar findings have also been reported by Kamble et al. (2022), Kumar et al. (2022), Rachana et al. (2023) and Jain et al. (2023). Overall, both genotypic and phenotypic path analysis highlighted that harvest index, biological yield and 1000-seed weight are the most influential traits for improving seed yield per plant in pearl millet. These findings suggested that direct selection for these traits could be highly effective in yield enhancement programmes, as earlier suggested by Sumathi et al. (2016), Rajpoot et al. (2023a) and Angel et al. (2024).

**Table 5 Genotypic path coefficients for yield and its attributing traits of 77 pearl millet restorer lines**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **DTF** | **DTM** | **PH** | **NPTC** | **PL** | **PD** | **SW** | **BY** | **HI** |
| **DTF** | **0.0020** | 0.0002 | -0.0004 | -0.0007 | -0.0003 | -0.0005 | -0.0008 | -0.0004 | 0.0001 |
| **DTM** | 0.0102 | **0.1121** | -0.0031 | 0.0207 | -0.0013 | 0.0010 | 0.0132 | 0.0113 | -0.0102 |
| **PH** | 0.0010 | 0.0001 | **-0.0049** | -0.0017 | -0.0014 | -0.0018 | -0.0017 | -0.0004 | -0.0007 |
| **NPTC** | 0.3739 | -0.2011 | -0.3749 | **-1.0872** | -0.1614 | -0.2571 | -1.0612 | -0.7896 | -0.1986 |
| **PL** | -0.0080 | -0.0005 | 0.0132 | 0.0069 | **0.0467** | 0.0207 | 0.0050 | -0.0045 | 0.0101 |
| **PD** | -0.0030 | 0.0001 | 0.0047 | 0.0030 | 0.0056 | **0.0127** | 0.0030 | -0.0006 | 0.0018 |
| **SW** | -0.3671 | 0.1046 | 0.3127 | 0.8664 | 0.0958 | 0.2128 | **0.8877** | 0.5498 | 0.1163 |
| **BY** | -0.2048 | 0.0936 | 0.0709 | 0.6740 | -0.0886 | -0.0450 | 0.5748 | **0.9281** | -0.2122 |
| **HI** | 0.0631 | -0.0936 | 0.1398 | 0.1877 | 0.2214 | 0.1460 | 0.1347 | -0.2351 | **1.0280** |
| **SYPP** | -0.1328 | 0.0155 | 0.1581 | 0.6693 | 0.1165 | 0.0888 | 0.5548 | 0.4587 | 0.7346 |

Residual Effect = 0.2169

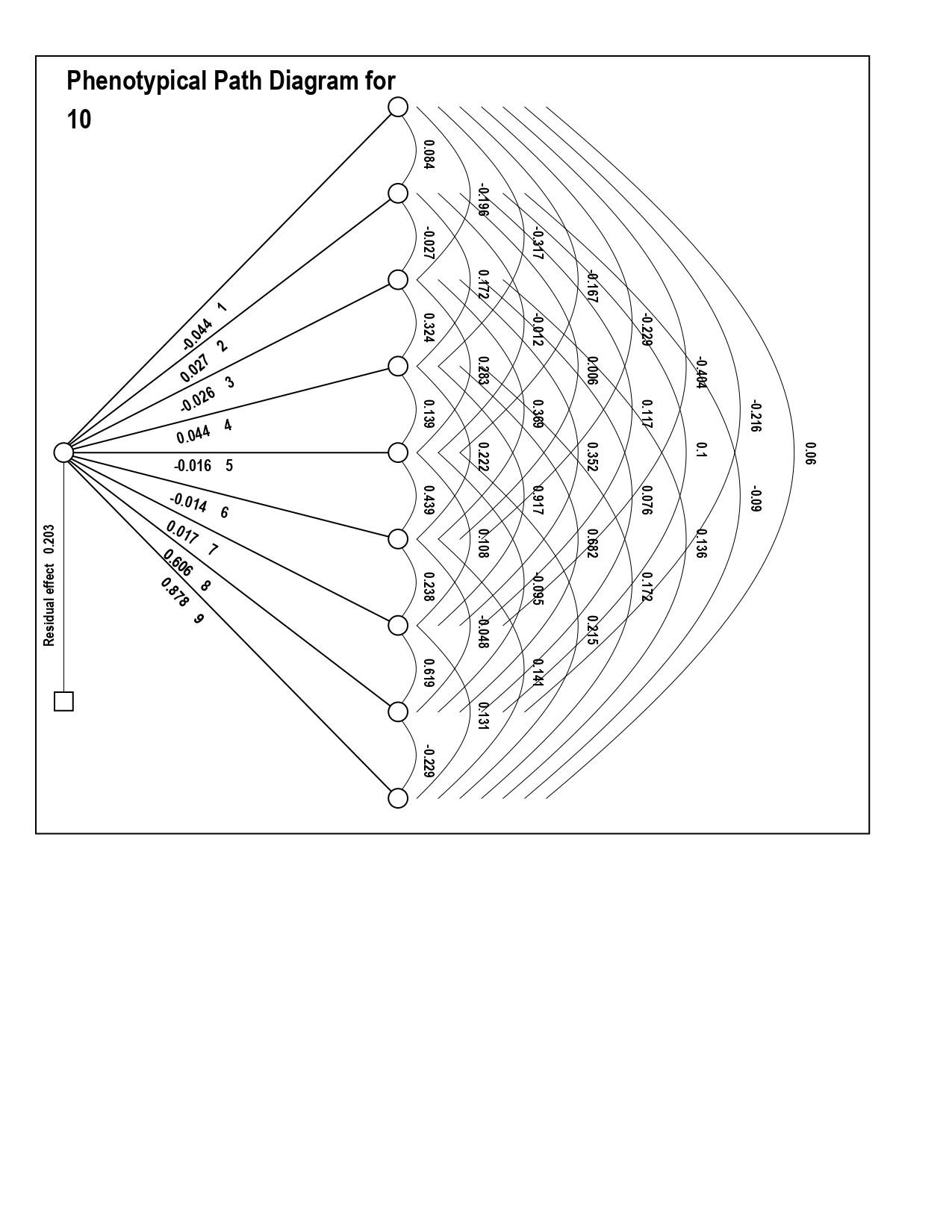
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**Fig. 2: Genotypic path diagram for yield and its attributing traits**

**Table 6 Phenotypic path coefficients for yield and its attributing traits of 77 pearl millet restorer lines**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **DTF** | **DTM** | **PH** | **NPTC** | **PL** | **PD** | **SW** | **BY** | **HI** |
| **DTF** | **-0.0442** | -0.0037 | 0.0087 | 0.0140 | 0.0074 | 0.0102 | 0.0179 | 0.0095 | -0.0027 |
| **DTM** | 0.0023 | **0.0274** | -0.0007 | 0.0047 | -0.0003 | 0.0002 | 0.0032 | 0.0027 | -0.0025 |
| **PH** | 0.0051 | 0.0007 | **-0.0261** | -0.0085 | -0.0074 | -0.0096 | -0.0092 | -0.0020 | -0.0035 |
| **NPTC** | -0.0139 | 0..0075 | 0.0142 | **0.0437** | 0.0061 | 0.0097 | 0.0401 | 0.0298 | 0.0075 |
| **PL** | 0.0027 | 0.0002 | -0.0046 | -0.0023 | **-0.0162** | -0.0071 | -0.0017 | 0.0015 | -0.0035 |
| **PD** | 0.0032 | -0.0001 | -0.0051 | -0.0031 | -0.0061 | **-0.0139** | -0.0033 | 0.0007 | -0.0020 |
| **SW** | -0.0070 | 0.0020 | 0.0061 | 0.0158 | 0.0019 | 0.0041 | **0.0173** | 0.0107 | 0.0023 |
| **BY** | -0.1308 | 0.0607 | 0.0463 | 0.4136 | -0.0579 | -0.0291 | 0.3756 | **0.6063** | -0.1387 |
| **HI** | 0.0527 | -0.0793 | 0.1193 | 0.1505 | 0.1890 | 0.1237 | 0.1150 | -0.2007 | **0.8777** |
| **SYPP** | -0.1299 | 0.0154 | 0.1580 | 0.6286 | 0.1165 | 0.0880 | 0.5548 | 0.4587 | 0.7346 |

Residual Effect = 0.2029

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**Fig. 3 Phenotypic path diagram for yield and its attributing traits**

**Conclusion**

The present investigation revealed presence of significant genetic variability among the 77 pearl millet restorer lines, providing ample scope for improvement of yield *via* enhancing its component traits through selection. High heritability estimates coupled with substantial genetic advance for key traits such as seed yield per plant, harvest index, 1000-seed weight, biological yield, and numbers of productive tillers indicate the predominance of additive gene action, thus making them highly amenable to selection. Correlation analysis identified strong positive associations of seed yield with harvest index, seed weight, biological yield, and numbers of productive tillers, reinforcing their critical role in yield determination. Path coefficient analysis further validated the direct and indirect effects of these traits on seed yield. Harvest index, biological yield, and 1000-seed weight emerged as the most influential traits exerting strong direct effects, while traits like numbers of productive tillers contributed indirectly *via* their interaction with seed weight and biomass. The low residual effects in path analysis signified that the studied traits sufficiently explain the variation in grain yield. Overall, the integration of genetic parameters, correlation, and path analysis provides a comprehensive framework for selecting superior genotypes. The identified traits *viz*., harvest index, biological yield, and seed weight can be prioritized in pearl millet breeding programmes aimed to enhance yield under rainfed and stress-prone environments. These findings offer valuable insights for genetic enhancement and development of high-yielding, climate-resilient pearl millet cultivars.

**Disclaimer (Artificial Intelligence)**

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

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