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Assessment of genetic variability, character association and path analysis for morphological, yield and yield attributing traits in advance Wheat (*Triticum aestivum* L) breeding lines

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Abstract

A study was conducted to assess genetic variability, correlation, and path coefficient analysis for morphological, yield, and yield-related traits in 50 wheat genotypes. The experiment was laid out in a randomized block design with two replications at the Wheat and Maize Research Unit, Parbhani (Maharashtra) during the *Rabi* season of 2023-24. The analysis of variance revealed significant differences among the genotypes for all traits, confirming the presence of considerable genetic variability in the material studied. High genotypic coefficients of variation were recorded for number of grains per spike, number of productive tillers per plant, grain yield per plant, and 1000-grain weight. Traits such as number of productive tillers per plant, number of grains per spike, and grain yield per plant exhibited high heritability along with high genetic advance as a percentage of the mean, indicating that these traits are mainly governed by additive gene action. Correlation analysis showed that grain yield per plant had a highly significant and positive association with harvest index, number of productive tillers per plant, number of grains per spike, spike length, 1000-grain weight, and biological yield per plant at both genotypic and phenotypic levels. Path coefficient analysis further indicated that number of grains per spike, number of productive tillers per plant, biological yield per plant, and harvest index exerted positive direct effects on grain yield per plant. Biological yield, followed by harvest index and 1000-grain weight, contributed the most directly to grain yield, identifying them as key determinants for yield improvement.

Overall, these results provide useful guidance for developing wheat breeding strategies focused on enhancing grain yield potential.

Keywords: Genetic variability, heritability, genetic advance, correlation, direct effect, indirect effect, grain yield

Introduction

Wheat (*Triticum aestivum* L. em. Thell; 2n=42) is a major cereal crop belonging to the family Gramineae (Poaceae) and the genus Triticum. Bread wheat is an allohexaploid species with a chromosome number of 2n=42 and carries the AABBDD genome constitution (Sleper and Poehlman, 2006) [26]. It is a self-pollinated crop adapted to cool-season conditions and grows best in areas receiving 750-1600 mm of annual rainfall. Self-pollination in wheat is largely due to its chasmogamous flowers, where anthers release pollen before the florets open. Optimal growth conditions include cool, moist weather during vegetative development and warm, dry conditions during grain filling and maturity. Conversely, hot and humid climates are generally unfavorable for wheat production, as they hinder crop establishment and increase susceptibility to diseases.

Wheat exhibits remarkable adaptability, thriving across a wide range of soil types and agro-climatic conditions. Wheat recognized as the "king of cereals" serves as a staple food for a significant portion of the global population and plays a crucial role in meeting their nutritional demands. Its wide adaptability and resilience make it a key focus in genetic improvement and plant breeding programs aimed at enhancing food security.

Wheat is one of the most important food crops in the world and plays a big role in global trade. It comes second only to rice as the most produced food grain worldwide.

Farmers grow wheat on about 224 million hectares of land globally, harvesting around 793 million tonnes every year. In India, wheat is a key crop too. It's grown on roughly 31.8 million hectares and gives about 113 million tonnes of grain. On average, each hectare produces around 3.5 tonnes (or 35 quintals).

The main wheat-growing states in India are Punjab, Haryana, Uttar Pradesh, Bihar, Gujarat, Rajasthan, and Madhya Pradesh. Among them, Uttar Pradesh has the largest area under wheat and the highest total production, while Punjab gets the best yield per hectare (Anonymous, 2023) [3].

Genetic variability refers to the extent to which individual genotypes within a population differ from one another. It influences how much a trait can change in response to genetic and environmental factors. A population must possess genetic variability to adjust to shifting conditions, with diverse varieties being more adaptable, whereas purelines have limited flexibility. In agriculture, genetic diversity is essential for crop improvement, as the success of breeding programs depends on the availability of genetic variability within a population. Enhancing wheat genotypes to develop superior varieties is one strategy to boost wheat production and productivity. Correlation analysis combined with path coefficient analysis offers a more comprehensive understanding of the relationships between different traits and grain yield. While correlation helps in determining the strength and direction of the association between yield and its contributing characters, path analysis further partitions these correlations into direct and indirect effects. The path coefficient quantifies the direct influence of an independent variable on the dependent variable, while also accounting for the indirect effects mediated through other traits (Dewey & Lu, 1959) [10]. Therefore, keeping the above facts in view, the present investigation has been carried out at Wheat and Maize Research Unit, VNMKV, Parbhani.

Materials and Methods

Experimental Site and Experimental Design

The experiment was conducted at the Wheat and Maize Research Unit, Parbhani, during the *Rabi* season of 2023-24 under normal irrigated conditions. The study material comprised fifty bread wheat genotypes obtained from the Wheat and Maize Research Unit, Parbhani.

The genotypes were evaluated in a randomized block design with two replications. Each plot measured 4.0 m × 0.20 m, with a row-to-row spacing of 20 cm and plant-to-plant spacing of 10 cm. All recommended agronomic practices were followed to raise a healthy crop.

Characters Studied

Data were recorded on ten morphological traits from five randomly selected plants of each genotype. The traits studied were: Days to 50% heading, days to maturity, plant height (cm), number of effective tillers per plant, spike length (cm), number of grains per spike, 1000-grain weight (g), grain yield per plant (g), biological yield per plant (g), and harvest index (%).

Observations for days to 50% heading and days to maturity were taken on a whole-plot basis only once, while the remaining characters were recorded from the five selected plants.

Statistical Analysis

The mean values of all traits were analyzed statistically. Analysis of variance (ANOVA) was carried out following the randomized block design procedure described by Panse and Sukhatme (1985) [21]. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated using the method proposed by Burton and Devane (1953) [7]. Heritability (broad sense) and expected genetic advance as a percentage of the mean were estimated according to Johnson *et al.* (1955) [15]. Genotypic, phenotypic, and environmental correlations were computed from the respective variance and covariance components as suggested by Searle (1961) [24].

Path coefficient analysis was performed following the method originally developed by Wright (1921) [29] and later elaborated by Dewey and Lu (1959) [10]. Grain yield per plant was treated as the dependent (resultant) variable, while the other nine traits were considered independent (causal) variables that affect grain yield both directly and indirectly through one another.

Result and Discussion

Genetic Variability

An analysis of variance for ten characteristics was conducted, and the sums of mean squares are summarized in (Table 1). In this study, significant genotypic differences were identified for all ten traits. The presence of variability suggests that there is considerable opportunity to select superior genotypes that can either be used directly as a new variety or as parent sources in upcoming breeding programs. This study indicated that the variability observed in these fifty genotypes is due to the presence of diverse genotypes with different genetic backgrounds, as well as environmental influences. Similar results were also earlier reported by Kumar *et al.* (2016) [17], Prasad *et al.* (2020) [22] and Rahman *et al.* (2016) [23] in wheat.

Table 1: Analysis of variance for yield and yield contributing characters in fifty genotypes of wheat

S. No.	Characters	Mean sum of squares		
		Replications (DF=1)	Treatments (DF=49)	Error (49)
1	Days to 50% heading	5.290	25.740**	2.657
2	Days to maturity	1.210	29.357**	6.679
3	Plant height	28.048	37.601**	13.130
4	Number of tillers per plant	0.003	0.920**	0.179
5	Spike length	0.274	0.802**	0.112
6	Number of grains per spike	4.335	25.346**	1.753
7	1000 seed weight	1.734	36.918**	8.081
8	Biological yield per plant	0.006	6.653**	1.669
9	Grain yield per plant	0.304	2.297**	0.310
10	Harvest index	9.183	28.848**	13.173

*, ** Significant at P=0.05 and P=0.01 levels of probability, respectively

The mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense), and genetic advance as percentage of mean for the ten characters are presented in Table 2. For all traits, phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation (GCV), but the differences were narrow, suggesting limited environmental influence on the expression of these traits. Relatively high values of both PCV and GCV were recorded for number of grains per spike (PCV: 17.20%, GCV: 15.88%), number of effective tillers per plant (PCV: 13.84%, GCV: 12.26%), grain yield per plant (PCV: 13.47%, GCV: 11.76%), and harvest index (PCV: 11.97%, GCV: 7.31%). These results indicate substantial genetic variability and good scope for improvement of these traits through direct selection. However, moderate PCV and GCV was observed for 1000 grain weight (10.31) and (8.26), biological yield per plant (9.19) and (7.11), spike length (8.05) and 6.99). The lowest estimates of PCV and GCV were observed for days to maturity (3.93) and (3.11) respectively followed by plant height and days to 50% heading. The magnitude of PCV ranged from 3.93 for days to maturity to 17.02 for number of grains/spike while GCV ranged from 3.11 for days to maturity to 15.88 for number of grains/spike. Similar results on variability for different characters were reported by Arya *et al.* (2017) [4], Fikre *et al.* (2015) [12], Abinasa *et al.* (2011) [1], Chauhan *et al.* (2023) [8].

Heritability estimates were highest for number of grains/spike (87.06), followed days to 50% heading (81.28), grain yield/plant (76.21), spike length (75.45). Lowest heritability shown by harvest index (37.21) followed by plant height (48.24).

The highest genetic advance as percentage of mean was recorded for number of grains per spike (30.53%), followed by number of effective tillers per plant (22.80%) and grain yield per plant (21.15%). High heritability combined with high genetic advance (as per cent of mean) was observed for number of effective tillers per plant, number of grains per spike, and grain yield per plant. This indicates that these traits are primarily governed by additive gene action and would respond well to direct selection. High heritability coupled with moderate genetic advance was exhibited by 1000-grain weight, spike length, and harvest index. In contrast, days to maturity and plant height showed low genetic advance as per cent of mean, suggesting limited scope for rapid improvement through selection. These findings are in agreement with the results reported by Arya *et al.* (2017) [4], Meles *et al.* (2017) [20].

Correlation Analysis

The genotypic and phenotypic correlation coefficients between yield and its related components are presented in (Table 3 and Table 4). A significant positive correlation were observed for grain yield/plant with number of effective tillers/plants (G: 0.7772, P: 0.5754), spike length (G: 0.8653, P: 0.6013), number of grains/spike (G: 0.8425, P: 0.6968), 1000-grains weight (G: 0.5316, P: 0.4043), biological yield/plant (G: 0.7947, P: 0.5140) and harvest index (G: 0.8234, P: 0.7282) at genotypic and phenotypic level. Correlation of days to heading (G:-0.003, P:-0.0146) and days to maturity (G:-0.2747, P:-0.1655) showed negative non-significant association with the grain yield. Also plant height showed positive but non-significant association with grain yield at both the level. Spike length, number of grains per spike and number of productive tillers per plant showed positive significance with biological yield per plant and harvest index at both the levels. These results were in accordance with Jeannie *et al.* (2022) [14], Singh *et al.* (2021) [25], Mecha *et al.* (2017) [19], Meles *et al.* (2017) [20] and Wani *et al.* (2018) [28].

In most cases, the genotypic correlation coefficients were higher in magnitude than the corresponding phenotypic correlation coefficients. This indicates that the associations between traits are largely genetic in nature, with relatively little masking effect from the environment. The strong genotypic correlations suggest that selection for one trait is likely to bring about correlated responses in associated traits. These observations are consistent with the findings of Kumar *et al.* (2024) [16] and Varsha *et al.* (2019) [27].

Path Coefficient Analysis

The direct and indirect effects of grain yield and its component traits are shown in (Table 5). Also the diagram of path analysis showing direct and indirect effects represented in (Figure 3). The genotypic path coefficient analysis revealed that 1000 grain weight (0.01560), number of productive tillers per plant (0.07223), biological yield per plant (0.751562) and harvest index (0.693662) had exhibited positive direct effect and significant positive genotypic correlation with grain yield/plant. Therefore, direct selection for these characters would be easy and would be rewarding. Days to maturity (-0.06492), spike length (-0.10386), number of grains per spike (-0.06149) showed negative direct effect on grain yield at genotypic level. Maximum contribution towards the grain yield shown by the biological yield followed by harvest index and 1000 grain weight. These indicate that true relationship between these traits and grain yield. Similar results were found in Gupta and Nigam (2023) [13], Alemu *et al.* (2020) [2], Dutamo *et al.* (2015) [11], Abinasa *et al.* (2011) [1] and Ayer *et al.* (2017) [5].

The residual effect in genotypic path analysis (0.0019) is below one, it indicates that the independent traits included in the analysis account for a large proportion of the variability in the dependent variable (e.g., grain yield). Same results were observed by the Kumar *et al.* (2023) [18] and Dashora *et al.* (2022) [9].

Conclusion

The present study demonstrated that the presence of wide range of variations for all of the traits among wheat genotypes provide the opportunities of the genetic gain through selection or hybridization. Traits with moderate to high levels of heritability and genetic advance indicates predominance of additive gene action, which is heritable and has high selection value. Focus on this should be prioritized for effective yield improvement. Selection is expected to be more successful when traits exhibit moderate to high heritability combined with moderate to high genetic advance. Also, the Phenotypic Coefficient of Variation (PCV) exceeded the Genotypic Coefficient of Variation (GCV) for all traits indicate that influence of environmental factors on expression of traits. The small difference between PCV and GCV for certain traits further suggests strong genetic control, enhancing the potential for effective selection. Both phenotypic and genotypic correlation analyses revealed a positive association of grain yield per plant with all the studied agro-morphological traits.

Table 2: Estimates of variability parameters for ten characters for yield and yield contributing characters in 50 genotypes of wheat

S. No	Characters	Mean	Range		PCV (%)	GCV (%)	Heritability in broad sense (H^2), (%)	Genetic Advance as % of mean
			Min.	Max.				
1	Days to 50% heading	70.15	60	77.5	5.37	4.84	81.28	8.994
2	Days to maturity	107.99	101	116	3.93	3.11	62.93	5.09
3	Plant height (cm)	87.86	77.86	96.8	5.7	3.9	48.24	5.69
4	Number of tillers/plant	8.38	7.35	9.35	13.84	12.26	67.45	22.80
5	Spike length (cm)	8.39	7.05	10.10	8.05	6.99	75.45	12.52
6	Number of grains/spike	21.61	15.22	30.47	17.02	15.88	87.06	30.53
7	1000 grain weight (g)	45.96	34.30	54.29	10.31	8.26	64.08	13.62
8	Biological yield/plant (g)	22.18	17.97	27.33	9.19	7.11	59.93	11.35
9	Harvest index%	38.27	33.14	47.84	11.97	7.31	37.31	14.20
10	Grain yield/plant (g)	8.47	6.50	10.65	13.47	11.76	76.21	21.15

GCV=Genotypic coefficient of variation, PCV=Phenotypic coefficient of variation

Table 3: Genotypic correlation coefficient for 10 different characters in wheat

Traits	DH	DM	PH	TPP	SL	NGS	TGW	BY	HI	GY
DH	1 **	0.5991 **	0.0194	-0.1509	-0.0742	-0.1245	0.0692	-0.2453	0.2251	-0.003
DM		1 **	0.3991 **	-0.3895 **	-0.3818 **	-0.4539 **	0.0277	-0.6712 **	0.2375	-0.2747
PH			1 **	0.2307	-0.0015	0.1782	0.1784	0.2009	0.0663	0.1773
TPP				1 **	0.5733 **	0.6868 **	0.5035 **	0.8097 **	0.4441 **	0.7772 **
SL					1 **	0.839 **	0.524 **	0.9905 **	0.4145 **	0.8653 **
NGS						1 **	0.4941 **	0.9501 **	0.4161 **	0.8425 **
TGW							1 **	0.5668 **	0.2956 *	0.5316 **
BY								1 **	0.3074 *	0.7947 **
HI									1 **	0.8234 **
GY										1 **

**-Significant at P=0.01 *-Significant at P=0. 05

DH-Days to 50% heading, DM-Days to maturity, PH-Plant height, TPP-Number of productive tillers per plant, SL-Spike length, NGS-Number of grains per spike, BY-Biological yield per plant, TGW-1000 grain weight,HI-Harvest index, GY-Grain yield per plant

Table 4: Phenotypic correlation coefficient for 10 different characters in wheat

Traits	DH	DM	PH	TPP	SL	NGS	TGW	BY	HI	GY
DH	1**	0.4738 **	0.098	-0.0311	-0.0491	-0.0843	0.0417	-0.199 *	0.1374	-0.0146
DM		1**	0.1841	-0.2774 **	-0.2743 **	-0.3135 **	-0.0476	-0.3414 **	0.0802	-0.1655
PH			1**	0.0921	0.0725	0.1182	0.1144	0.1100	0.0637	0.1198
TTP				1**	0.3711 **	0.5427 **	0.3356 **	0.4212 **	0.3166 **	0.5754 **
SL					1**	0.6812 **	0.3421 **	0.6643 **	0.1607	0.6013 **
NGS						1**	0.359 **	0.7057 **	0.2301 *	0.6968 **
TGW							1**	0.3274 **	0.2133 *	0.4083 **
BY								1**	-0.2096 *	0.514 **
HI									1**	0.7282 **
GY										1**

**-Significant at P=0.01 *-Significant at P=0. 05

DH-Days to 50% heading, DM-Days to maturity, PH-Plant height, TPP-Number of productive tillers per plant, SL-Spike length, NGS-Number of grains per spike, BY-Biological yield per plant, TGW-1000 grain weight, HI-Harvest index, GY-Grain yield per plant

Table 5: Genotypic path coefficient analysis showing direct (diagonal) and indirect effects of nine causal variables on grain yield per plant in 50 genotypes of wheat

Trait	DH	DM	PH	TPP	SL	NGS	TGW	BY	HI	GY
DH	0.036206	-0.03889	0.000585	0.010901	0.007704	0.007656	0.001079	-0.18438	0.156143	-0.003
DM	0.021691	-0.06492	0.012046	0.028136	0.039648	0.027913	0.000432	-0.50441	0.164738	-0.2747
PH	0.000702	-0.02591	0.030187	-0.01666	0.00016	-0.01096	0.002784	0.150959	0.045997	0.1773
TPP	-0.00546	0.025291	0.006963	0.07223	-0.05954	-0.04223	0.007857	0.608532	0.308055	0.7772 **
SL	-0.00269	0.024785	-0.00005	-0.04141	-0.10386	-0.05159	0.008178	0.744399	0.287523	0.8653 **
NGS	-0.00451	0.02947	0.005381	-0.0496	-0.08713	-0.06149	0.007711	0.714059	0.288605	0.8425 **
TGW	0.002504	-0.0018	0.005385	-0.03636	-0.05442	-0.03038	0.015606	0.425993	0.205033	0.5316 **
BY	-0.00888	0.043573	0.006063	-0.05848	-0.10287	-0.05842	0.008846	0.751562	0.21326	0.7947 **
HI	0.00815	-0.01542	0.002002	-0.03208	-0.04305	-0.02558	0.004613	0.23106	0.693662	0.8234 **

** -Significant at P=0.01 * -Significant at P=0. 05 Residual effect= 0.0019

DH-Days to 50% heading, DM-Days to maturity, PH-Plant height, TPP-Number of productive tillers per plant, SL-Spike length, NGS-Number of grains per spike, BY-Biological yield per plant, TGW-1000 grain weight, HI-Harvest index, GY-Grain yield per plant.

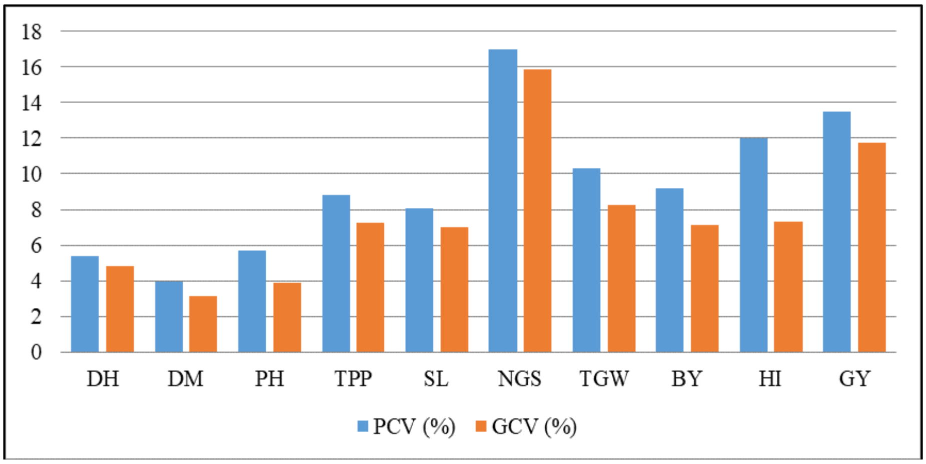

Fig 1: Genotypic and phenotypic coefficient of variation for ten characters in wheat

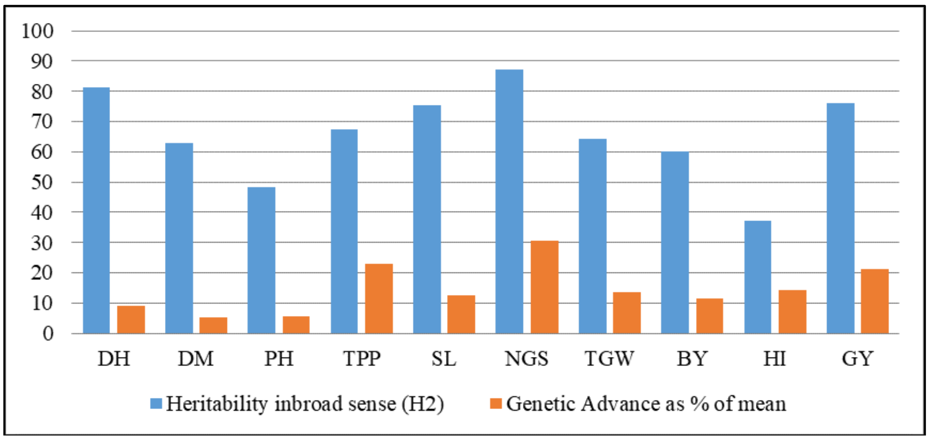

Fig 2: Heritability and genetic advance as per cent of mean for ten characters in wheat

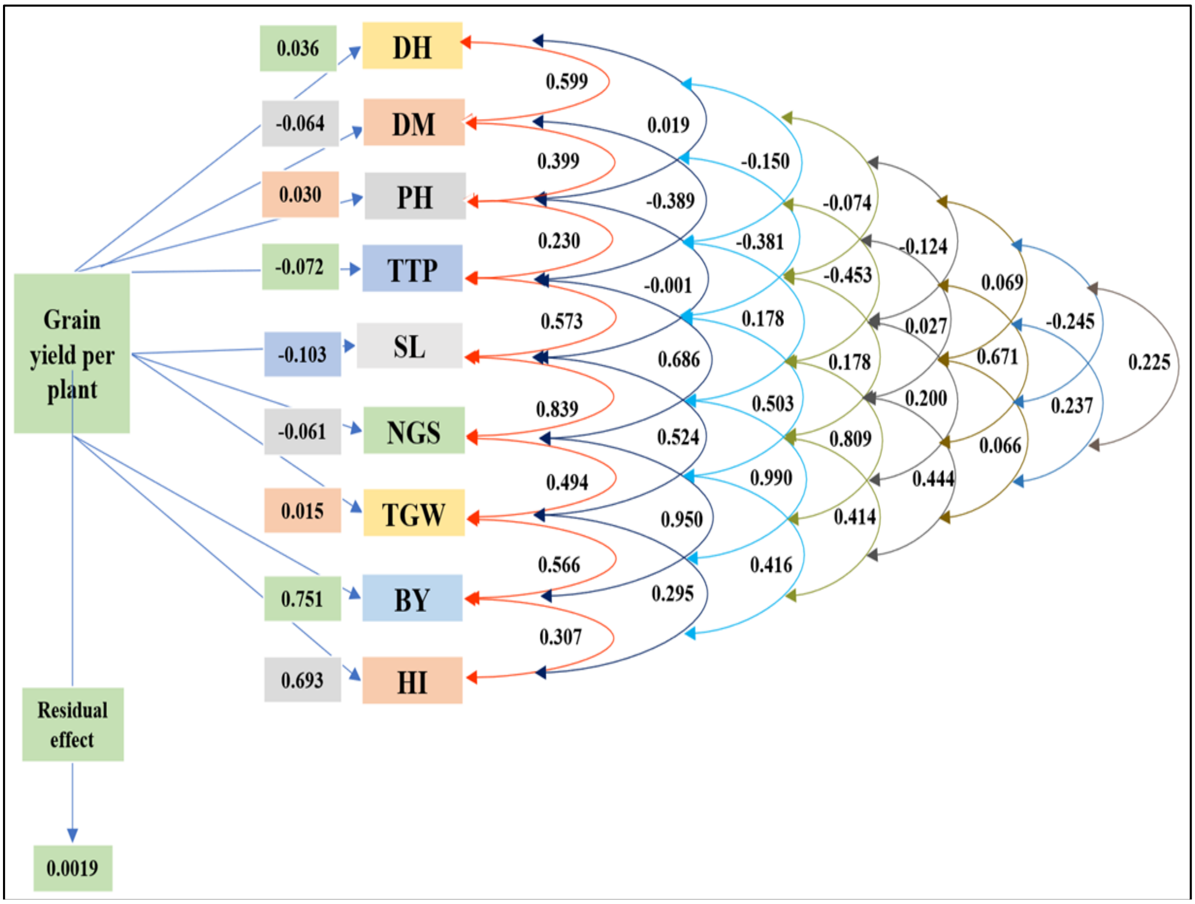

Fig 3: Genotypic path analysis diagram showing direct and indirect effects of nine independent variables on grain yield per plant

This indicates that improvement in one or more of these traits would lead to higher grain yield. Among these, biological yield per plant, harvest index, and number of effective tillers per plant exhibited a positive and significant genotypic correlation with grain yield, coupled with a positive direct effect on grain yield in the path coefficient analysis. These traits can therefore be considered reliable selection criteria for improving grain yield through direct selection.

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