



Genetic variability and multivariate assessment of wheat–*Aegilops* derivatives under diverse agro-climatic environments

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Abstract

Cultivated wheat has a narrow genetic base; therefore, wild relatives represent an invaluable source of novel alleles for broadening genetic diversity and enhancing yield potential. We evaluated 109 wheat–*Aegilops* derivatives including parents and three check varieties across four diverse agro-climatic environments (Baru Sahib, Palampur, Ludhiana and Ayodhya) to examine genetic variability, trait associations and diversity using multivariate approaches. The combined analysis of variance (ANOVA) revealed that genetic variability, environmental conditions and $G \times E$ interactions significantly impact the agronomic performance and yield potential of the wheat–*Aegilops* derivatives. Significant phenotypic variation was observed for all morpho-physiological and yield-related traits, showing genetic diversity and environmental effects on trait expression. Broad-sense heritability ranged from 38.30 to 91.69 %, while genetic advance mean varied from 2.15 to 44.69 %, with grain yield recording the highest genetic advance over mean. Grain yield exhibited strong positive associations with spike length, grains per spike and thousand-grain weight. The first two principal components together explained 83.4 % of the variation (PC1=72.9 % and PC2 10.5 %) and were associated with grain yield, thousand-grain weight, spike length and grains per spike. Five stable wheat–*Aegilops* derivatives, such as MB-13-2-2, PRH3-62-1-4, B-56-2-5-1, B-52-1-4 and PRH3-45-3 were observed across locations. The findings of this study provide valuable insights for utilization wheat–*Aegilops* derivatives in future breeding programs aimed to developing climate-resilient high yielded wheat cultivars.

Keywords: *Aegilops* introgression, genetic variability, heritability, multivariate analysis, principal component analysis, wheat improvement

INTRODUCTION

Wheat (*Triticum aestivum* L.) is among the most widely cultivated cereal crops and serves as a primary source of food and nutrition for the global population (Akbar *et al.*, 2025). Wheat production globally is expected to reach 796-809 million metric tons in 2025, driven by improved harvest performance across countries. In India, the crop is grown over an area of approximately 31.76 million hectares with a production of 109.52 million tons, showing a 1.8 % increase over the previous year (FAO, 2025-26). Enhancing wheat productivity requires the development of high-yielding cultivars possessing broad genetic diversity and adaptability to diverse agro-climatic regions. Wheat contributes nearly 20 % of the total edible biomass produced globally, signifying its importance in global food security. Further, in resource-poor regions, it provides up to 60 % of daily caloric intake,

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indicating its role in alleviating global food insecurity (Akbar *et al.*, 2025). Production can be enhanced through high-yielding varieties that provide stable output with efficient resource exploitation. Adaptability refers to the ability of a genotype to combine high yield with stability under climate change, while those showing pronounced responses to environmental conditions are considered sensitive (Havryliuk and Kovalyshyna, 2024). The wild relative of wheat, particularly species belonging to the genus *Aegilops*, represents an important reservoir of genetic diversity for wheat improvement. Wheat-*Aegilops* derivatives have been extensively used in breeding programs to introgress desirable genes associated with abiotic stress tolerance, disease resistance, yield stability and environmental adaptability (Kishii, 2019).

The assessment of genetic variability and trait associations is essential for effective wheat breeding and grain yield can be improved through indirect selection of yield-contributing traits (Kumar *et al.*, 2017). Therefore, direct selection for yield alone is not effective and efficient breeding depends on understanding genetic variability and the relationships between agro-morphological and yield traits (Ali *et al.*, 2008). Path coefficient analysis further partitioned this relationship into direct and indirect effects, making it more informative than simple correlation analysis (Arshad *et al.*, 2006). Therefore, correlation and path analyses are effective tools for identifying key traits to enhance wheat yield (Pandit *et al.*, 2025). The performance of genotypes is strongly influenced by environmental conditions, resulting in significant genotype $\times$ environment interactions. Multi-location trials are therefore essential for evaluating the stability, adaptability and yield performance of genotypes across diverse climatic regions (Mullualem *et al.*, 2024). Multi-environment testing also assists in understanding the magnitude of genotype $\times$ environment interaction and selecting superior genotypes with broad or specific adaptation under diverse agro-climatic conditions (Kassie *et al.*, 2025). Therefore, the evaluation of wheat-*Aegilops* derivatives under diverse environments can facilitate the identification of superior genotypes with enhanced agronomic performance and adaptability.

MATERIALS AND METHODS

The experimental material includes 109 wheat-*Aegilops* derivatives introgression lines developed through crosses between commercial wheat cultivars (Chinese Spring, HD2687, WL711, UP2338 and PBW343) and non-progenitors *Aegilops* species (*Aegilops kotschy* 396, *Aegilops kotschy* 3573, *Aegilops kotschy* 3790 and *Aegilops peregrine* 3519, *Aegilops peregrina* 3774, *Aegilops peregrina* 3772). These crosses were carried out at the Indian Institute of Technology, Roorkee (Uttarakhand) and Eternal University, Baru Sahib, Sirmour (Himachal Pradesh) using pollen radiation hybridization and induced homeologous pairing approaches (Tiwari *et al.*, 2010).

The experimental material comprised advanced wheat-*Aegilops* derivative genotypes (stable BC₂F₁₀/BC₂F₁₁ introgression lines), along with the parental lines and check cultivars. The experimental material was sown during the *Rabi* season 2024-25, in the last week of October to the first week of November at the four different agro-climatic locations, viz. Eternal University, Baru Sahib, Himachal Pradesh (30.7537° N, 77.2965° E), Rice and Wheat Research Station, Malan, Himachal Pradesh (32.1792° N, 76.3882° E), Punjab Agricultural University, Ludhiana, Punjab (30.9019° N, 75.8078° E) and Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh (26°32'08" N, 81°50'07" E), India. Each genotype was sown in paired rows of 1 m length and row-to-row spacing of 20-22 cm was maintained for the wheat-*Aegilops* introgression lines, whereas a spacing of 60-80 cm was maintained for the wild parental lines. The experiment was conducted using an Augmented Block Design comprising five blocks, with 109 genotypes and three check varieties. Four blocks accommodated 22 test entries each, while the fifth contained 21 entries; 'Chinese Spring' was included as a filler to maintain uniformity. Check varieties were replicated across all blocks. The layout of the experiment ensured random distribution of entries within each block to minimize environmental variation.

Statistical analysis

Analysis of variance (ANOVA) was estimated for each location and variability components analysis was assessed using pooled data over the environments by following standard procedures. ANOVA for the Augmented Block Design was estimated using the *Augmented RCB*D package (Aravind *et al.*, 2020) in R version 4.4.2. Broad-sense heritability and genetic advance as per cent of mean were estimated from the pooled variance components. Correlation coefficients were computed and visualized using the *corrplot* package (Wei and Simko, 2021); the statistical significance of each correlation coefficient was tested using the corresponding p-value matrix, with significance denoted at $p < 0.05$, $p < 0.01$ and $p < 0.001$. Path coefficient analysis was carried out with grain yield per plot as the dependent variable to partition the correlations into direct and indirect effects and the residual effect was estimated as $\sqrt{1 - R^2}$, where R^2 is the variation in grain yield explained by the causal traits. Principal component analysis was performed using the *stats* package (R Core Team, 2023) and the *FactoMineR* package (Husson *et al.*, 2020). Hierarchical cluster analysis was carried out using the *cluster* package (Maechler *et al.*, 2023), with *factoextra* (Kassambara and Mundt, 2020) and *dendextend* (Galili, 2015) used for visualization.

RESULTS AND DISCUSSION

Analysis of variance across environments

The combined analysis of variance revealed highly significant ($p < 0.001$) effects of environments and

genotypes for all the studied morpho-physiological and yield-related traits, indicating the presence of substantial environmental influence and genetic variability among the wheat-*Aegilops* derivatives (Table 1). The genotype $\times$ environment interaction was also significant for all the studied traits, demonstrating differential performance across locations. The significant genotypic effects observed for all traits provide substantial opportunities for selection and genetic improvement. Similar findings were also reported earlier by Kassie *et al.* (2025), significant contribution of genotype $\times$ environment sources of variation in multi-environment wheat trials.

Descriptive statistics across environments

The descriptive statistics indicated substantial differences among wheat-*Aegilops* derivatives across the four testing environments viz., Baru Sahib, Palampur, Ludhiana and Ayodhya, suggesting significant genetic diversity along with environmental effects on trait expression (Table 2). The days to flower initiation showed variation from 82.93 days in Ayodhya to 105.89 days in Baru Sahib, revealing earlier flowering behaviour in Ayodhya and Ludhiana environments and emphasizing distinct differences among genotypes. Days to maturity showed comparatively low variation across the four environments, ranged from 123.69 days in Ayodhya to 168.10 days in Baru Sahib, which indicates relative stability of this trait despite an observable diversity (40, 42, 53, 53 days) range. Plant height displayed moderate variability, with maximum mean value in Ayodhya (106.93 cm) and minimum in Palampur (95.64 cm), indicating the availability of both dwarf and tall plant types across locations. Spike length varied from 12.38 cm in Palampur to 14.53 cm in Ludhiana, suggesting moderate variability for the improvement and selection of high-yielding spike type. Among all the traits, productive tillers per plant exhibited maximum variability, despite comparable mean values across the four environments (10.23-10.90), highlighting substantial genotypic and environmental influence on this character. The number of grains per spike ranged between 23.44

in Baru Sahib and 38.58 in Ayodhya, reflecting superior grain setting in Ayodhya and significant diversity among genotypes. Thousand-grain weight remained relatively consistent across environments, varying from 43.63 g in Baru Sahib to 47.89 g in Ayodhya, which indicates stable expression and the presence of bold-seeded genotypes. Grain yield per plot showed marked variation among the four environments, with the highest average grain yield of 220.68 g in Palampur, followed closely by Baru Sahib (220.08 g), whereas the lowest mean was recorded in Ayodhya (178.82 g). This variation reflects the significant impact of environmental conditions and differential responses of genotypes across locations. The genotypes showed extensive phenotypic heterogeneity, suggesting wheat breeding programs could benefit from selection and genetic enhancement. The present study found wide genetic variability among wheat-*Aegilops* derivatives for morpho-physiological and yield-related variables across environments, showing genetic diversity and diverse environmental responses. Variation in descriptive statistics revealed potential for selection and genetic enhancement. The high environmental influence on trait performance, especially days to maturity and grain per spike, suggests that environmental factors determine phenotypic expression. Multi-environment wheat studies showed that environmental variability greatly affects yield and its components (Gupta *et al.*, 2022).

Genetic variability parameters

The magnitude of variability among wheat-*Aegilops* derivatives across environments was assessed through phenotypic coefficient of variation, genotypic coefficient of variation and environmental coefficient of variation estimated for the studied traits (Table 3). Among all the traits, thousand-grain weight exhibited the highest genotypic coefficient of variation (18.70 %) followed by grain yield per plot (17.24 %). In contrast, grain yield also recorded the highest phenotypic coefficient of variation (27.87 %) along with thousand-grain weight (19.68 %), suggesting considerable scope for yield improvement.

Table 1. Analysis of variance for morpho-physiological and yield-related traits of wheat-*aegilops* derivatives across four agro-climatic environments

Source of variation	Environment (E)	Genotype (G)	Environment $\times$ Block	G $\times$ E interaction	Residual
Df	3	111	16	333	36
Days to flower initiation	17168***	534***	92***	27*	15
Days to maturity	54334***	233***	51***	31***	7
Plant height	2771.90***	879.90***	121.30***	79.00***	28
Spike length	132.19***	18.51***	3.29**	2.36**	1.07
Productive tillers per plant	10.40***	448.70***	3.10***	1.80***	0.3
Grains per spike	6648***	86***	20***	11***	3
Thousand grain weight	504.90***	289.70***	18.30***	7.90*	4.4
Grain yield	53111***	6898***	4021***	2179***	153

Significance levels: * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$

Table 2. Descriptive statistics of morpho-physiological and yield-related traits of wheat-*aegilops* derivatives across four agro-climatic environments

Trait	Environments	Mean	SD	SE	Minimum	Maximum
Days to flower initiation	BS	105.89	13.02	1.16	80.00	146.00
	PL	101.08	11.07	0.99	73.00	137.00
	LDH	84.05	11.38	1.02	72.00	135.00
	AY	82.93	11.99	1.07	71.00	132.00
Days to maturity	BS	168.10	6.55	0.59	146.00	186.00
	PL	151.26	9.17	0.82	135.00	177.00
	LDH	127.72	9.18	0.82	114.00	167.00
	AY	123.69	9.46	0.85	115.00	166.00
Plant height (cm)	BS	99.76	16.81	1.50	29.30	135.30
	PL	95.64	14.11	1.26	42.00	146.00
	LDH	99.46	14.31	1.28	40.70	135.00
	AY	106.93	18.36	1.64	32.00	147.60
Spike length (cm)	BS	12.94	2.18	0.20	5.10	17.10
	PL	12.38	2.23	0.20	5.70	16.50
	LDH	14.53	2.62	0.23	4.70	19.00
	AY	14.23	2.65	0.24	5.50	18.60
Productive tillers per plant	BS	10.43	9.70	0.87	5.00	67.00
	PL	10.37	9.67	0.86	6.00	68.00
	LDH	10.90	10.82	0.97	5.00	71.00
	AY	10.23	10.12	0.91	5.00	68.00
Grains per spike	BS	23.44	4.22	0.38	10.00	31.00
	PL	23.70	3.84	0.34	9.00	30.00
	LDH	32.10	6.16	0.55	11.00	49.00
	AY	38.58	6.18	0.55	10.00	46.00
Thousand grain weight (g)	BS	43.63	8.55	0.77	11.90	60.00
	PL	43.84	9.11	0.81	10.40	59.80
	LDH	44.24	8.16	0.73	11.90	57.20
	AY	47.89	7.84	0.70	13.30	58.30
Grain yield per plot (g)	BS	220.08	46.62	4.17	95.60	288.00
	PL	220.68	47.72	4.27	92.60	300.00
	LDH	193.73	68.52	6.13	78.80	361.80
	AY	178.82	58.70	5.25	76.80	316.00

Note: BS = Baru Sahib, PL = Palampur, LDH = Ludhiana and AY = Ayodhya, SD-Standard Deviation, SE-Standard Error, Min.-Minimum, Max.-Maximum

Plant height exhibited moderate phenotypic coefficient of variation and genotypic coefficient of variation estimates, reflecting the availability of considerable genetic variability for selection. The narrow gap between phenotypic coefficient of variation and genotypic coefficient of variation values indicated that these traits were less affected by environmental factors and predominantly governed by genetic components. Whereas, days to flower initiation and days to maturity showed relatively lower phenotypic coefficient of variation and genotypic coefficient of variation values, suggesting relatively narrow variability and stable performance

across environments. Phenotypic coefficient of variation (PCV) values was higher than corresponding genotypic coefficient of variation (GCV) values for all the studied traits, indicating the influence of environmental factors on phenotypic expression. Numbers of tiller per plant for *Aegilops* derivatives was excluded due to a large amount of variation, demonstrating the role of environmental factors in trait expression. However, the close association between phenotypic coefficient of variation and genotypic coefficient of variation for most traits showed that genetic factors dominated variability, suggesting that phenotypic selection is effective for crop improvement programs. All

Table 3. Estimates of genetic variability parameters for morpho-physiological and yield-related traits of wheat-*aegilops* derivatives

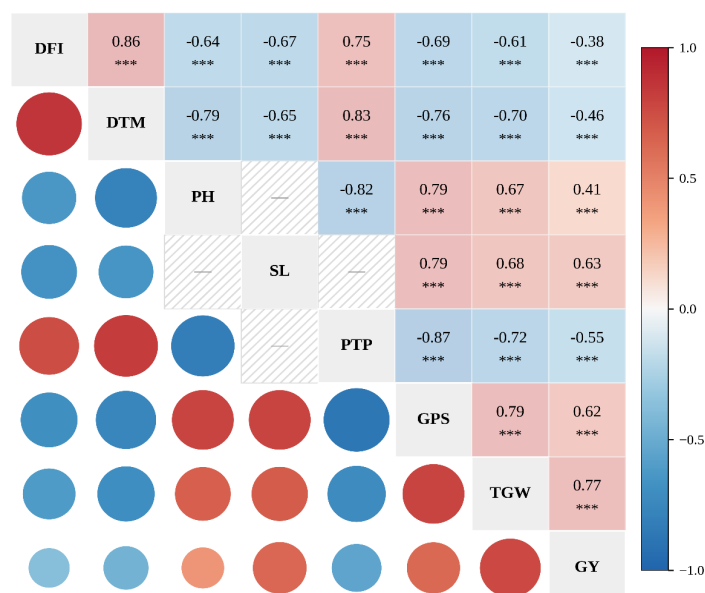
Trait	GCV (%)	PCV (%)	ECV (%)	Heritability (bs) (%)	GAM (%)
Days to flower initiation	12.06	13.21	5.40	83.30	21.19
Days to maturity	5.01	6.26	3.75	64.14	11.80
Plant height	14.13	16.52	8.57	73.12	25.00
Spike length	14.92	18.57	11.07	64.50	3.34
Productive tillers per plant	13.90	14.52	12.24	91.69	2.15
Grains per spike	14.82	18.23	10.62	66.00	7.31
Thousand grain weight	18.70	19.68	6.12	90.30	16.44
Grain yield per plot	17.24	27.87	21.89	38.30	44.69

Note: GCV-Genotypic Coefficient of Variation; PCV-Phenotypic Coefficient of Variation; ECV-Environmental Coefficient of Variation; Heritability (bs)-Broad-Sense Heritability; GAM-Genetic Advance as Percent of Mean

evaluated variables show significant genotypic variation, indicating genetic diversity in wheat-*Aegilops* derivatives. This genetic diversity helps identify and choose superior genotypes for agricultural improvement. Previous studies have shown that introgression lines from wild relatives need genetic variety to improve stress tolerance and yield performance (Kaur and Sangha, 2025; Antwi-Boasiako *et al.*, 2026).

Broad-sense heritability (h^2) ranged from 38.30 % for grain yield per plot to 91.69 % for productive tillers per plant (Table 3). Genetic advance as per cent of mean (GAM) varied from 2.15 % for productive tillers per plant to 44.69

% for grain yield per plot. High heritability was observed for productive tillers per plant (91.69 %) and thousand-grain weight (90.30 %), whereas grain yield per plot exhibited the highest GAM (44.69 %), indicating greater potential for improvement through selection. The high heritability with high GAM for days to flower initiation and thousand-grain weight supports predominant additive gene action and efficiency of selection for these traits. Grain yield per plot had low heritability but high GAM, indicating a greater influence of environmental factors, although there was substantial expected genetic gain. Similar results have been reported by Chauhan *et al.* (2023).

**Fig. 1. Pearson's correlation matrix of morpho-physiological and yield-related traits of wheat-*aegilops* derivatives**

Note: DFI-Days to flower initiation, DTM- Days to maturity, PH- Plant height, SL- Spike length, PTP- Productive tillers per plant, GPS- Grains per spike, TGW-Thousand-grain weight, GY- Grain yield per plant.

Significance levels: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

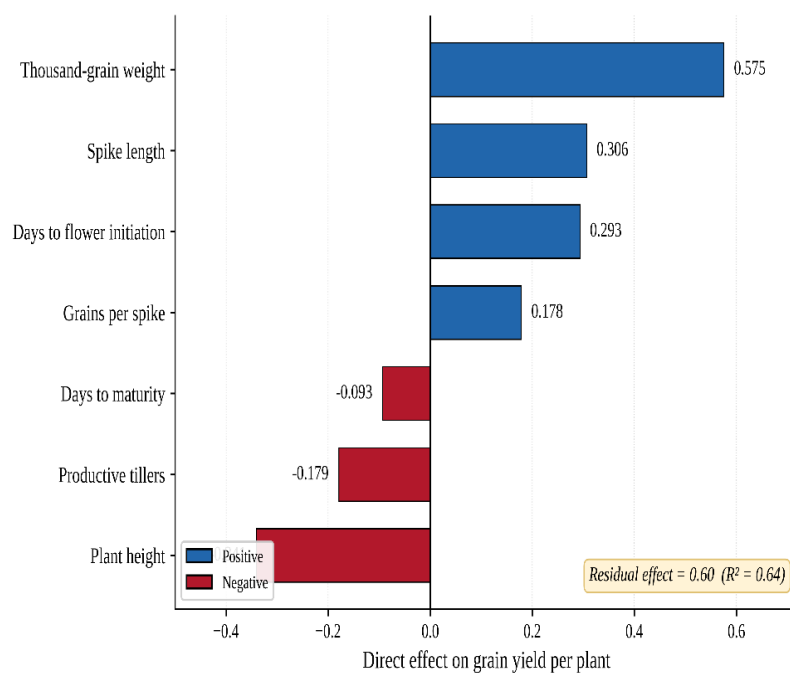
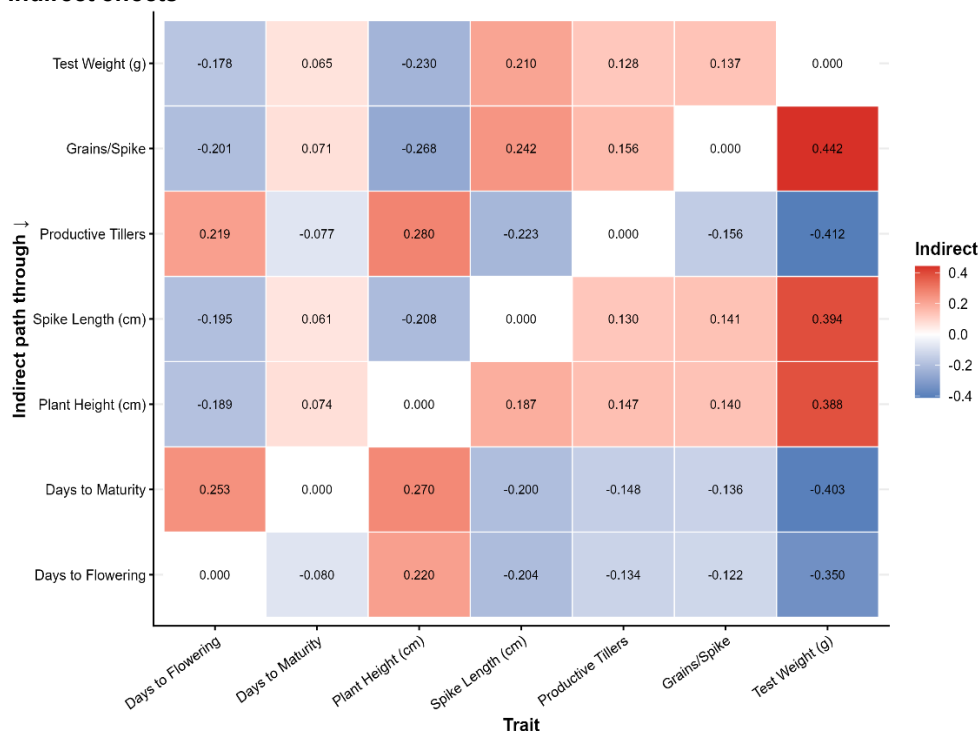
A. Direct effect**B. Indirect effects**

Fig. 2. Path coefficient analysis of morpho-physiological and yield-related traits in Wheat-*Aegilops* derivatives. (a) Direct effects; (b) Indirect effects.

Correlation of morpho-physiological and yield-related traits

Correlation analysis of morpho-physiological and yield-related traits in wheat–*Aegilops* derivatives showed important relationships useful for breeding strategies (Fig. 1). Days to flower initiation showed a strong positive correlation with days to maturity (0.86) and productive tillers per plant (0.75), but negative associations with plant height (-0.64), spike length (-0.67), grains per spike (-0.69), thousand-grain weight (-0.61) and grain yield (-0.38). Similarly, days to maturity was positively correlated with productive tillers (0.83) but negatively associated with yield-related traits. Plant height showed positive correlations with grains per spike (0.79), thousand-grain weight (0.67) and grain yield (0.41), while negatively correlated with productive tillers (-0.82). Spike length was positively associated with grains per spike (0.79), thousand-grain weight (0.68) and grain yield (0.63), indicating its role in yield improvement. Productive tillers showed negative correlation with grains per spike (-0.87), thousand-grain weight (-0.72) and grain yield (-0.55), suggesting that higher tillering did not necessarily improve productivity. Grain yield was strongly associated with thousand-grain weight (0.77), grains per spike (0.62) and spike length (0.63), highlighting these traits as important selection criteria. Similar positive effects of test weight on yield were reported by Pandit *et al.* (2025), while the negative relationship between tillers and yield agrees with Singh *et al.* (2023).

Path coefficient analysis of morpho-physiological and yield-related traits

Path coefficient analysis revealed the direct and indirect contribution of morpho-physiological and yield-related traits towards grain yield in wheat–*Aegilops* derivatives (Fig. 2). Thousand-grain weight exhibited the highest positive direct effect on grain yield (0.575), followed by spike length (0.306), days to flowering initiation (0.293) and grains per spike (0.178), indicating their strong direct contribution towards yield improvement. In contrast, plant height (-0.341), productive tillers per plant (-0.179) and days to maturity (-0.093) showed negative direct effects on grain yield (Fig 2 a). Thousand-grain weight emerged as the most influential mediating trait, through which grains per spike (0.442), spike length (0.394) and plant height (0.388) exerted substantial positive indirect effects on grain yield. Positive indirect contributions were also observed for productive tillers via plant height (0.280) and days to maturity via days to flowering (0.253) and plant height (0.270) (Fig 2 b). The residual effect was 0.60, indicating that the studied traits explained 64% ($R^2 = 0.64$) of the total variation in grain yield, while the remaining variation may be attributed to other unexplored traits and environmental factors. The result indicated that thousand-grain weight played a vital role in mediating the relationships among yield-contributing traits and grain yield, highlighting its significant role in yield improvement. Similar findings have been reported

where kernel weight contributed significantly to final yield (Abdurezake *et al.*, 2024).

Principal component analysis of morpho-physiological and yield-related traits

Principal component analysis of morpho-physiological and yield-related traits in wheat–*Aegilops* derivatives showed that PC1 and PC2 explained 83.4 % of the total variation, contributing 72.9 % and 10.5 %, respectively (Fig. 3). Genotypes located near the origin (MB-13-2-2, PRH3-62-1-4, B-56-2-5-1, B-52-1-4 and PRH3-45-3) showed balanced trait expression (Fig. 4). The higher contribution of PC1 indicated that yield and related traits were the main sources of variation among genotypes. Grain yield showed a strong positive association with thousand-grain weight, spike length and grains per spike, indicating their importance in yield improvement. Plant height was also positively related to yield traits but contributed mainly through PC2. In contrast, days to flower initiation, days to maturity and productive tillers per plant showed negative associations with major yield traits. Similar findings were reported by Alemayehu *et al.* (2025), where the first two principal components explained major variability and supported selection of superior wheat genotypes. Muhammad *et al.* (2024) also reported similar relationships between yield and phenological traits in wheat.

Hierarchical cluster analysis

Hierarchical cluster analysis using Ward's method based on D^2 statistics classified the wheat–*Aegilops* derivatives into two major clusters (I and II) with Cluster II further portioned into four subclusters (II a - II d) showing high genetic diversity among genotypes (Fig. 5). Major Cluster A, comprising six *Aegilops* accessions (*Ae. kotschy* 3573, 3790, 396; *Ae. peregrina* 3519, 3772, 3774) and major Cluster B, a secondary split at ~31% dissimilarity (~69% similarity) divided the panel into two arms, which further divided into four subclusters at ~20% dissimilarity (~80% similarity): Subcluster II a (n=26) and II b (n=22), and in the second, Subclusters II c (n=31) and II d (n=27). Cluster mean values were significantly distinct for morpho-physiological and yield related traits (Table 4). Subcluster II c recorded the highest grain yield (239.00 g), thousand-grain weight (50.14 g), spike length (14.59 cm) and grains per spike (30.84) and hence, it was the most promising group for yield improvement. Subcluster II b recorded the tallest plants (111.77 cm) and subcluster II a had the earliest flowering (84.42 days) and maturity (138.72 days), which was suitable for short-duration environments. Subcluster II d was intermediate but had the highest grains per spike (30.87). Cluster I (*Aegilops* accessions) highest reproductive tillers (52.54) but the lowest spike length (6.32 cm), grains per spike (11.54), thousand-grain weight (16.54 g) and grain yield per plot (102.57 g) proving that high tillering alone did not reflect in productivity. Similar clustering of diverse wheat genotypes based on morphological and yield traits was also reported by Zewdu *et al.* (2024).

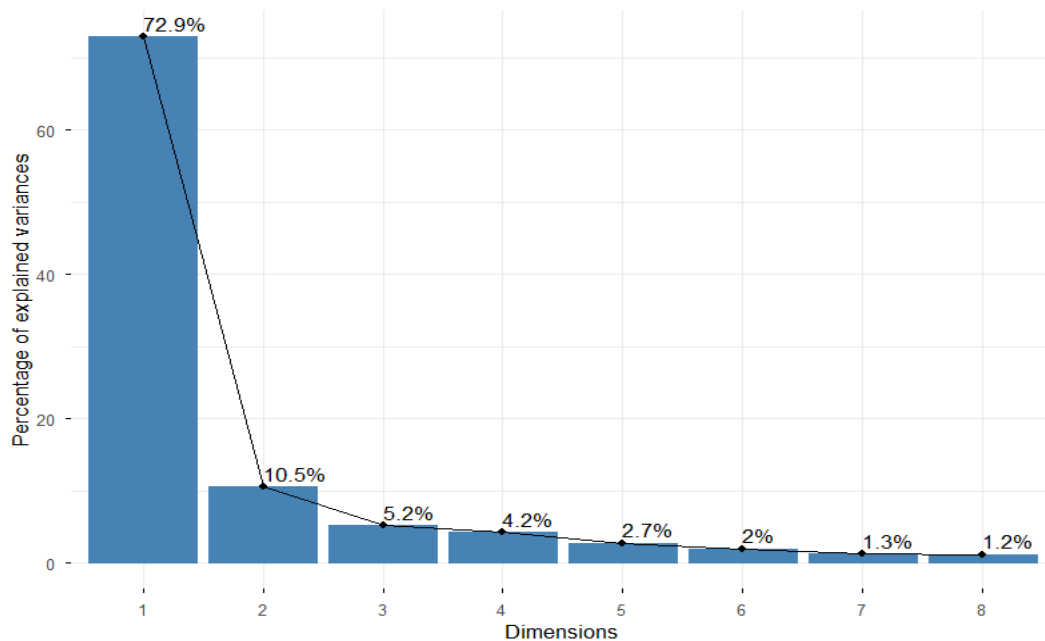


Fig. 3. Scree plot showing the percentage of variance explained by principal components for morpho-physiological and yield-related traits of wheat-*aegilops* derivatives

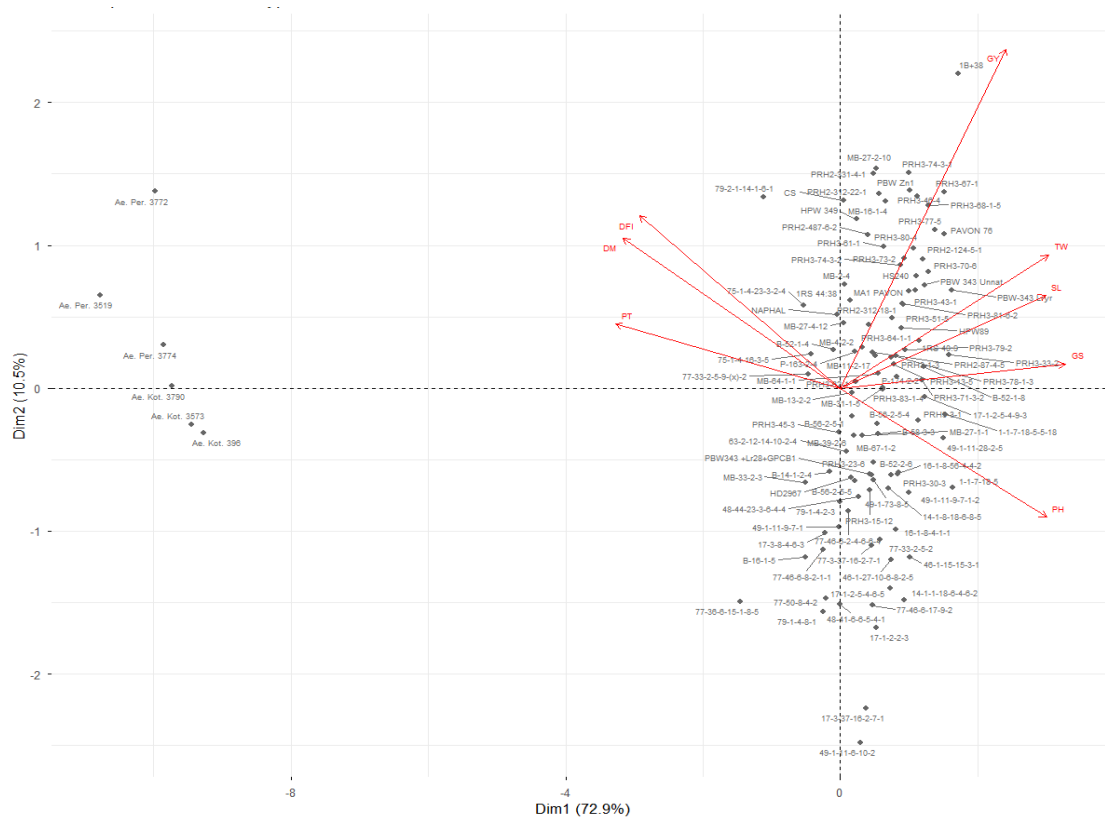


Fig. 4. PCA score plot showing the distribution of wheat-*aegilops* derivatives based on morpho-physiological and yield-related traits

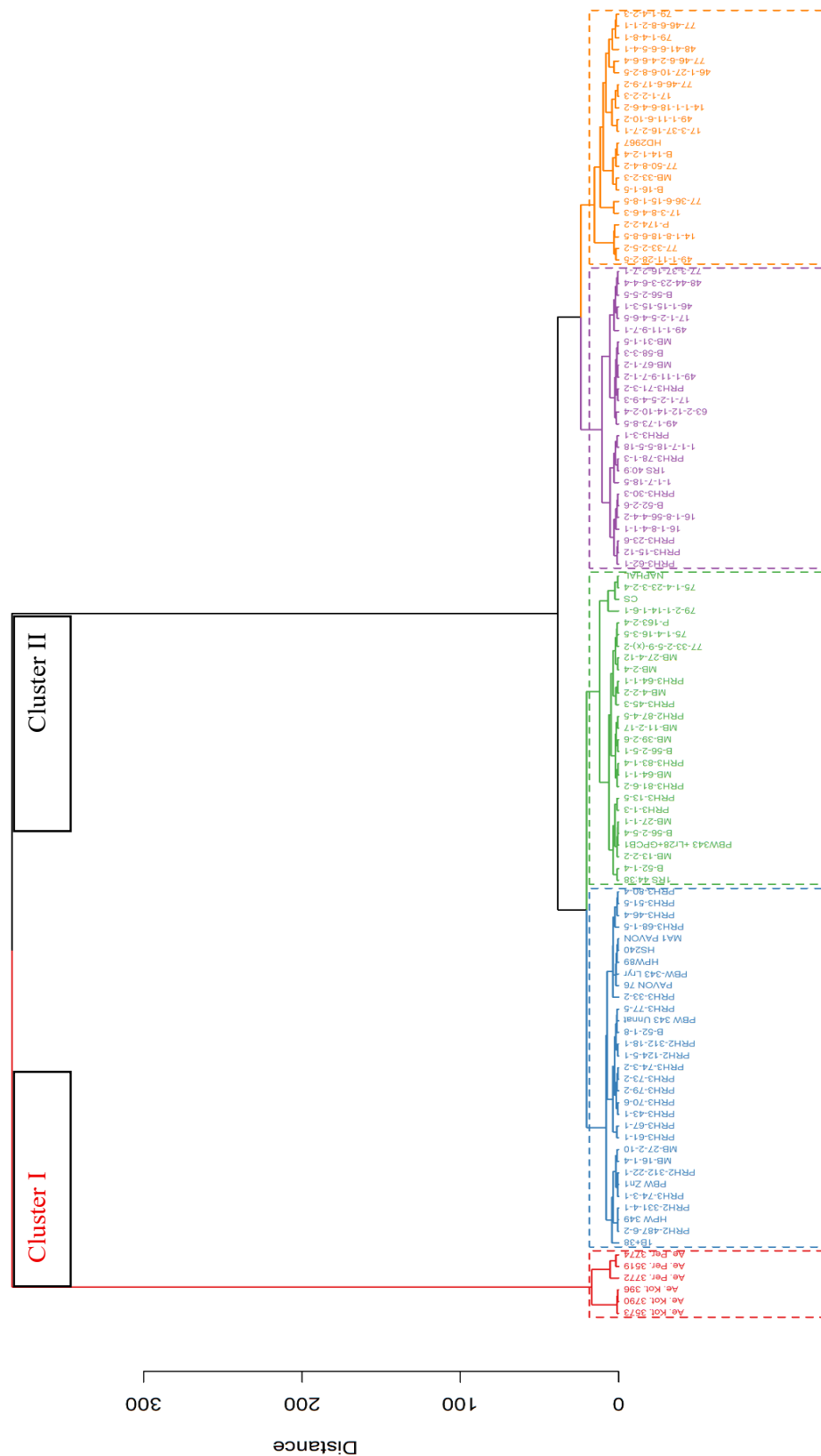


Fig. 5. Hierarchical clustering dendrogram of wheat-*aegilops* derivatives using ward's d^2 method

Table 4. Mean performance of morpho-physiological and yield-related traits across major clusters and subclusters

Cluster	I (n=6)		II (n=106)		
Subcluster	–	II a (n=26)	II b (n=22)	II c (n=31)	II d (n=27)
Days to flower initiation	130.12	84.42	91.27	92.25	97.03
Days to maturity	169.92	138.72	139.35	141.56	143.57
Plant height (cm)	46.24	100.2	111.77	100.41	101.52
Spike length (cm)	6.32	14.36	12.49	14.59	13.67
Productive tillers per plant	52.54	8.38	8.08	8.48	8.31
Grains per spike	11.54	30.05	29.61	30.84	30.87
Thousand grain weight (g)	16.54	44.89	42.34	50.14	45.19
Grain yield per plot (g)	102.57	191.81	170.57	239.00	202.50

The wheat-*Aegilops* derivatives confirmed significant genetic variability across all four different agro-climatic environments, indicating strong potential for effective selection and genetic improvement. Significant variation was recorded for most of the studied traits. Thousand-grain weight, spike length and grains per spike were important contributors to grain yield, showing significant direct as well as indirect effects. The wheat-*Aegilops* derivatives have substantial genetic divergence along with differential responses across environments. Five stable wheat-*Aegilops* derivatives, such as MB-13-2-2, PRH3-62-1-4, B-56-2-5-1, B-52-1-4 and PRH3-45-3 were observed across locations. The identified superior and genetically diverse wheat-*Aegilops* introgression lines provide valuable genetic resources for enhancing yield, broadening the genetic base and improving the adaptability of wheat under diverse agro-climatic conditions thereby offering significant potential for future wheat improvement programmes.

REFERENCES

- Arshad, M., Ali, N. and Ghafoor, A. 2006. Character correlation and path coefficient in soybean *Glycine max* (L.) Merrill. *Pakistan Journal of Botany*, **38**(1): 121.
- Abdurezake, M., Bekeko, Z. and Mohammed, A. 2024. Genetic variability and path coefficient analysis among bread wheat (*Triticum aestivum* L.) genotypes for yield and yield-related traits in Bale Highlands, southeastern Ethiopia. *Agrosystems, Geosciences & Environment*, **7**(2): e20515. [\[Cross Ref\]](#)
- Akbar, A., Ahmad, I., Jehan, A., Ali, I. and Haris, M. 2025. Genetic variability among advanced wheat lines for yield and yield related traits. *Sarhad Journal of Agriculture*, **41**(1): 154–164. [\[Cross Ref\]](#)
- Alemayehu, L., Kebede, M. and Wada, E. 2025. AMMI analysis of elite bread wheat (*Triticum aestivum* L.) selections for genotype by environment interaction and stability of grain yield in Southern Ethiopia. *PLOS ONE*, **20**(1): e0318559. [\[Cross Ref\]](#)
- Ali, Y., Atta, B.M., Akhter, J., Monneveux, P. and Lateef, Z. 2008. Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm. *Pakistan Journal of Botany*, **40**(5): 2087–2097.
- Antwi-Boasiako, A., Dormatey, R., Baafi, E., Ghanney, P., Opoku, J.A., Boateng, A.B. and Dapaah, H.K. 2026. Role of genetic diversity in crop improvement. In: *Advances in Genetic Diversity-Recent Advances, Challenges, and Prospects*. IntechOpen, London. [\[Cross Ref\]](#)
- Aravind, J., Mukesh Sankar, S., Pandhari Wankhede, D. and Kaur, V. 2020. Augmented RCBD: Analysis of augmented randomised complete block designs. *Zenodo*.
- Chauhan, S., Gupta, A., Tyagi, S.D. and Singh, S. 2023. Genetic variability, heritability and genetic advance analysis in bread wheat (*Triticum aestivum* L.) genotypes. *International Journal of Plant & Soil Science*, **35**(19): 164–172. [\[Cross Ref\]](#)
- FAO. 2025. Wheat outlook report 2024–25. Food and Agriculture Organization of the United Nations, Rome, Italy.
- Gupta, V., Kumar, M., Singh, V., Chaudhary, L., Yashveer, S., Sheoran, R. and Nagpal, S. 2022. Genotype by environment interaction analysis for grain yield of wheat (*Triticum aestivum* L. em. Thell) genotypes. *Agriculture*, **12**(7): 1002. [\[Cross Ref\]](#)
- Havryliuk, I. and Kovalyshyna, H. 2024. Characteristics of soft winter wheat varieties by crop structure and grain quality indicators. *Ukrainian Black Sea Region Agrarian Science*, **28**(4): 68–84. [\[Cross Ref\]](#)

- Husson, F., Josse, J., Le, S. and Mazet, J. 2020. Multivariate exploratory data analysis and data mining. R package version 2.4.
- Kassambara, A. and Mundt, F. 2020. Factoextra: Extract and visualize the results of multivariate data analyses. R package version 1.0.7.
- Kassie, M.M., Abebe, T.D., Desta, E.A. and Tadesse, W. 2025. Multi-environment evaluation of bread wheat genotypes for yield stability in Ethiopia using AMMI and GGE-biplot analyses. *Crop Breeding, Genetics and Genomics*, **7**(2). e250004. [\[Cross Ref\]](#)
- Kaur, A. and Sangha, M.K. 2025. Crop wild relatives (CWRs) a genetic pool for crop improvement: A review. *Agricultural Reviews*, **46**(1): 109–115.
- KC, B., Pandit, R., Maharjan, B., Adhikari, N.R., Poudel, M.R., Thapa, D.B. and Poudel, S. 2025. Genetic parameters, correlation and multivariate analysis of yield and yield components in 30 promising wheat (*Triticum aestivum* L.) genotypes. *International Journal of Agronomy*, **2025**: 3774228. [\[Cross Ref\]](#)
- Kishii, M. 2019. An update of recent use of *Aegilops* species in wheat breeding. *Frontiers in Plant Science*, **10**: 585. [\[Cross Ref\]](#)
- Kumar, S., Kumar, A. and Kumar, J. 2017. Genetic analysis for heterotic traits in bread wheat (*Triticum aestivum* L.) using six parameters model. *Electronic Journal of Plant Breeding*, **8**(1):206-215. [\[Cross Ref\]](#)
- Maechler, M., Rousseeuw, P., Struyf, A., Hubert, M. and Hornik, K. 2023. Cluster: cluster analysis basics and extensions. *R Package Version 2.1. 4*.
- Muhammad, H. K., Mujtaba, H., Khan, M. S., Khan, M. F., Jabeen, N., Shafqat, N. and Rehman, K. U. 2024. Correlation and path analysis for yield and yield linked traits in wheat (*Triticumaestivum* L.). *Pakistan Journal of Biotechnology*, **21**(2): 565-570.
- Mullualem, D., Tsega, A., Mengie, T., Fentie, D., Kassa, Z., Fassil, A. and Astatkie, T. 2024. Genotype-by-environment interaction and stability analysis of grain yield of bread wheat (*Triticum aestivum* L.) genotypes using AMMI and GGE biplot analyses. *Heliyon*, **10**(12). e32918. [\[Cross Ref\]](#)
- R Core Team. stats: Statistical Functions. R package version 4.3.2; 2023. In: R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria Analyses. R package version 1.0.7; 2020.
- Singh, P. K., Singh, L., Singh, S. V., Nath, S., Yadav, V., Mishra, A. and Kuswaha, C. 2023. Estimation of genetic variability, correlation and path analysis for yield and some yield contributing traits in bread wheat (*Triticum aestivum* L.). *International Journal of Environment and Climate Change*, **13**(11): 2429-2440. [\[Cross Ref\]](#)
- Tiwari, V. K., Rawat, N., Neelam, K., Kumar, S., Randhawa, G. S. and Dhaliwal, H. S. 2010. Substitutions of 2S and 7U chromosomes of *Aegilops kotschy* in wheat enhance grain iron and zinc concentration. *Theoretical and Applied Genetics*, **121**(2): 259-269. [\[Cross Ref\]](#)
- Wei, T. and Simko, V. R. 2021. package “corrplot”: Visualization of a Correlation Matrix (Version 0.92). *Package Corrplot for R Software*.
- Zewdu, D., Mekonnen, F. and Geleta, N. 2024. Cluster and principal component analysis for yield and yield-related traits of bread wheat (*Triticum aestivum* L.) genotypes. *AGBIR*, **40**(2): 962-967. [\[Cross Ref\]](#)