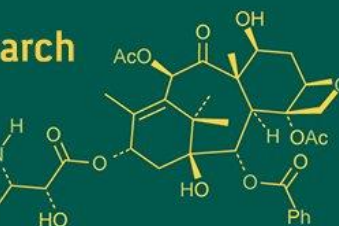
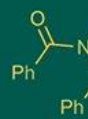


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(8): 2234-2238
www.biochemjournal.com
Received: 16-05-2026
Accepted: 20-06-2026

Shaurya Singh
Department of Genetics and
Plant Breeding, College of
Agriculture, G.B. Pant
University of Agriculture and
Technology, Pantnagar,
Uttarakhand, India

JP Jaiswal
Department of Genetics and
Plant Breeding, College of
Agriculture, G.B. Pant
University of Agriculture and
Technology, Pantnagar,
Uttarakhand, India

Mitali Tiwari
Department of Genetics and
Plant Breeding, College of
Agriculture, G.B. Pant
University of Agriculture and
Technology, Pantnagar,
Uttarakhand, India

Amit Kumar Singh
Division of Genomic
Resources, ICAR-National
Bureau of Plant Genetic
Resources, New Delhi, Delhi,
India

Corresponding Author:
Shaurya Singh
Department of Genetics and
Plant Breeding, College of
Agriculture, G.B. Pant
University of Agriculture and
Technology, Pantnagar,
Uttarakhand, India

Genetic variability, heritability, character association and principal component analysis in indigenous Indian wheat (*Triticum aestivum* L.) germplasm

Shaurya Singh, JP Jaiswal, Mitali Tiwari and Amit Kumar Singh

DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i8Sy.9730>

Abstract

Indigenous landraces retain alleles lost from modern wheat cultivars, but their use in breeding requires prior characterisation. Two hundred indigenous bread wheat (*Triticum aestivum* L.) accessions from the ICAR-National Bureau of Plant Genetic Resources were evaluated over two rabi seasons in an augmented block design, and best linear unbiased predictions were obtained for fifteen agro-morphological and phenological traits. Wide variation was recorded for all traits, the coefficient of variation ranging from 4.08% for days to flowering to 34.72% for biological yield. Broad-sense heritability was high throughout (81.5-97.1%) and was coupled with high genetic advance as per cent of mean for twelve traits, indicating predominantly additive gene action and effective response to phenotypic selection. Grain yield per plot was significantly correlated with biological yield ($r=0.824$), thousand-grain weight ($r=0.232$), grains per spike ($r=0.200$) and plant height ($r=0.196$), while biological yield and harvest index were strongly negatively associated ($r=-0.574$). Principal component analysis extracted six components explaining 80.16% of the variation, PC1 (22.88%) representing a plant-size and spike-architecture axis and PC2 (15.61%) a duration-and-partitioning versus biomass axis. Accessions IC1802, IC1895 and IC1056 are recommended as donors for yield improvement.

Keywords: *Triticum aestivum*, landrace, genetic variability, heritability, genetic advance, correlation, principal component analysis

Introduction

In India, bread wheat (*Triticum aestivum* L., $2n = 6x = 42$) supplies a large share of the calories and protein consumed daily, yet gains from breeding have decelerated, a slowdown traced in large measure to the repeated recycling of a narrow set of elite parents and the consequent erosion of diversity in present-day cultivars (Cavanagh *et al.*, 2013) [4]. Indigenous accessions and landraces held in national gene banks provide one way past this constraint: shaped under low-input, stress-prone cultivation, they retain combinations of phenology, stature and spike architecture that have become uncommon in improved backgrounds (Lopes *et al.*, 2015) [12]. Deploying them, however, requires that the material first be characterised. Reading heritability alongside expected genetic advance reveals whether variation is largely additive and how far selection is likely to shift a trait; inter-trait correlations show which characters can be advanced together and which oppose one another; and principal component analysis isolates those characters accounting for most of the divergence within a collection. The present study was undertaken to assess genetic variability, heritability and genetic advance for fifteen agro-morphological and phenological traits in a panel of 200 indigenous Indian wheat accessions, to determine the pattern of trait association with reference to grain yield, and to identify promising donor accessions.

Materials and Methods

Two hundred indigenous bread wheat accessions (IC997 to IC2131) procured from the National Bureau of Plant Genetic Resources, New Delhi, together with three released check varieties (HD 3086, DBW 88 and WH 1105), were evaluated at the Norman E. Borlaug Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar,

Uttarakhand (29 degrees above mean sea level), during the rabi seasons of 2023-24 and 2024-25. The trial followed an N, 79 degrees E, 243.8 m augmented block design (Federer, 1956) ^[5], the 200 test accessions being distributed unreplicated over ten blocks each season with the three checks repeated in every block, giving 230 plots per season. Each plot measured 1 m² and was sown at a seed rate of 100 kg/ha under the recommended package of practices for timely-sown irrigated wheat.

Fifteen agro-morphological and phenological traits were recorded: days to heading, flowering and maturity and grain filling duration; plant height, peduncle length, spike length, spikelets per spike, leaf length and leaf breadth; and grains per spike, thousand-grain weight, grain yield per plot, biological yield and harvest index.

Best linear unbiased predictions of genotypic values were obtained from a linear mixed model with genotype random and block-within-season fixed using lme4 (Bates *et al.*, 2015) ^[2] in R (R Core Team, 2023); prediction of genotypic values as BLUPs is appropriate where test entries are unreplicated, shrinkage towards the population mean improving the precision with which genotypes are ranked (Piepho *et al.*, 2008). Broad-sense heritability was computed as the ratio of genotypic to total phenotypic variance, genotypic and phenotypic coefficients of variation were expressed as percentages of the trait mean (Burton and Devane, 1953) ^[3], and expected genetic advance was calculated at 5% selection intensity ($k = 2.06$) and expressed as per cent of mean (Johnson *et al.*, 1955) ^[7]. Pearson correlations among all 105 trait pairs were estimated from the adjusted entry means (Singh and Chaudhary, 1985) ^[16], and principal component analysis was performed on the standardised matrix of adjusted entry means, components with eigenvalue exceeding unity being retained and the ordination visualised with factoextra (Kassambara and Mundt, 2020) ^[18].

Results and Discussion

Variability, heritability and genetic advance

All fifteen traits showed wide variation (Table 1). Days to maturity spanned 106.55 to 145.22 days, a difference of nearly six weeks in crop duration, and plant height 53.56 to

173.82 cm, reflecting the coexistence of tall traditional types and semi-dwarf introductions. Grain yield per plot varied nearly twelve-fold across the panel (0.083-0.982 kg), and biological yield close to sixteen-fold. Days to flowering returned the smallest coefficient of variation (4.08%), whereas biological yield (34.72%) and grain yield per plot (26.63%) returned the largest, indicating that phenological characters were the most strongly buffered against environment and yield-related characters the most plastic. Skewness was close to zero for most traits, indicating approximately normal distributions typical of polygenic inheritance.

Estimates of broad-sense heritability spanned 81.5% for days to maturity to 97.1% for biological yield, ten traits exceeding 90%, among them grain yield per plot, thousand-grain weight, plant height, peduncle length and spike length. Since these estimates derive from BLUP variance components pooled over two seasons with block effects removed, genotype-by-environment interaction was not separately partitioned; they represent an upper bound on the repeatability of genotypic ranking rather than narrow-sense estimates. For every trait the phenotypic coefficient of variation was the larger of the two, though never by a wide margin, so that environment contributed comparatively little to the expression observed. Twelve traits combined high heritability with high genetic advance as per cent of mean, a joint pattern conventionally read as evidence of additive control, including biological yield (97.1, 72.3), grain yield per plot (93.7, 55.2), harvest index (87.6, 33.4), grains per spike (92.0, 32.8), leaf breadth (91.1, 32.8), thousand-grain weight (94.2, 32.7) and peduncle length (94.3, 31.7); for these, selection on phenotype alone should prove productive; the same joint pattern has been recorded previously in Indian bread wheat material (Kumar *et al.*, 2019). Days to heading, days to flowering and days to maturity behaved otherwise, pairing high heritability with low genetic advance (7.5 to 18.8%), a combination usually taken to reflect non-additive control together with a restricted range of variation.

Table 1: Mean, range, variability and genetic parameters for fifteen agro-morphological traits in 200 indigenous wheat accessions evaluated over two rabi seasons

Trait	Mean	Range	CV (%)	h ² _{bs} (%)	GCV (%)	PCV (%)	GAM (%)
Days to heading (d)	79.32	59.28-91.28	9.48	95.3	9.15	9.60	18.83
Days to maturity (d)	125.38	106.55-145.22	5.61	81.5	4.99	6.02	10.10
Grain filling duration (d)	38.96	25.62-55.28	16.00	88.7	14.63	16.39	29.94
Days to flowering (d)	86.42	76.10-94.93	4.08	84.5	3.66	4.28	7.46
Plant height (cm)	109.08	53.56-173.82	15.35	94.5	14.65	15.47	30.12
Peduncle length (cm)	37.86	22.13-57.31	16.05	94.3	15.40	16.30	31.68
Spike length (cm)	11.32	7.12-16.26	15.83	93.2	15.00	16.06	30.83
Spikelets per spike	18.02	11.72-24.88	16.00	93.5	15.32	16.35	31.49
Leaf length (cm)	27.55	15.76-38.51	15.80	89.0	14.80	16.54	30.31
Leaf breadth (cm)	1.85	0.99-2.81	16.76	91.1	15.98	17.47	32.80
Grains per spike	43.55	25.67-62.33	16.82	92.0	15.99	17.31	32.83
1000-grain weight (g)	38.50	19.22-55.87	16.62	94.2	15.91	16.86	32.71
Grain yield per plot (kg)	0.54	0.08-0.98	26.63	93.7	26.87	28.63	55.24
Biological yield (kg)	1.35	0.19-3.21	34.72	97.1	35.10	36.14	72.28
Harvest index (%)	41.29	26.39-52.70	18.17	87.6	16.34	18.51	33.41

CV = coefficient of variation; h²_{bs} = broad-sense heritability; GCV, PCV = genotypic and phenotypic coefficients of variation; GAM = genetic advance as per cent of mean at 5% selection intensity.

Character association

Of the 105 trait pairs examined, 41 were significant at $p < 0.05$ and 35 at $p < 0.01$ (Figure 1). The strongest association involving grain yield per plot was with biological yield ($r = 0.824$), which identifies total biomass accumulation as the principal determinant of yield in this panel; yield was additionally correlated with thousand-grain weight ($r = 0.232$), grains per spike ($r = 0.200$) and plant height ($r = 0.196$) (Table 2). Biomass therefore predicted yield far better than any single component did, implying that within this collection it is variation in how much assimilate a plant captures, rather than how that assimilate is later apportioned among spike components, that separates the accessions.

Harvest index bore no relation to grain yield ($r = -0.053$) while standing in strong opposition to biological yield ($r = -0.574$). Such a configuration is characteristic of landrace collections, where tall high-biomass forms divert proportionally less dry matter into grain while dwarf forms partition efficiently from a smaller biomass base; improvement must therefore address biomass and partitioning together rather than either in isolation, consistent with the view that further gains in wheat yield

potential will depend more on raising total biomass than on further increases in partitioning (Reynolds *et al.*, 2009); in tall material of this kind the scope for improving partitioning is further limited by the need to maintain lodging resistance (Foulkes *et al.*, 2011). Days to maturity was strongly correlated with grain filling duration ($r = 0.866$) and days to heading with days to flowering ($r = 0.793$), while grains per spike was correlated with spikelets per spike ($r = 0.729$) and spike length ($r = 0.553$), so that spike architecture behaves as one coherent unit for improvement. Plant height and peduncle length were likewise associated ($r = 0.529$), reflecting the contribution of internode elongation to overall stature.

Table 2: Characters showing significant association with grain yield per plot

Trait	r	p-value	Significance
Biological yield (kg)	0.824	<0.0001	**
1000-grain weight (g)	0.232	0.0009	**
Grains per spike	0.200	0.0045	**
Plant height (cm)	0.196	0.0055	**

** significant at $p < 0.01$; * significant at $p < 0.05$.

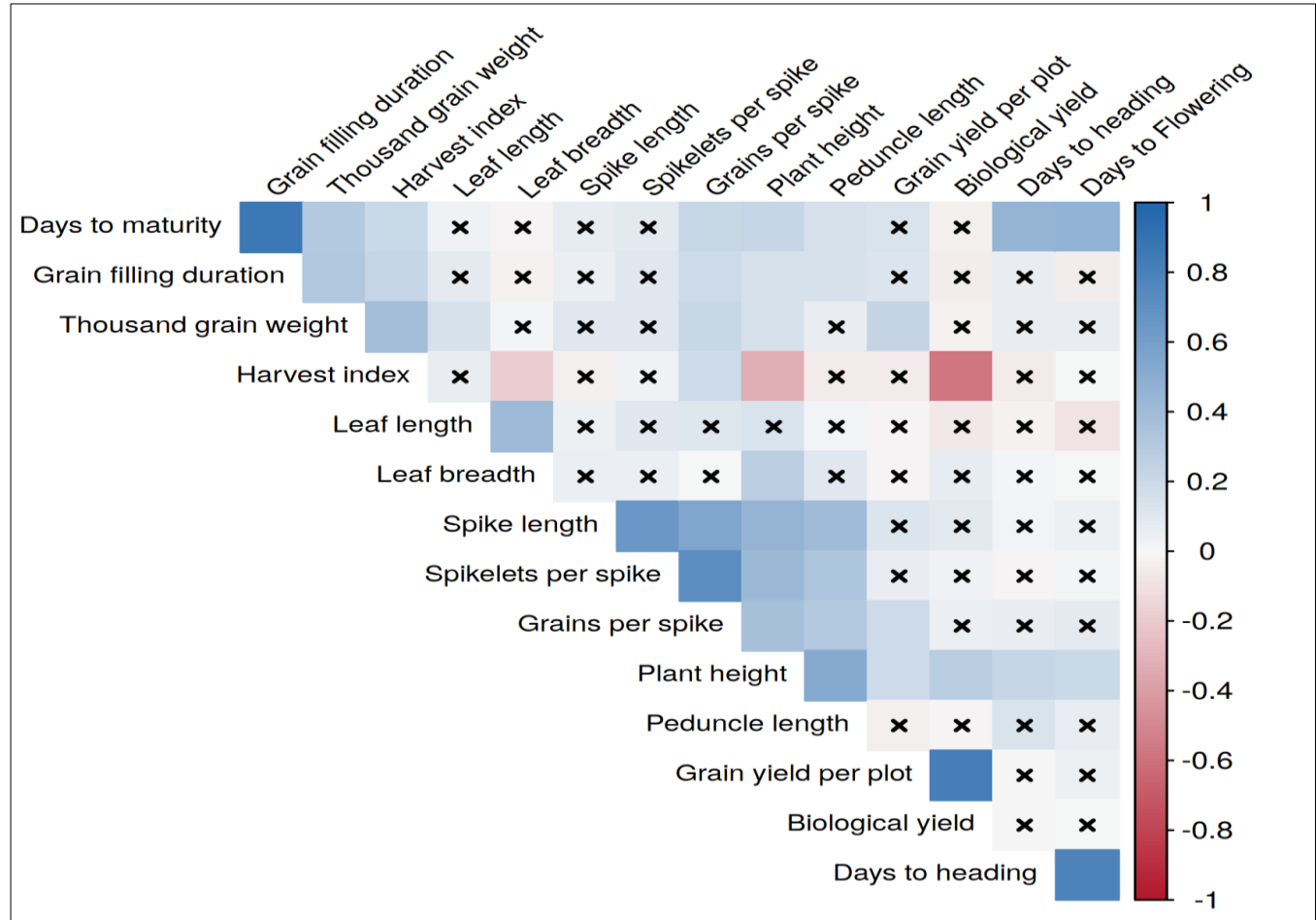


Fig 1: Pearson correlation matrix among fifteen agro-morphological traits. Blue denotes positive and red negative correlation, shading intensity being proportional to the coefficient; crossed cells are not significant at $p < 0.05$.

Principal component analysis and promising accessions

Six components had eigenvalue exceeding unity and together accounted for 80.16% of the total variation, the first two explaining 22.88% and 15.61% and the first five 72.99%. That six axes are required, none of them dominant, indicates that variation in this collection is dispersed across

several largely independent dimensions rather than organised around a single gradient of productivity. Such dispersal is characteristic of a genetically broad, unselected germplasm set; in elite breeding panels, where directional selection has aligned many characters and eroded diversity at numerous loci (Cavanagh *et al.*, 2013) ^[4], the first

component commonly absorbs a considerably larger share of the variance. Dispersion of a similar order characterised 74 landraces drawn from Pakistan and Central Asia, where PC1 and PC2 jointly captured 48.59%, again under half the total (Khan *et al.*, 2025) ^[10], and six components with eigenvalue exceeding unity were likewise required to account for 78.47% of the variation among 22 durum wheat landraces scored for sixteen descriptors (Almarri *et al.*, 2023) ^[10]. For the breeder the dispersion is itself informative, since it implies that accessions cannot be ranked along any one axis of merit and that complementary parents must be sought on several axes simultaneously. It is equally favourable for association mapping, the several independent dimensions offering distinct targets for marker-trait analysis.

PC1 was dominated by grains per spike (-0.391), plant height (-0.389), spikelets per spike (-0.368), spike length (-0.358), days to maturity (-0.314) and peduncle length (-0.303), all loading in the same direction, and therefore represents an axis of general plant size and spike architecture: accessions at one extreme are tall and long-spiked with numerous spikelets and grains and mature late, while those at the other are short, small-spiked and early. An equivalently undifferentiated first component, carrying loadings of the same sign for every character and receiving its largest contribution from spike length, was recovered from 77 wheat genotypes scored for six agro-morphological traits (Khalid *et al.*, 2023) ^[9], suggesting that a composite size axis of this kind is a general feature of morphologically diverse wheat collections. Harvest index was almost orthogonal to this axis (-0.017), showing that size and partitioning efficiency vary independently in this material and that a large plant type carries no necessary penalty in the proportion of biomass converted to grain. PC2 separated harvest index (0.432), days to maturity (0.416), grain filling

duration (0.337) and thousand-grain weight (0.229) from biological yield (-0.415), grain yield per plot (-0.214), plant height (-0.211) and spike length (-0.197), and thus contrasts long-duration accessions that fill grain slowly and partition efficiently with vigorous high-biomass accessions of greater stature. The opposition of harvest index and biological yield on this axis restates the negative correlation between the two in multivariate form, confirming it as a structural feature of the panel rather than an artefact of any single pair of measurements.

PC3 (13.50%) set days to heading (0.412), days to flowering (0.410) and biological yield (0.407) against harvest index (-0.324) and spikelets per spike (-0.307), isolating a late-flowering, high-biomass, low-partitioning syndrome. PC4 (11.35%) was defined by grain yield per plot (0.512), grain filling duration (0.339), biological yield (0.334) and thousand-grain weight (0.328) opposed to days to heading (-0.358) and days to flowering (-0.347), and is agronomically the most interesting of the minor axes, describing accessions that flower early, fill grain over an extended period and combine heavy grain with high yield. Because this combination is expressed independently of the size axis captured by PC1, it can in principle be recombined with the large-spike phenotype without the two objectives competing. The distribution of accessions in the PC1-PC2 biplot (Figure 2) was broad and continuous, without discrete clustering, indicating a gradational spread of trait combinations rather than distinct morphological groups; accessions lying at the extremes, among them IC1942 and IC1924 at the large-plant end of PC1 and IC1018 and IC1662 at the opposite end, are the most divergent and therefore the most promising parents for hybridisation, while pairs drawn from opposite quadrants of the PC1-PC2 plane are divergent in both size and partitioning simultaneously.

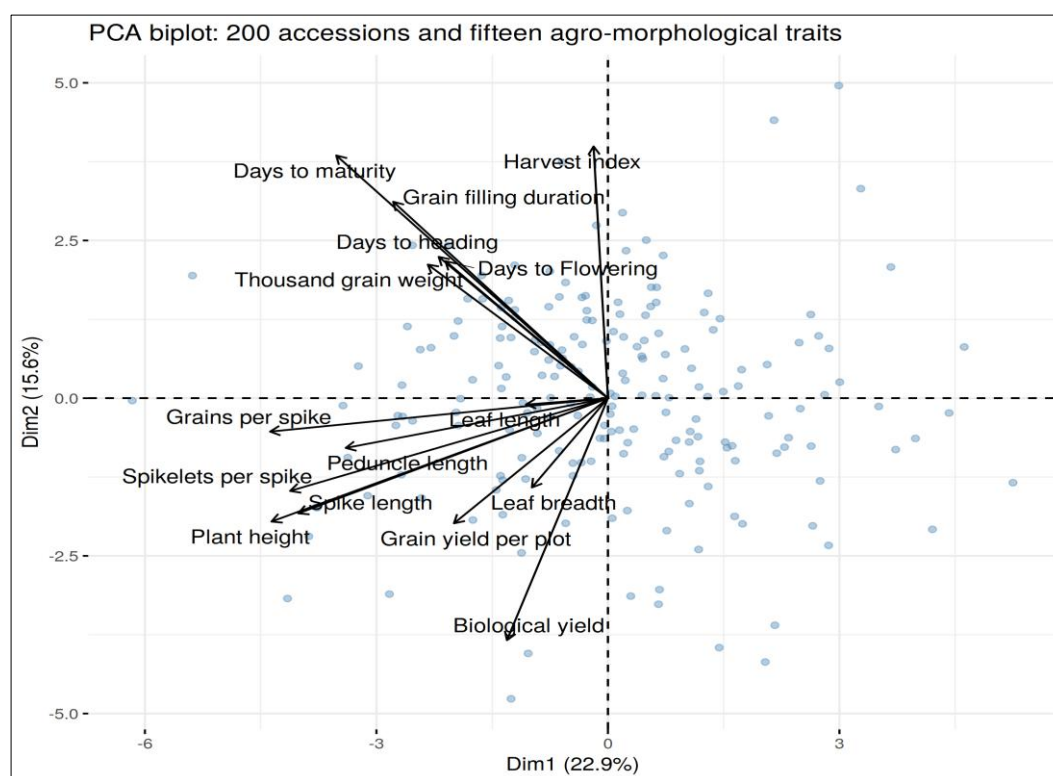


Fig 2: Ordination of the 200 accessions (points) and the fifteen traits (vectors) on PC1 and PC2.

Ranked on across-season BLUP values, IC1802 and IC1895 led for grain yield per plot (1.000 and 0.965 kg), each pairing biological yield above 3.0 kg with a moderate harvest index; IC1048 (0.907 kg) and IC1237 (0.884 kg) followed. IC1056 reached 0.855 kg from a comparatively modest biological yield (2.015 kg) by virtue of the highest harvest index in the group (42.95%), a complementary route to the same end; a cross of IC1895 with IC1056 would therefore bring biomass and partitioning together, and transgressive segregants might reasonably be anticipated. The same contrast is recoverable from the ordination, IC1802 and IC1048 lying towards the low-PC2 extreme that characterises high-biomass types, so that selection guided by the biplot and selection on yield per se converge on the same complementary parents.

Conclusion

The panel of 200 indigenous Indian wheat accessions harbours substantial and largely heritable variation for phenological, morphological and yield-attributing traits. High broad-sense heritability coupled with high genetic advance for twelve traits indicates predominantly additive gene action, so that direct phenotypic selection would be effective. Grain yield was governed primarily by biological yield and secondarily by thousand-grain weight, grains per spike and plant height, while the negative association between biological yield and harvest index indicates that biomass and partitioning must be targeted jointly. Principal component analysis resolved the variation into six independent axes, the first describing plant size and spike architecture and the second duration and partitioning, and showed the collection to be continuously rather than discretely structured. Accessions IC1802, IC1895 and IC1056 are recommended as donors for yield improvement. The magnitude of variation and the broad multivariate spread establish this panel as well suited to genome-wide association analysis.

Acknowledgements

The authors acknowledge the ICAR-National Bureau of Plant Genetic Resources, New Delhi, for providing the wheat germplasm and the Director of Research, G.B. Pant University of Agriculture and Technology, Pantnagar, and the Department of Genetics and Plant Breeding for providing field and laboratory facilities.

Conflict of Interest

The authors declare that they have no conflict of interest.

References

1. Almarri NB, Alghamdi SS, ElShal MH, Afzal M. Estimating genetic diversity among durum wheat (*Triticum durum* Desf.) landraces using morphological and SRAP markers. *J Saudi Soc Agric Sci*. 2023;22:273-282.
2. Bates D, Mächler M, Bolker B, Walker S. Fitting linear mixed-effects models using lme4. *J Stat Softw*. 2015;67(1):1-48.
3. Burton GW, Devane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron J*. 1953;45(10):478-481.
4. Cavanagh CR, Chao S, Wang S, Huang BE, Stephen S, Kiani S, *et al*. Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. *Proc Natl Acad Sci U S A*. 2013;110(20):8057-8062.
5. Federer WT. Augmented designs. *Hawaiian Planters Rec*. 1956;55:191-208.
6. Foulkes MJ, Slafer GA, Davies WJ, Berry PM, Sylvester-Bradley R, Martre P, *et al*. Raising yield potential of wheat. III. Optimizing partitioning to grain while maintaining lodging resistance. *J Exp Bot*. 2011;62(2):469-486.
7. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. *Agron J*. 1955;47(7):314-318.
8. Kassambara A, Mundt F. factoextra: Extract and Visualize the Results of Multivariate Data Analyses. R package version 1.0.7. 2020.
9. Khalid A, Hameed A, Tahir MF. Estimation of genetic divergence in wheat genotypes based on agromorphological traits through agglomerative hierarchical clustering and principal component analysis. *Cereal Res Commun*. 2023;51(1):217-224.
10. Khan S, Ali N, Khan FU, Din IU, Amjad M, Ahmad I. Genetic diversity in wheat landraces for agronomic traits and yellow rust resistance. *Genet Resour Crop Evol*. 2025;72(5):6165-6179.
11. Kumar J, Kumar A, Kumar M, Singh SK, Singh L. Assessment of genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.) genotypes. *J Pharmacogn Phytochem*. 2019;8(1):206-209.
12. Lopes MS, El-Basyoni I, Baenziger PS, Singh S, Royo C, Ozbek K, *et al*. Exploiting genetic diversity from landraces in wheat breeding for adaptation to climate change. *J Exp Bot*. 2015;66(12):3477-3486.
13. Piepho HP, Möhring J, Melchinger AE, Büchse A. BLUP for phenotypic selection in plant breeding and variety testing. *Euphytica*. 2008;161(1-2):209-228.
14. R Core Team. R: A Language and Environment for Statistical Computing. Vienna, Austria: R Foundation for Statistical Computing; 2023.
15. Reynolds M, Foulkes MJ, Slafer GA, Berry P, Parry MAJ, Snape JW, *et al*. Raising yield potential in wheat. *J Exp Bot*. 2009;60(7):1899-1918.
16. Singh RK, Chaudhary BD. Biometrical Methods in Quantitative Genetic Analysis. New Delhi, India: Kalyani Publishers; 1985.