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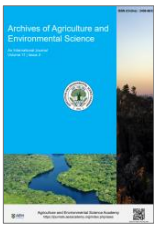

Original Research Article

Identification of high-performing wheat landraces using morphological characterization and multi-trait genotype-ideotype distance index

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ABSTRACT

Wheat landraces are an invaluable source of germplasm for developing climate-resilient and high-yielding cultivars. To characterize morphological diversity and select superior wheat landraces using the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) to maximize genetic gain and productivity, 58 wheat landraces from across Nepal were studied in a randomized complete block design for 12 qualitative and 19 quantitative traits at Khumaltar, Nepal. We analyzed quantitative traits using linear mixed models to estimate broad-sense heritability and Best Linear Unbiased Predictors (BLUPs). MGIDI at 15% selection intensity was computed based on the Euclidean distance of each landrace from an ideal ideotype for multi-trait selection, and the results were compared with FAI-BLUP and two Smith-Hazel indices. Significantly high Shannon-Weaver diversity was observed in qualitative traits, guiding selection. Pronounced genotypic differences and high broad-sense heritability (h^2 = 0.89-1.00; $p<0.001$) were observed for most quantitative traits. Factor analysis revealed six factors explaining 80.34% of the total variation. MGIDI successfully identified nine elite landraces with desirable gains, with maximum selection gains obtained for spike length (30.12%) and grain yield (15.57%). MGIDI showed a perfect coincidence index (CI=100%) with FAI-BLUP but substantially lower coincidences with Smith Hazel indices. Four genotypes, G41 (NGRC-7819), G34 (NGRC-7615), G22 (NGRC-6554), and G31 (NGRC-7586), were selected concurrently in the study across all four indices and are recommended for further study. Overall, the findings highlight MGIDI as an effective, reliable, and data-driven approach for selecting and leveraging wheat germplasm to develop climate-resilient varieties to ensure food security.

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INTRODUCTION

Wheat is one of the oldest staple crops and the second most produced crop in the world, with an average global production of 844.15 million metric tons (FAOSTAT, 2026). Wheat has undergone a series of domestication events from an early diploid (genome AA) (einkorn type) to tetraploid (genome AABB) (emmer type) and later to hexaploid cultivars (Heun *et al*., 1997; Dubcovsky & Dvorak, 2007). The development of the earliest cultivated forms of wheat, known as landraces, was an important part of this evolutionary trajectory, characterized by non-shattering, free-threshing, naked spike, and, more importantly, their broad adaptation to local environmental stresses (Shewry, 2009). Furthermore, these landraces exhibit exceptional genetic diversity for abiotic stress tolerance (drought, salt, cold, and heat) and biotic stress resistance, which enhances their adaptation to diverse environmental conditions (Özkan *et al*., 2011; Khan *et al*., 2013). Wheat is unrivalled in its range of cultivation and trait diversity (Shewry, 2009). Historically, landraces have been an indispensable source of gene pools for modern agriculture; notably, the *Norin 10* Japanese wheat landrace, originating from Shiro Daruma, provided the critical

gene for reduced height (*Rht*) dwarfing gene, which drove the Green Revolution (Reitz & Salmon, 1968; Dreisigacker *et al.*, 2005; Royo & Briceño-Félix, 2011). Thus, characterizing wheat landraces is crucial for the selection of suitable lines as donors of desirable traits for breeding high-yielding, climate-resilient cultivars (Gurcan *et al.*, 2017). Elite lines are desirable genotypes with both morphological and physiological traits that contribute to maximizing yield and quality (Donald, 1968). Elite crops are selected with the objective of combining presumably low-frequency alleles with known economic importance (Lyu *et al.*, 2013). Multiple studies have supported that features like leaf erectness, reduced leaf area, and height in wheat boost the yield potential (Bugbee & Koerner, 1997). Breeding of such elite lines helps in the accumulation of beneficial traits in one variety, which helps to meet the current need for improved crops. Genetic improvement has been continuously playing a fundamental role in crop improvement and will continue to do so in the future (Paramasivam *et al.*, 2025). The objective of crop improvement can only be attained with the selection and breeding of elite lines based on their desirable traits.

The rapid expansion of the global population and urbanization has urged the immediate need for a sustainable and improved production approach to ensure food security. Climate change-induced drought and altered rainfall patterns have been impacting the agricultural system by altering crop phenology and increasing the incidence of insect pests in wheat, thereby limiting productivity and threatening food security and sustainability (Nalley *et al.*, 2018). Therefore, an increasing interest has been observed in harnessing and selecting elite wheat landraces for the development of climate-resilient cultivars with high yield and nutritional quality. However, the use of landrace diversity in conventional breeding is a challenge for an effective assessment and utilization of this diversity. Traditionally, crop selection has been based on a univariate strategy using only yield, overlooking other undesirable traits and not considering trait interactions, environmental interactions, or underlying polygenic architectures (Paramasivam *et al.*, 2025). Yield has a complex nature, as it is influenced by multiple ideotype morphological and physiological traits and is a quantitative trait (Donald, 1968; Bugbee & Koerner, 1997), so crop selection cannot be done based on yield alone. This results in improvement of one trait at the expense of others, thereby limiting progress in developing resilient cultivars (Lyu *et al.*, 2013). MGIDI, FAIBLUP, and Smith-Hazel are advanced tools designed to achieve joint selection for several desirable traits (Entringer *et al.*, 2016; Coutinho *et al.*, 2019). Nevertheless, Smith-Hazel (SH) indexes are classical linear indices that often face severe multicollinearity among correlated traits and require subjective assignment of arbitrary economic weights, resulting in biased estimates of genetic gain (Smith, 1936; Bizari *et al.*, 2017). This study used the multi-trait genotype ideotype distance index (MGIDI), a novel tool that uses factor analysis and linear mixed models (BLUPs) to evaluate genotypes by measuring their Euclidean distance from an ideal ideotype without assigning economic weight to the traits (Olivoto & Nardino, 2019b; 2021). While various crops have been extensively studied under MGIDI, its application to wheat landraces is yet to be researched and remains unexplored (Farhad *et al.*, 2022). Nepalese wheat landraces are an important but underused source of climate-resilient alleles. Despite the potential, there is a clear gap in studies that recognize the need to use the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) to screen local wheat landraces systematically and validate whether the performance of the index actually outperforms conventional approaches.

Therefore, bridging this gap is crucial to sustain wheat production amid rapid population growth, climate fluctuations, and geopolitical threats to food security (Chapagain *et al.*, 2025). Therefore, this study was conducted with the main objective of assessing the variation in qualitative and quantitative traits of the diverse set of Nepalese wheat landraces for selecting elite landraces by using MGIDI to maximize the selection response and expected gains of the traits and to compare the coincidence and efficiency of selection of elite landraces by MGIDI, FAIBLUP, and the Smith-Hazel index to establish a better system for the selection of elite landraces (Céron-Rojas & Crossa, 2018).

MATERIALS AND METHODS

Experimental site

The research aimed at characterizing and identifying the best-performing wheat landraces was conducted in the experimental plot of the National Agriculture Genetic Resource Centre (NAGRC), Khumaltar, Lalitpur, Nepal, situated in the subtropical mid-hill region at an altitude of 1368 m, at 27°42´N latitude, and 85°20´E longitude. The experiment was carried out during the winter season of 2025. The soil at the research site was loamy clay, with a pH range of 5-7.

Methodology

A total of 58 wheat landraces representing diverse agro-ecological regions of Nepal were evaluated to characterize morphological variation and to capture genotype × environment interactions using a randomized complete block design with three replications. Each plot measured 3 m in length and 1.5 m in breadth, comprising six rows of plants with row-to-row spacing of 25 cm and plant-to-plant spacing of 10 cm, covering a total area of 4.5 m^2. Adjacent plots were separated by 50 cm. FYM was incorporated at the recommended dose of 6 t/ha, 10 days prior to land preparation. NPK was applied at a rate of 100:50:50 Kg/ha^{-1}. This structured approach ensured the adequate and timely availability of all the necessary nutrients and water during critical growth periods. Weeding was performed manually three times, first at 35 days after sowing, and subsequently at 15-day intervals. Irrigation was also provided, taking the critical period into account. No chemical measures were used for insect or weed control, to facilitate the identification of true ideotypes.

Data collection

Data on twelve qualitative and nineteen quantitative traits of wheat were collected and recorded based on the wheat descriptor developed by the International Board for Plant Genetic Resources (1989) at an appropriate stage for each trait. Data were collected from five plants, selected randomly from each plot, excluding border plants. Qualitative traits observed at respective growth stages were growth habit, leaf color, anther color, awedness, glume color, glume hairiness, spike density, lodging resistance, seed color, seed surface, seed shape, and seed size. The nineteen quantitative traits assessed were days to emergence (DTE), days to 1st (DT1H) and 50% heading (DT50H), days to flowering (DTF), days to maturity (DTM), flag leaf length (FLL), flag leaf width (FLW), plant height (PH), peduncle length (PL), spike exertion (SE), spike length (SL), number of spikelets per spike (SKPS), number of seeds per spikelet (SDPSK), number of seeds per spike (SDPS), seed length (SDL), seed width (SDW), seed thickness (SDT), hundred grain weight (HGW), and grain yield (GY).

Data analysis

Distribution and Shannon-Weaver diversity estimation of qualitative traits

Qualitative traits were subjected to frequency, percentage distribution, and the Shannon-Weaver diversity index (H'), to quantify diversity prior to selection among landraces, using Microsoft Excel 2016. The standardized Shannon-Weaver Diversity Index was calculated (Shannon & Weaver, 1949) using the formula in equation (1):

$$H' = [\Sigma(n/N) * Log2(n/N) * (-1)]/log2k \quad (1)$$

Where (H' is the standardized Shannon-Weaver diversity index, (K) is the number of phenotypic classes for a particular trait, (n) is the frequency of a phenotypic class of that trait, and (N) is the number of observations for that trait.

Mixed-Model Analysis and BLUP Estimation

The identification of superior landraces was based entirely on quantitative traits. These traits were analyzed using a linear mixed-effects model (Olivoto & Lucio, 2020) using equation (2):

$$y = Xb + Zu + e \quad (2)$$

Where y is the observed values of the trait, b is the block effect, u is the genotype effect, e the is random error, and X and Z are design matrices. Best Linear Unbiased Predictors (BLUP) for each genotype were obtained using this model analysis and were organized into a table with 58 rows (genotypes) and 19 columns (trait). The gamem () and get_model_data () functions of the metan package were used for mixed model analysis in R 4.00 software (Olivoto & Lucio, 2020). Genetic and residual variances were estimated using Restricted Maximum Likelihood (REML), and their significance was statistically tested using the Likelihood Ratio Test (LRT) (Olivoto & Nardino, 2021).

Broad-sense heritability (h^2) was subsequently calculated (Buntaran *et al.*, 2020), equation 3:

$$h2 = (\sigma^2 g)/(\sigma^2 p) \quad (3)$$

Where σ^2g is genotypic variance, and σ^2p is phenotypic variance.

Multi-trait genotype-ideotype distance index

As a first step, all traits were scaled to a 0–100 range (Olivoto *et al.*, 2019a, b). The rescaled value for the *j*th trait of *i*th genotype (rX_{ij}) was generated using equation (4):

$$rXij = (\eta nj - \phi nj)/(\eta oj - \phi oj) \times (\theta ij - \eta oj) + \eta nj \quad (4)$$

and are the new maximum and minimum values after rescaling, while are the original maximum and minimum values for the *j*th trait of the *i*th ideotype. = 0 and was for the traits desiring lower values (DTE, DTH, PH, PL, SE), in contrast, = 100 and was used for high-value-desiring traits such as HGW and GY). To reduce dimensionality and group correlated traits into factors, factor analysis (FA) was employed (Norman *et al.*, 2022) using equation (5):

$$F = Z(ATR - 1)T \quad (5)$$

F is a *g* × *f* matrix of factorial scores. Z is a *g* × *p* matrix with the standardized means (rX), A is a *p*×*f* matrix of loadings, and F is a genotype × factors matrix of factorial scores, and R is a *p*×*p* correlation matrix between the traits. *g*, *f*, and *p* refer to the number of genotypes, factors retained, and analyzed traits, respectively. Each of the 58 genotypes received a score on each factor. An ideotype was then defined, providing a maximum value (100) for positively desired traits and a minimum (0) for negatively desired traits. The last step was the estimation of the multi-trait genotype-ideotype distance index (MGIDI) as suggested by Olivoto & Nardino (2021) using equation (6).

$$\text{MGIDI}_i = \sum_{j=1}^{f} \left[(\gamma_{ij} - \gamma_j)^2\right]^{0.5} \quad (6)$$

γ_{ij} is the score of the ith genotype in the jth factor, and γ_j is the jth score of the ideotype. ω_{ij}, the jth factor, explained the MGIDI index proportion and was computed using equation (7) (Olivoto & Nardino, 2021).

$$\omega ij = \sqrt{(D_i j^2)}/(_(j = 1)^f \sqrt{(D_i j^2)}) \quad (7)$$

Where D_{ij} is the distance between the *i*th genotype and the ideotype for the *j*th factor.

Selection gain and index benchmarking

Selection gain was estimated for each trait based on 15 % selection intensity (Paramasivam *et al.*, 2025) using equation (8).

$$SG(\%) = \left(\frac{(X_s - X_o) \times h^2}{X_o}\right) \times 100 \quad (8)$$

is the mean of the selected genotypes, is the mean of the original population, and h^2 is the broad-sense heritability. MGIDI was benchmarked with two alternative selection indices. So, the FAIBLUP Index was calculated by using the function "fai_blup ()" in metan (Norman *et al.*, 2022) based on equation (9).

$$P_{ij} = \frac{\frac{1}{d_{ij}}}{\sum_{i=1}^{n}\sum_{j=1}^{m}\frac{1}{d_{ij}}} \quad (9)$$

Where d_{ij} is the standardized Euclidean distance between defined ideotypes and P_{ij} is the spatial probability. The Smith-Hazel (SH) index was evaluated using Smith_Hazel () in metan (Smith, 1936; Hazel, 1943) via equation (10):

$$b = P - 1Gw \quad (10)$$

Where b is a vector of index coefficients, P is the phenotypic variance-covariance matrix, and G is the genetic variance-covariance matrix; w is the economic weight, and w = +1 was assigned for positive selection traits and -1 for negative selection traits, respectively. During the selection, all 19 traits were integrated by SH-1, while multicollinear traits were excluded in SH-2 using non_collinear_vars () in metan according to Hamblin & Zimmerman (1986). Lastly, the coincidence index (CI) was computed using the formula in equation (11).

$$CI = (A - C)/(M - C) \times 100 \quad (11)$$

Here, A is the number of common genotypes selected between two indices, M is the total number of genotypes selected, and C

is the number of genotypes selected as an outcome of random chance at 15% selection intensity (M×0.15).

RESULTS AND DISCUSSION

Analysis of diversity based on qualitative traits

The phenotypic diversity of 12 qualitative traits was evaluated using the Shannon-Weaver diversity index (H'), as shown in Table 1. Most traits revealed substantial diversity, indicating ample genetic variability within the germplasm conserved at the National Agriculture Genetic Resource Centre (NAGRC). The estimate of Shannon-Weaver diversity indices (H') reflects both richness and evenness of the phenotypic classes for each trait. Anther color exhibited the highest diversity (H'=1.22), followed by growth habit, spike density, seed color, and seed shape (all with H' > 0.85), highlighting the importance of qualitative traits in the differentiation of wheat genotypes. These findings are consistent with Karkee *et al.* (2023). In contrast, no diversity was observed for seed shape and seed surface, and relatively low diversity was obtained for glume color (H' = 0.42) as well as for lodging resistance (0.48). The diversity pattern of these traits reflected a substantial influence of natural selection pressure, emphasizing breeders to identify desirable genotypes for targeted breeding, conservation, and sustainable use (Haque *et al.*, 2021).

Analysis for selection of elite lines based on quantitative traits

Variance components

The chi-square (χ^2) statistical likelihood ratio test ($p < 0.001$) across all 19 quantitative traits showed significant genotypic variance (Table 2), indicating that the traits met the predefined criteria for efficient selection. Genotypic variance ($\sigma^2 g$) accounted for most of the variance, ranging from 72.5% for days to emergence (DTE) to 99.0% for seed thickness (SDT). Broad-sense heritability (h^2) was high, ranging from 0.89 for days to ear emergence (DTE) to 1.00 for spike length (SL). Consistent with high genotypic variance, the genotypic-to-residual coefficient of variation (CVg/CVr) exceeded one for most traits (1.63 to 9.33), suggesting a favorable environment for selection (Olivoto & Lúcio, 2020). High heritability was observed for phenological traits, such as DT1H, DT50H, DT1F, and DTM (h^2 = 0.99), which is significant given the critical role of day length and temperature conditions in wheat breeding (Hickey *et al.*, 2019).

Table 1. Frequency of different categories of qualitative traits observed in wheat accessions.

S. No.	Variables	Descriptive score	Frequency	Percentage (%)	H'
1	Growth habit	3 Upright	34	58.62	0.87
		5 Intermediate	9	25.86	
		7 Prostrate	15	15.52	
2	Leaf color	3 Light green	14	24.14	0.81
		5 Green	7	12.07	
		7 Dark green	37	63.79	
3	Anther color	3 Purple	9	15.52	1.22
		5 yellow	49	84.48	
4	Spike density	1 Very Lax	0	0	0.99
		3 Lax	19	32.76	
		5 Intermediate	23	39.66	
		7 Dense	15	25.86	
		9 Very dense	0	0	
5	Awedness	7 Awned	38	65.52	0.78
		3 Awnletted	6	10.34	
		0 Awnless	14	24.14	
6	Glume color	1 White	53	91.38	0.42
		2 Red to brown	5	8.62	
		3 Purple to black	0	0	
7	Glume hairiness	0 Absent	35	60.34	0.85
		3 Low	9	15.52	
		7 High	14	24.14	
8	Lodging resistance	0 Resistance	49	84.48	0.48
		L Low	3	5.17	
		M Medium	6	10.34	
9	Seed color	1 White	33	56.90	0.99
		2 Red	0	0	
		3 Purple	25	43.10	
10	Seed surface	1 Rough	58	100	0.00
		2 Smooth	0	0	
11	Seed size	3 Small	16	27.59	0.81
		5 Intermediate	36	62.07	
		7 Large	6	10.34	
12	Seed shape	5 Ovate	34	58.62	0.98
		7 Elliptical	24	41.38	
		3 Round	0	0	

Table 2. Estimated variance components, heritability estimates, and genetic parameters for 19 traits studied in 58 wheat genotypes.

Variable	σ^2g	σ^2r	σ^2p	h^2	CVg	CVr	CVg/CVr	Pr(>Chisq)
DTE	2.42	0.92	3.34	0.89	14.01	8.61	1.63	9.75E-23
DT1H	47.87	1.05	48.93	0.99	6.14	0.91	6.74	1.10E-83
DT50H	64.88	1.04	65.92	0.99	6.80	0.86	7.88	2.87E-91
DT1F	28.20	1.05	29.25	0.99	4.50	0.87	5.18	3.96E-71
DTM	33.12	0.71	33.83	0.99	3.51	0.51	6.85	1.76E-84
FLL	6.88	0.57	7.45	0.97	16.89	4.86	3.48	9.91E-53
FLW	0.50	0.03	0.53	0.98	16.04	3.74	4.29	2.70E-62
PH	334.24	6.35	340.59	0.99	17.98	2.48	7.25	3.00E-87
PL	51.35	1.08	52.42	0.99	19.87	2.88	6.91	6.97E-85
SE	71.66	1.57	73.23	0.99	42.30	6.26	6.76	7.57E-84
SL	9.26	0.13	9.40	1.00	25.06	3.03	8.28	1.08E-93
SKPS	1.70	0.05	1.74	0.99	12.71	2.15	5.90	2.66E-77
SDPSK	0.11	0.00	0.11	1.00	14.54	1.56	9.33	1.79E-99
SDPS	56.75	4.06	60.81	0.98	17.15	4.59	3.74	5.39E-56
SDL	0.32	0.02	0.34	0.98	9.38	2.06	4.55	4.67E-65
SDW	0.10	0.00	0.10	0.99	9.52	1.96	4.84	6.03E-68
SDT	0.06	0.00	0.06	0.99	8.77	1.62	5.42	2.63E-73
HGW	0.80	0.05	0.84	0.98	22.21	5.44	4.09	4.93E-60
GY	0.67	0.02	0.68	0.99	38.18	6.39	5.98	6.45E-78

Note: DTE: Days to emergence, DT1H: Days to 1st heading, DT50H: Days to 50% heading, DT1F: Day to 1st flowering, DTM: Days to maturity, PH: Plant height (cm), PL: Peduncle length (cm), FLL: Flag leaf length (cm), FLW: Flag leaf width (cm), SL: Spike length (cm), SE: Spike exertion (cm), SKPS: No. of spikelets per spike, SDPSK: No. of seed per spikelet, SDPS: No. of seed per spike, SDL (mm): Seed length (mm), SDW: Seed width, SDT (mm): Seed thickness, HGW (gm): Hundred grain weight, GY: Grain yield (t/ha), σ^2g: Genotypic Variance, σ^2r: Residual Variance, σ^2p: Phenotypic variance, h^2: Broad-sense heritability estimates, CVg: genotypic coefficient of variation„ CVr: residual coefficient of variation, and Pr(>Chisq): Probability greater than chi square

Table 3. Principal component analysis of studied traits observed in wheat accessions.

Eigenvalues	5.857	3.770	1.784	1.471	1.328	1.054	Communality
Variance (%)	30.828	19.843	9.392	7.740	6.991	5.548	
Cum. variance (%)	30.828	50.671	60.062	67.802	74.793	80.341	
VAR	FA1	FA2	FA3	FA4	FA5	FA6	
DTE	-0.113	0.033	0.078	-0.026	-0.021	0.923	0.874
DT1H	-0.252	0.171	0.146	-0.255	0.750	0.107	0.753
DT50H	-0.270	0.210	0.015	-0.115	0.880	-0.062	0.908
DT1F	-0.122	-0.028	0.226	-0.016	0.795	-0.023	0.700
DTM	-0.150	0.045	-0.029	-0.087	0.816	-0.248	0.760
FLL	-0.157	-0.072	0.141	-0.925	0.089	0.018	0.914
FLW	-0.230	-0.113	0.012	-0.935	0.113	0.029	0.955
PH	-0.267	-0.890	0.117	-0.156	-0.033	-0.009	0.903
PL	-0.076	-0.944	0.093	0.007	-0.106	0.050	0.919
SE	-0.297	-0.831	0.022	-0.009	-0.343	-0.062	0.901
SL	-0.643	-0.450	-0.291	-0.055	0.091	0.115	0.726
SKPS	0.104	0.270	-0.762	0.206	-0.326	0.012	0.812
SDPSK	-0.015	-0.565	-0.183	-0.422	0.240	-0.104	0.599
SDPS	0.116	-0.070	-0.901	-0.016	0.089	-0.091	0.846
SDL	-0.886	-0.160	0.036	-0.079	0.057	0.102	0.832
SDW	-0.531	-0.240	0.107	-0.356	0.427	-0.047	0.662
SDT	-0.669	0.005	0.262	-0.216	0.323	-0.179	0.700
HGW	-0.795	-0.233	0.242	-0.205	0.166	0.119	0.829
GY	0.154	-0.044	-0.241	0.019	0.711	0.289	0.673

Note: DTE: Days to emergence, DT1H: Days to 1st heading, DT50H: Days to 50% heading, DT1F: Day to 1st flowering, DTM: Days to maturity, PH: Plant height (cm), PL: Peduncle length (cm), FLL: Flag leaf length (cm), FLW: Flag leaf width (cm), SL: Spike length (cm), SE: Spike exertion (cm), SKPS: No. of spikelets per spike, SDPSK: No. of seed per spikelet, SDPS: No. of seed per spike, SDL (mm): Seed length (mm), SDW: Seed width, SDT (mm): Seed thickness, HGW (gm): Hundred grain weight, GY: Grain yield (t/ha)

Similar high heritability was confirmed by Farhad *et al.* (2022), reinforcing that the predominance of genotypic variance over residual variance in trait expression was largely attributed to genetic control under proper replication and uniform experimental design. Moreover, the findings corroborate those of Rahmati & Karimizadeh (2025), who reported high heritability for yield-related traits, including thousand-kernel weight and spike characteristics.

Loadings and factor delineation

Based on factor analysis that integrates the correlation of component variables, the MGIDI-based selection process was initiated (Paramasivam *et al.*, 2025). After rescaling the traits, six factors, each with an eigenvalue > 1, were extracted by factor analysis. The factors together accounted for 80.341% of the variance across the evaluated traits (Table 3). These findings agree with Chapagain *et al.* (2025), who reported that

five principal components accounted for 80.8 % of total variance. Communality estimates ranged from 0.599 for seeds per spikelet (SDPSK) to 0.955 for flag leaf width (FLW), with an average of 0.825, indicating that most phenotypic variation in the traits was explained by the extracted factors with minimal loss of information (Rocha *et al.*, 2018). The lowest communality score (0.599) for seeds per spikelet (SDPSK) suggests that this trait was associated with both spike architecture-related (FA2) and grain number-related (FA3) factors, illustrating complex pleiotropic trade-offs among yield components (Gupta *et al.*, 2020). The Six factors (FA) were agronomically interpretable: FA1 represented seed morphological traits (seed length, spike length, seed width, seed thickness); FA2 represented plant structural traits (plant height, peduncle length, stem elongation, etc.); FA3 represented spikelets per spike and seeds per spike; FA4 represented flag leaf length and flag leaf width; FA5 represented phenological and yield traits, such as days to heading, flowering, maturity, and grain yield; and FA6 consisted only of days to ear emergence (DTE). This factor delineation reflects underlying biological relationships, particularly the correlation between plant development traits (FA5) and the differentiation between seed morphological traits (FA1) and plant structural traits (FA2).

Coincidence index and selected genotypes

The Coincidence index was calculated (Table 4) to evaluate the consistency, reliability, and degree of agreement among different selection indices. At 15% selection intensity, MGIDI identified nine elite genotypes (G41, G34, G22, G37, G38, G26, G28, G31, and G21) that moved in the desired direction for all 19 traits, thereby outperforming the Smith-Hazel index (Figure 1), consistent with Olivoto & Nardino (2020). These genotypes were selected because of their lower factor contribution scores, indicating their trait closeness to the ideotype. The perfect coincidence (CI = 100%) between MGIDI and FAI-BLUP is likely attributed to the common orthogonal factor-analytic structure used by both methods, which led to high heritability associated with the factors and, consequently, the selection of the same genotypes. Conversely, coincidence between the MGIDI and Smith-Hazel indices was lower (47.09% with SH-1, sharing five common genotypes: G41, G34, G22, G28, and G31, and 60.32% with SH-2, sharing six common genotypes, that is, G41, G34, G22, G37, G26, and G31). This reduced agreement may reflect the susceptibility of SH indices to multicollinearity among correlated traits, leading to unstable economic weights. Although omission of three collinear traits (FLW, DT50H, and PL) in SH-2 improved agreement with MGIDI from 47.09% to 60.32%, it reduced the biological information linked to canopy and reproductive development (Paramasivam *et al.*, 2025). Similarly, Fellahi *et al.* (2024) showed high alignment between MGIDI and FAI-BLUP while selecting superior wheat genotypes. The orthogonal factor-analytic structure in the MGIDI effectively handles multicollinearity (Graham, 2003; Olivoto *et al.*, 2019a, b), more effective selection can be achieved through MGIDI. Four genotypes, G41, G34, G22, and G31, were selected consistently across all indices because each excels in a distinct agronomic trait. G41 was selected mainly because of its outstanding yield capability, with high values for all of the main yield components: grain yield, spike length, hundred grain weight, and plant vigor. G34 had highly desirable physical grain quality, grain weight, and overall harvest efficiencies; thus, it ensures no compromise in seed payload through a reduction in crop architecture. G22 is outstanding for phenological targets and has a very short development period with optimum days to flowering, heading, and maturity parameters, making it a great choice for short duration cropping systems or early drought avoidance. Lastly, G31 is an all-rounder, with good multi-trait balance and environmental resilience across lodging and stable spike parameters. These four selections will encompass important breeding goals by combining raw production with seed quality, accurate maturity date, and seed and yield stability, underscoring their suitability as reliable candidates for further testing, crossing, and use in breeding programs.

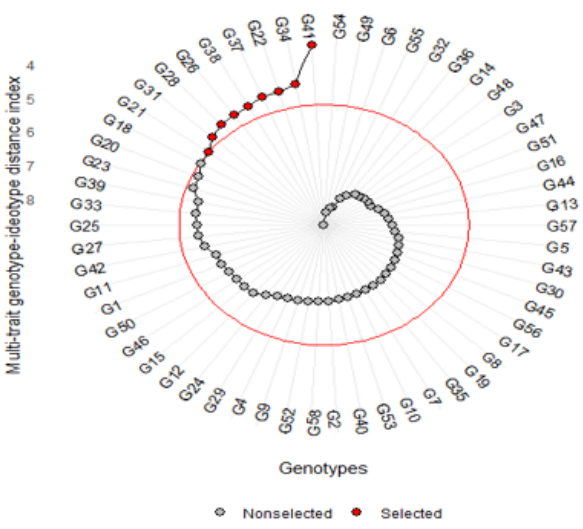

Figure 1. *Genotypes selected for the MGIDI index. Selected genotypes are shown in red, and the red circle represents the cut point according to the selection pressure.*

Table 4. Coincidence index, number of common genotypes, and shared genotypes for each pair of indices evaluated.

Index 1	Index 2	Coincidence	Common	Genotypes
mgidi_index	fai_blup_index	100	9	G4, G34, G22, G37, G38, G26, G28, G31, G21
mgidi_index	sh1_index	47.09	5	G41, G34, G22, G28, G31
mgidi_index	sh2_index	60.32	6	G4, G34, G22, G37, G26, G31
fai_blup_index	sh1_index	47.09	5	G4, G34, G22, G28, G31
fai_blup_index	sh2_index	60.32	6	G4, G34, G22, G37, G26, G31
sh1_index	sh2_index	73.54	7	G33, G41, G31, G22, G23, G35, G34

Predicted selection gains

The estimated selection gains for the 19 traits across the four indices are presented in Table 5. MGIDI index ensured desirable gains for all 19 traits, achieving positive gains for traits to be increased and negative gains for traits to be decreased, as shown in Figure 2. The FAI-BLUP index yielded the same gains as the MGIDI. By contrast, SH-1 did not yield the desired

direction, achieving a low gain for (DTE - 0.01%), whereas SH-2 achieved the desired gains for all 16 retained traits after the exclusion of traits affected by multicollinearity, thereby improving its overall response. In agreement with the findings, Farhad *et al.* (2022) reported that combining MGIDI increases the positive gain of yield traits in wheat while decreasing plant height and shortening maturity duration of wheat. Both MGIDI and FAI-BLUP achieved the desired highest gain for spike length (SL, 30.12%), surpassing the SH indices. For plant architecture traits (FA2), the desired negative gains were made for plant height (-10.63%), peduncle length (-5.51%), and stem elongation (-17.12%), together with a positive gain for seeds per spikelet (8.79%). The SH indexes had greater negative gains for PH and SE. The superior outcomes of MGIDI and FAI-BLUP are attributed to their explicit consideration of a priori ideotype and the multivariate relationships between traits. The MGIDI considers the multivariate distance between each genotype and the pre-defined ideal genotype after considering the underlying factor structure. This allowed the effective performance of correlated traits for genotype selection retarding the distortion of the index coefficient by strong correlation among traits.

Table 5. Predicted genetic gains for the indices MGIDI, FAI-BLUP, SH-1, and SH-2.

Factor	Traits	sense	Genetic Value	Genetic gain %			
				MGIDI	FAI_BLUP	SH-1	SH-2
FA1	SL	increase	12.14±3.68	30.12	30.12	19.72	24.46
FA1	SDL	increase	6.06±0.42	6.82	6.82	7.08	7.02
FA1	SDW	increase	3.26±0.23	6.88	6.88	8.11	8.65
FA1	SDT	increase	2.73±0.08	3.01	3.01	2.89	5.28
FA1	HGW	increase	4.02±0.45	11.07	11.07	15.16	17.14
FA2	PH	decrease	101.66±10.88	-10.63	-10.63	-13.45	-14.84
FA2	PL	decrease	36.07±2.00	-5.51	-5.51	-13.41	
FA2	SE	decrease	20.01±3.45	-17.12	-17.12	-30.30	-23.01
FA2	SDPSK	increase	2.25±0.20	8.79	8.79	7.51	10.18
FA3	SKPS	increase	10.25±0.65	6.32	6.32	0.74	2.75
FA3	SDPS	increase	43.93±8.57	19.05	19.05	7.64	12.61
FA4	FLL	increase	15.53±1.41	8.86	8.86	11.43	8.16
FA4	FLW	increase	4.41±0.58	12.87	12.87	13.00	
FA5	DT1H	decrease	112.68±109.95	-2.41	-2.41	-4.10	-3.74
FA5	DT50H	decrease	118.38±3.21	-2.70	-2.70	-4.53	
FA5	DT1F	decrease	118.11±0.77	-0.65	-0.65	-2.88	-1.32
FA5	DTM	decrease	163.80±2.74	-1.66	-1.66	-1.75	-1.68
FA5	GY	increase	2.14±0.34	15.57	15.57	18.89	13.26
FA6	DTE	decrease	11.11±0.13	-1.04	-1.04	0.01	-1.56

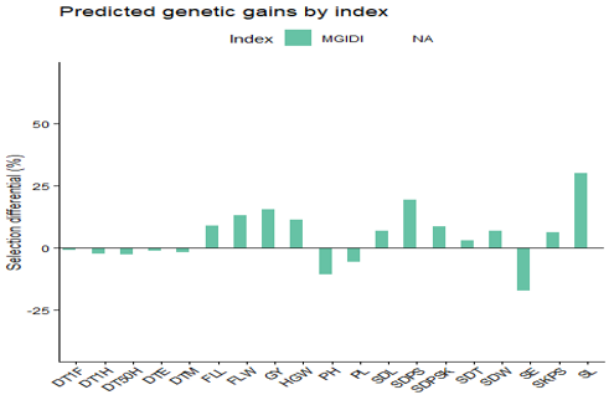

Figure 2. *Predicted selection gain of evaluated traits by MGIDI index.*

Strengths and weaknesses of factors on the genotype MGIDI Index

A distinct advantage of MGIDI is that it pinpoints which trait groups perform best in the selected genotypes, which can be used as a guide for designing crossing blocks. This plot (Figure 3) depicts the percentage contribution of factors FA1–FA6 to the MGIDI score for the selected genotypes. A factor line extending far from the origin (high contribution) indicates strength, whereas a shorter line closer to the origin (lower contribution) indicates weakness because of the strong influence of factors on that genotype, resulting in poor performance of those factor-associated traits. G37 and G26 exhibited notable strength for FA1; G34, G38, and G36 for FA2; G37 and G41 for FA3; G41 and G28 for FA4; and G31 and G22 for FA5. Overall, the plot reveals the strengths and weaknesses of each genotype and provides practical guides to choose potential parents in breeding programs.

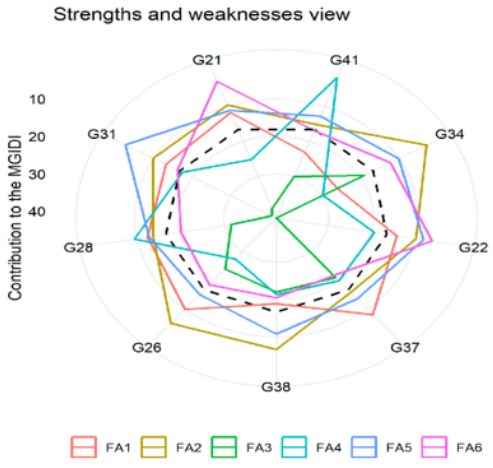

Figure 3. *Strengths and weaknesses of the factors on the MGIDI index.*

Performance of selected genotypes by MGIDI

A heat map of standardized (Z-score) trait values for the nine genotypes selected by MGIDI at 15% selection intensity was generated in R using the ggplot2 package (Figure 4). In this heat map, dark green represents highly favorable performance, whereas red denotes poor performance. Selected Genotypes G41 and G22, ranked first and third by the MGIDI score, were predominantly represented by green cells across almost all 19 traits and had particularly higher values for seed-related traits, such as seeds per pod (SDPS) and seed length (SL). All selected genotypes showed a consistent desirable pattern for traits related to pod and seed characteristics, including SDPS, SDL, and SL. Some genotypes, however, exhibited trade-offs. For instance, G37 ranked fourth, despite its relatively low value for yield (GY = -1.1), because of its strong contribution to FA1. This confirms that the selection of these nine genotypes relied on multiple traits rather than yield alone.

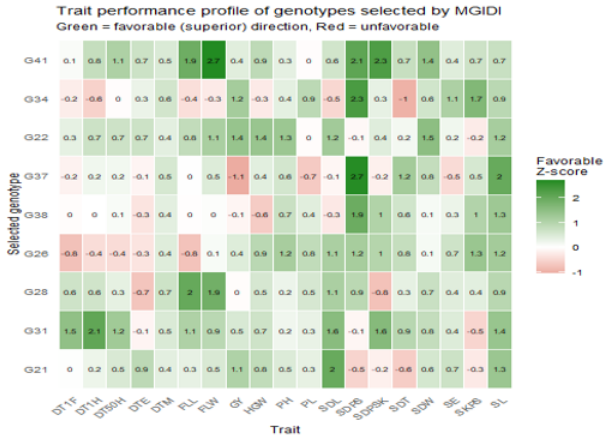

Figure 4. *Trait performance profile of genotypes selected by MGIDI at 15 % selection intensity.* ***Note:*** *DTE: Days to emergence, DT1H: Days to 1st heading, DT50H: Days to 50% heading, DT1F: Day to 1st flowering, DTM: Days to maturity, PH: Plant height (cm), PL: Peduncle length (cm), FLL: Flag leaf length (cm), FLW: Flag leaf width (cm), SL: Spike length (cm), SE: Spike exertion (cm), SKPS: No. of spikelets per spike, SDPSK: No. of seeds per spikelet, SDPS: No. of seeds per spike, SDL (mm): Seed length (mm), SDW: Seed width, SDT (mm): Seed thickness, HGW (gm): Hundred grain weight, GY: Grain yield (t/ha).*

Conclusion

This study showed the effectiveness of MGIDI in identifying superior-performing wheat landraces in the mid-hill agro-ecological conditions of Khumaltar, Nepal. The high broad-sense heritability values and genotypic variances across the evaluated traits verified the presence of high genetic control and provided a solid basis for data-driven selection. In all three selection methods (MGIDI, FAI-BLUP, and Smith-Hazel), four elite landraces (G41, NGRC-7819; G34, NGRC-7615; G22, NGRC-6554; G31, NGRC-7586) were selected consistently for their balanced performance in the key agronomic parameters, particularly in plant height, maturity, hundred-grain weight, and yield potential. The four landraces are potential candidates for further breeding, crop improvement, and elite germplasm conservation programs for enhancing food security. This study was based on a single-season and single-location framework. So, a multi-season, multi-environment trial incorporating molecular profiling is further recommended to validate these landraces' trait consistency and genetic stability under diverse agro-climatic conditions. In this context, integrating MGIDI provides a comprehensive methodology that boosts selection precision, optimizes genetic improvement potential, and directs the breeding workflow for the improvement of several traits in wheat.

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DECLARATIONS

Author contribution statement: Conceptualization: A.S. and M.B; Methodology: A.S.; Software and validation: A.S.; Formal analysis and investigation: A.S.; Resources: M.B; Data curation: A.S.; Writing-original draft preparation: A.S.; Writing-review and editing: A.S.; Visualization: A.S.; Supervision: B.K. and M.B. All authors have read and agreed to the published version of the manuscript.

Conflicts of interest: The authors declare that there are no conflicts of interest regarding the publication of this manuscript.

Ethics approval: This study was conducted in view of the institutional ethical guidelines and did not harm the human participants.

Consent for publication: All co-authors gave their consent to publish this paper in AAES.

Data availability: The data that support the findings of this study are available on request from the corresponding author.

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