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Integrating Morpho-Phenological and Agronomical Traits to Explore Genetic Diversity of Wheat (*Triticum aestivum* L.) Landraces in Lalitpur, Nepal

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ABSTRACT

Wheat (*Triticum aestivum* L.) is the king of cereal crops, with the largest genomic size (~ 17 Gb), the oldest domesticated crop, with high and increasing demand, making its continuous crop improvement essential for climate resilience and food security. To characterize and evaluate 70 Nepalese wheat landraces, this research was carried out in the National Agriculture Genetic Resources Centre (NAGRC), Khumaltar, Lalitpur, from November 12, 2024, to May 22, 2025. Seventy wheat landraces collected from different districts of Nepal were characterized and evaluated using an augmented block design. Twenty quantitative and thirteen qualitative traits were assessed to determine the extent of variability and identify elite genotypes for breeding programs. Statistical tools like Principal Component Analysis (PCA), descriptive statistics, Cluster analysis, Karl Pearson correlation coefficient were used for the analysis. Shannon-Weaver diversity indices (H') showed a moderate to low level of diversity for qualitative traits, and showed a high to moderate level of diversity for quantitative traits. The first four principal components (PC) explained 67.42% of the total phenotypic variation, while the first two PCs constituted 49.32% of the variation. Cluster analysis grouped the 70 wheat accessions into four genetically distinct clusters. Cluster-2 was the largest cluster with 35 (50%) accessions, and cluster-1 constituted 25 (35%) accessions. Pearson correlation analysis showed a highly significant positive correlation between days to heading and days to maturity, plant height and spike exertion, awn length and hundred grain weight, and seed length and hundred grain weight. Promising landraces were identified for high-yielding, desirable short-stature (lodging resistant), desirable early maturing traits, and quality seed-related traits for studying their suitable area of cultivation as elite candidates for evaluation across multiple environments and selection for potential use in the development of improved wheat varieties.

Keywords: Wheat Accession, Euclidean distance, Genetic variability, Principal Component

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INTRODUCTION

Wheat (*Triticum aestivum* L.) is the king of cereal crops, feeding approximately 35% of the global population. Wheat contributes around 41% of the world's food calories, thereby ensuring food security for millions. The most commonly cultivated species (Bread wheat) is an annual allohexaploid (2n=6x=42) with a (BBAADD) genome, having an estimated genomic size of ~17 Gb. It belongs to the Poaceae family and the Triticaceae tribe (Sears 1952). Bread wheat originated around 8,500-9000 years ago through hybridization between a domesticated, free-threshing tetraploid progenitor (BBAA genome) and *Aegilops tauschii,* the diploid donor of the D genome (Levy and Feldman 2022). The modern cultivated crop represents the result of the domestication of wild ancestors by early farmers, followed by diversification and improvement over more than ten thousand years (Gross and Olsen 2010). In 2024, global wheat production reached 800.79 million tons with its cultivation area of 220 million hectares, highlighting its importance in global agriculture (FAOSTAT 2024). The crop is widely grown across all agro-climatic regions of Nepal, ranging from 50m to 4,000m above sea level, and contributes 5.67% to the country's agricultural GDP. Since the 1960s, wheat cultivation in Nepal has expanded more than fivefold, significantly contributing to national food security (Bhattarai and Pandey 1997). At present, Nepal's wheat productivity is 2.99 t ha^{-1}, with a total production of 2.04 tons and 6,81,851 hectares under cultivation (MoALD 2025). Wheat ranks as the third most-produced crop in Nepal, following rice and maize. By 2030, the country's wheat demand is projected to increase by approximately 890,000 metric tons. However, Nepal is the fourth most vulnerable country to climate change globally (Upadhyay and Arora 2023), posing a significant threat to its agricultural sector. This highlights the need for further advancement in wheat breeding programs.

The growing dependency on improved and hybrid bread wheat varieties has led to a situation of a bottleneck, resulting in narrow genetic diversity. Although there is a lot of germplasm in the wild state in the different parts of the country, with better quality in terms of disease resistance, nutritional quality, drought resistance, early maturity, etc.) these genetic resources are neglected or underutilized by farmers due to their undesirable agronomic characteristics such as low yield, harvesting, and threshing problems, etc, but still a number of wheat landraces are still cultivated by farmers in mid-hill of Nepal, despite the widespread adoption of improved and hybrid varieties, However, many of these indigenous genetic resources remain poorly characterized and underutilized (Joshi et al 2020). The current status and importance of wheat in Nepal necessitate the importance of an agro-morphological and phenological characterization study, as well as diversity assessment of wheat landraces. The present scenario of genetic loss has triggered the conservationists to collect, conserve, characterize, and sustainably use wheat landraces for further genetic improvement in wheat breeding programs. Traditional cultivars, landraces, and wild relatives are crucial in addressing climate change impacts due to their genetic diversity, adaptability to local conditions, and resilience against biotic and abiotic stresses (Ehdaie et al 1989). Landraces, although lower-yielding than modern hybrid varieties, exhibit remarkable stability under low-input agricultural systems and possess drought tolerance, heat tolerance, insect pest resistance, and nutritional quality traits. Mineral content in modern cultivars has declined, but landraces often retain higher levels of essential nutrients like copper, iron, magnesium, manganese, phosphorus, selenium, and zinc. This suggests that landraces could contribute to improving the nutritional quality of wheat products (Distelfeld et al 2007, Genc et al 2005). Moreover, landraces developed in nutrient-poor environments may offer genetic material for breeding varieties suited to low-fertilizer condition (Manohara et al 2019). Understanding the morpho-phenological and agronomical variability in wheat landraces is therefore essential to identify superior genotypes that can perform well under changing environmental conditions and provide a valuable gene pool for developing improved, stress-tolerant, climate change resilient, and high-yielding varieties.

High diversity was reported in both quantitative and qualitative features of awedness, glume color, tillering capacity, seed size, and spike density in the previous study in 200 wheat accessions (Karkee et al 2023). And more than 20% coefficient of variation was contributed by the parameters spike per square meter, awn length, thousand grain weight, and yield individually. The specific objective of this study was to assess the extent of genetic diversity among wheat landraces, identify the superior genotypes with their key morphological traits that contribute significantly to this variability to utilize in wheat improvement programs This study will use qualitative and quantitative agro-morphological traits to assess the intra-varietal diversity among the wheat landraces collected from different regions of Nepal, and identify landraces with adaptability to local environment and tolerance to biotic and abiotic stress providing critical insights into their genetic variability and potential utilization in future breeding programs. The results will offer critical baseline data for future molecular research, multi-environment trials, and breeding strategies.

MATERIALS AND METHODS

Experimental site

The research to characterize and recommend the best-performing wheat landraces was conducted at the National Agriculture Genetic Resource Centre (NAGRC), Khumaltar, Lalitpur (Figure 1). The experiment was conducted from November 12 to May 22. The experimental site is located in the sub-tropical mid-hill region at an altitude of 1368 m, latitude of 27º42´N, and longitude of 85º20´E. The soil type at the research site was loamy clay, with a pH of 5-7. The site's agro ecology was categorized as mid-hill.

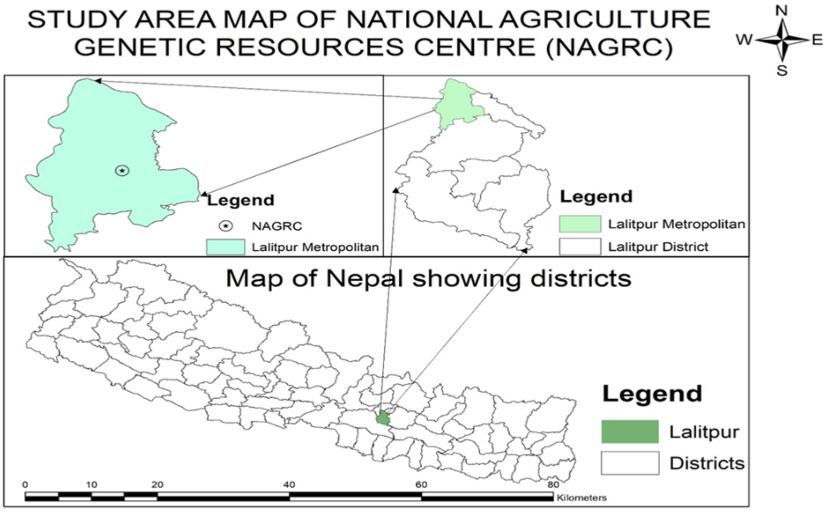

Figure 1.Study area showing Genebank, Khumaltar, Lalitpur, Nepal

Experiment design and materials

This study was conducted in 70 wheat landrace accessions sourced from 7 different districts of Nepal as plant material for experiments. The wheat landraces used for the study. The experiment was conducted using a non-replicated augmented block design. The experimental field was designed in 4 blocks comprising 21 plots in each block, and each plot was sown with a distinct accession. Each plot was designed with dimensions 3m ×1.5m, consisting six rows of plants. Plots were arranged in Row-Row distance of 25cm and Plant-Plant distance of 10cm. The distance between two plots was 25cm, and between 2 block was 50 cm. FYM was incorporated 10 days in advance of land preparation as per the recommended dose of 6 t/ha. Fertilizer was applied at a rate of 100:50:50 NPK/ha. This structured approach facilitated the adequate and timely availability of all the necessary nutrients and water during critical growth periods.

Data collection

Data for qualitative and quantitative traits of wheat were collected and recorded based on the wheat descriptor developed by the (International Board for Plant Genetic Resources, 1985) at an appropriate vegetative stage to the reproductive stage for each trait. Data were collected by selecting 5 plants randomly from each accession plot, avoiding border plants. Thirteen qualitative traits were observed at different growth stages growth habit, leaf color, anther color, awedness, glume color, glume hairiness, spike density, tillering capacity, lodging resistance, seed color, seed surface, seed shape, and seed size. Similarly, twenty quantitative traits were assessed through visual observation: days to emergence, days to 1st and 50% heading, days to flowering, days to maturity, flag leaf length, flag leaf width, plant height, peduncle length, spike exertion, spike length, awn length, number of spikelets per spike, number of grains per spikelet, number of grains per spike, length of grain, width of grain, thickness of grain, hundred grain weight, and grain yield.

Data analysis

For quantitative traits, descriptive statistics such as minimum, maximum, mean, standard deviation, coefficient of variation, correlation, and Principal Component Analysis (PCA) were calculated using R Studio version 2025.09. Principal component analysis was conducted to identify the major components contributing to the variability among genotypes. Dendrogram was constructed using Minitab 17 statistical software. To analyze diversity, the standardized Shannon-Weaver Diversity index was calculated using MS Excel 2016 using the formula in Equation (i)

Equation (i):

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

where, H′= standardized Shannon-Weaver diversity index,

K= number of phenotypic classes for a character,

n= frequency of a phenotypic class of that character,

and N= Number of observations/landraces for that character.

For Qualitative traits frequency and percentage distribution of different categories of 14 traits was calculated using Microsoft-Excel 2016.

Diversity based on qualitative traits

Diversity based on qualitative traits was assessed using Shannon-Weaver diversity index. Considerable variation was observed for the thirteen qualitative traits, with spike density exhibiting relatively high diversity index (H'=1.097), as shown in Table 1. The estimate of Shannon- Weaver diversity indices (H') considers both richness and evenness of the phenotypic classes of the traits. Among the thirteen qualitative traits, traits like growth habit (H'=1.097), spike density (H'=1.097), leaf color (H'=1.097), and seed size (H'=1.097) revealed high diversity index (H') > 1, which implied these traits highlighted importance of qualitative traits in the differentiation of wheat genotypes. This finding aligns with the finding by (Karkee et al 2023).

Table 1. Frequency of different categories of qualitative traits observed in wheat accessions at NAGRC, Khumaltar, Lalitpur, 2025

S. N	Variables	Descriptive score	Frequency	Percentage (%)	H'
1	Growth habit	3 Upright	33	47.14	1.027
		5 Intermediate	22	31.43	
		7 Prostrate	15	21.43	
2	Leaf color	3 Light green	30	42.86	1.019
		5 Green	11	15.71	
		7 Dark green	29	41.43	
3	Anther color	3 Purple	18	25.71	0.56
		5 yellow	52	74.29	
4	Tillering Capacity	7 High	64	91.43	0.295
		5 Medium	6	8.57	
		3 Low	0	0	
5	Spike density	1 Very Lax	0	0	1.096
		3 Lax	21	30	
		5 Intermediate	24	34.29	
		7 Dense	25	35.71	
		9 Very dense	0	0	
6	Awedness	7 Awned	44	62.86	0.88
		3 Awnletted	3	27.14	
		0 Awnless	19	10.00	
7	Glume color	1 White	60	85.71	0.41
		2 Red to brown	10	14.29	
		3 Purple to black	0	0	
8	Glume hairiness	0 Absent	42	60	0.94
		3 Low	14	20	
		7 High	14	20	
9	Lodging resistance	0 Resistance	47	67.14	0.86
		L Low	13	18.57	
		M Medium	10	14.29	
10	Seed color	1 White	32	45.71	0.69
		2 Red	0	0	
		3 Purple	38	54.29	
11	Seed surface	1 Rough	70	100	0.00
		2 Smooth	0	0	
12	Seed size	3 Small	20	28.57	0.97
		5 Intermediate	39	55.71	
		7 Large	11	15.71	
13	Seed shape	5 Ovate	46	65.71	0.64
		7 Elliptical	24	34.29	
		3 Round	0	0	

Note: H' = Shannon–Weaver diversity index.

In contrast, the lowest diversity was obtained for tillering capacity (H'=0.295). However, relatively low diversity was obtained for the seed surface and glume color, which implied that landraces were uniform for these traits. In addition to this, findings showed that the structure of agro-morphological traits is significantly influenced by natural selection factors. Studies have shown that diversity measures help in identifying various germplasm for breeding, conservation, and the sustainable use of wheat. The prevalence of high genetic diversity in Nepalese wheat landraces increases the space for selection and pre-breeding purposes of elite varieties. The relatively high Shannon-Weaver diversity index for qualitative traits inferred ample genetic variability within the collection and fairly even distribution across frequency classes, with implications for utilization in robust crop improvement and enhancement of genetic potential of wheat landraces.

Diversity based on quantitative traits

The range (minimum-maximum), mean, standard error of mean, variance, standard deviation, and coefficient of variation (CV%) and Shannon-Weaver diversity for 20 quantitative traits were used to characterize and measure the variation within and between wheat populations, as shown in Table 2. High to moderate level of diversity was assessed using Shannon-Weaver diversity index, ranging from (0.97-1.84) for quantitative traits. The days of emergence varied from 9 to 12 days, with an average of 10.13 days, and a standard error (SE) of 0.11, and coefficient of variation of 9.35%, and it showed moderate level of diversity, having Shannon weaver diversity index (1.09). Days to 50 % heading varied from 94 to 144 days, with an average of 118.13 days. Shannon-Weaver diversity index (1.59) implied high level of diversity in days to heading. Days to flowering varied from 110-142 days, with an average of 119.07 days, and showed moderate diversity with Shannon-Weaver diversity index value of 1.50. Days to flowering varied from 110-142 days, with an average of 119.07 days, and showed moderate diversity with Shannon-Weaver diversity index value of 1.50. Flag leaf length varied from 9.05 to 24.70 cm with an average of 15.33, and it showed a high level of diversity with Shannon-Weaver diversity index value (1.55). Flag leaf width varied from 0.92 to 2.22 cm with an average of 1.54 cm, and it also showed higher diversity value of 1.59.

Table 1. Descriptive statistics of parameters for different quantitative traits observed in wheat accessions at NAGRC, Khumaltar, Lalitpur, 2025

Variable	Min.	Max.	Mean	Median	SE.mean	SD	CV	H'
DTE	9.00	12.00	10.13	10.00	0.11	0.95	9.35	1.09
DT1H	87.00	139.00	112.19	110.50	1.35	11.28	10.05	1.59
DT50H	94.00	144.00	118.13	115.00	1.36	11.39	9.64	1.60
DT1F	110.00	142.00	119.07	116.50	1.00	8.36	7.02	1.50
DTM	158.00	186.00	164.89	162.50	0.84	7.05	4.27	0.97
FLL	9.05	24.70	15.33	15.22	0.31	2.61	17.05	1.55
FLW	0.92	2.22	1.54	1.52	0.03	0.24	15.32	1.59
PH	57.20	144.98	107.53	112.85	2.39	20.02	18.61	1.74
PL	12.60	53.10	38.74	40.25	1.03	8.65	22.32	1.71
SE	4.3	46.30	23.08	21.85	1.19	9.92	42.97	1.74
SpL	6.50	17.00	10.84	10.93	0.34	2.84	26.18	1.84
Sl.S	7.00	17.00	9.79	9.80	0.14	1.21	12.38	0.98
Sd.Sl	1.00	3.00	2.25	2.20	0.04	0.34	15.25	1.29
Sd.S	26.60	57.40	40.07	40.00	0.78	6.53	16.29	1.74
SL	4.82	7.19	5.99	5.88	0.06	0.53	8.81	1.79
SW	2.14	3.73	3.19	3.23	0.04	0.31	9.69	0.75
ST	2.17	6.45	2.78	2.72	0.06	0.53	19.22	1.29
HW	2.36	5.87	3.86	3.66	0.10	0.80	20.83	1.74
AL	0.00	7.00	3.34	3.99	0.29	2.46	73.57	1.79
Yd	0.60	4.78	2.08	1.97	0.10	0.87	41.73	1.72

Min. = Minimum, Max. = Maximum, SE.mean = Standard Error of mean, SD = Standard Deviation, CV= Coefficient of Variation %, H' = Notation for Shannon-Weaver diversity index. DTE: Days to emergence, DT1H: Days to 1st heading, DT50H: Days to 50 % heading, DT1F: Days 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), SpL: Spike length (cm), SE: Spike exertion (cm), Sl.S: No. of Spikelet per spike, Sd.Sl: No. of seed per spikelet, Sd.S: No. of seed per spike, SL: Seed length, SW: Seed width, ST: Seed thickness, HW: Hundred grain weight, AL: Awn length (cm), and Yd: Yield (t/ha)

Plant height varied from 57-144.98 cm with an average of 108.53 cm, showing higher level diversity value of 1.74. Spike exertion varied from 4.3 to 46.30 cm with an average of 23.08 cm. Shannon-Weaver diversity index value for it was 1.74, which implies a high level of diversity. Spike length in the landraces ranged from 6.50 to 17 cm, with an average of 10.84 cm, and it showed a very high level of Shannon Weaver diversity index value (1.84). Seed per spikelet varied from 1 to 3 in number, with an average of 2.25. Shannon-Weaver diversity index showed moderate value for this trait. Seed per spike varied from 26.6 to 57.4 with an average of 40.07, showing high diversity index value (1.74). Seed length varied from 4.82 to 7.19 mm with an average of 5.99 mm, showing high level of diversity index value (1.79). Hundred grain weight varied from 2.36 to 5.87 grams with an average of 3.86 grams and Shannon-Weaver diversity index value (1.74) implied a very high level of diversity. Awn length varied from 0 to 7 cm in length among 70 landraces, giving very high value of diversity (1.79). Yield varied from 0.6 to 4.78 t/ha with an average of 2.08 t, and it showed very high diversity value (1.72). These revealed variations between quantitative traits were found in the study conducted for wheat landraces by Bhattarai et al. (2025). Prioritizing the high-yielding landraces will facilitate breeders to deliver improved varieties in wheat.

Multivariate analysis

Principal Component Analysis (PCA)

PCA was employed to estimate the relative contribution of each quantitative trait to total variation and to characterize the agronomic diversity among 70 landraces. This method helps to identify the best parent for breeding programs. The PCA simplifies complex data by reducing the number of linked qualities to a smaller number of variables (PCs) using an eigenvalue greater than one as a measure for the significance of a principal component (PC). The Scree plot of the PCA (Figure 2) demonstrates that the first six dimensions accounted for the entire percentage of variance in the dataset. The total cumulative variance of these six factors was 79.87% (Table 3). The very first principal component (PC1) accounted for the most variability in the data with regard to succeeding components. The positive loadings on table imply that trait variation increases toward positive side of respective PC, and negative loadings imply that trait variation increases toward negative side of PC. The predicted wheat variables were divided into six major components using PCA, of which PC1 only explained roughly 27.44% of the variation.

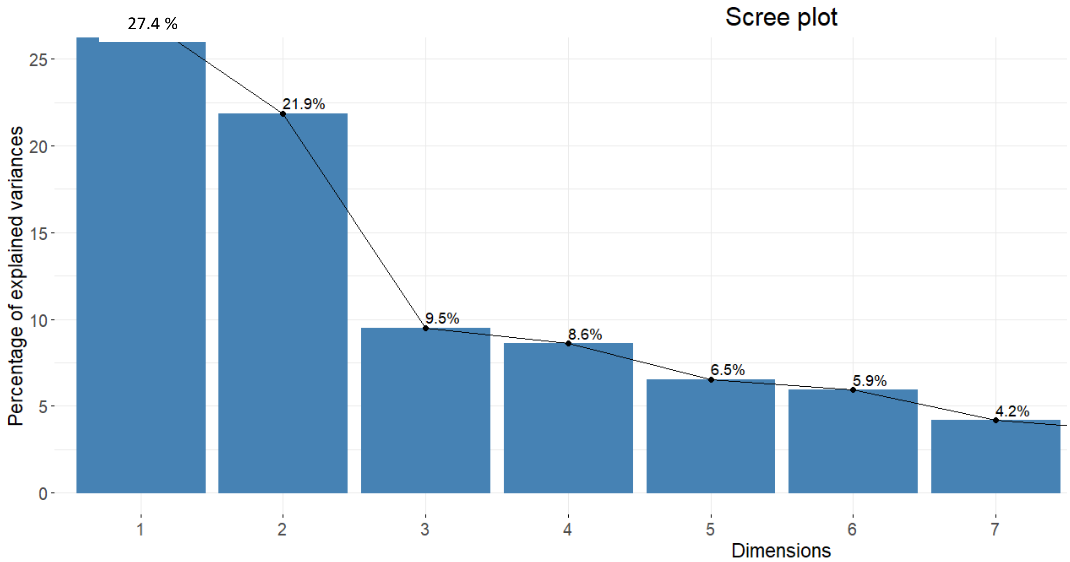

Figure 2. Scree Plot of the dimensions of Principal Component Analysis

First principal component variance was significantly contributed by the seed grain related traits like spike length (SpL) (4.79), seed per spike (Sd.S) (4.36), and seed per spikelet (Sd.Sl) (3.79). Traits like days to emergence (DTE) (-4.04), flag leaf width (FLW) (-0.54) had high contribution for variation in negative direction of PC1. The traits with high loadings (regardless of sign) had strong influence on variation in PC1. PC1 was followed by PC2 in the contribution to variance, which explained 21.88% of variance. PC2 was highly influenced by the traits like spike exertion (SE) (5.74), spikelet per spike (Sl.S) (4.55), seed per spikelet (Sd.Sl) (3.24). In contrast, it was highly influenced by days to flowering (DT1F) (-4.17), seed width (SW) (-3.86), seed thickness (ST) (-3.78), flag leaf width (FLW) (-3.65), plant height (PH) (-3.21) in the negative direction.

Third principal component (PC3) accounted for 9.49% of variance, indicating that traits like spikelet per spike (Sl.S) (2.60), seed per spike (Sd.S) (2.59), and days to emergence (DTE) (2.05) contributed the most. Days to flowering (DT1F), peduncle length (PL), spike exertion (SE), seed per spikelet (Sd.Sl), seed width (SW), and yield (Yd) had significant negative loadings. PC4 accounted for 8.61% of variance, which was contributed highly by spikelet per spike (Sl.S) (2.06), spike length (SpL) (1.82), and Spike exertion (SE) (1.73). PC5 explained roughly about 6.53 % of variance, which was mostly contributed by awn length (AL) (2.57), seed per spikelet (Sd.Sl) (2.52), hundred grain weight (HW) (2.48), seed per spike (Sd.S) (1.74), and spike exertion (SE) (1.59). PC6 explained about 5.92% of total variance, in which seed per spike (Sd.S) (0.83), awn length (AL) (0.79), seed width (SW) (0.72), and hundred grain weight (HW) (0.63) had contributions in positive direction. In a study by Mecha et al. (2017), 64 bread wheat genotypes were studied, and five principal components (PC1, PC2, PC3, PC4, PC5) were reported having eigenvalues greater than one that held 72.78% of total variation, which is similar to our findings and has similar variation exhibited by the five principal components in our study.

Table 2. PCA table of quantitative traits observed in wheat accessions at NAGRC, Khumaltar, Lalitpur, 2025

Variable	PC1	PC2	PC3	PC4	PC5	PC6
DTE	-4.04	0.11	2.05	1.16	-0.68	0.41
DT1H	-0.16	-1.76	0.55	-0.26	-0.14	-1.71
DT50H	-0.24	-2.67	0.31	-0.59	-0.87	-0.41
DT1F	0.17	-4.17	-0.84	0.76	0.15	-0.46
DTM	0.28	-2.07	0.90	-1.86	-0.70	-0.75
FLL	1.36	-2.36	0.64	0.74	-0.26	-0.21
FLW	-0.54	-3.65	1.63	1.59	-1.01	0.26
PH	0.60	-3.21	0.55	1.33	1.00	-1.33
PL	1.20	-2.32	-0.16	-0.53	1.01	-0.07
SE	2.98	5.74	-0.39	1.73	1.59	-0.26
SpL	4.79	1.65	0.55	1.82	-1.47	-0.51
Sl.S	1.48	4.55	2.60	2.06	-0.05	-1.19
Sd.Sl	3.79	3.24	-1.12	0.49	2.52	-1.50
Sd.S	4.36	0.92	2.59	-0.06	1.74	0.83
SL	1.31	-1.09	0.10	0.18	1.14	-0.65
SW	0.04	-3.86	-1.50	0.71	0.04	0.72
ST	-0.18	-3.74	1.75	0.87	-0.87	-0.29
HW	0.60	-2.68	0.18	-0.73	2.48	0.63
AL	-0.25	-2.74	1.57	0.59	2.57	0.79
Yd	1.78	-2.32	-0.16	-0.52	0.22	-2.12
Eigenvalue	5.49	4.38	1.90	1.72	1.31	1.18
Variance%	27.44	21.88	9.49	8.61	6.53	5.92
CV%	27.44	49.32	58.81	67.42	73.95	79.87

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), SpL: Spike length (cm), SE: Spike exertion (cm), Sl.S: No.of Spikelets per spike, Sd.Sl: No.of seed per spikelet, Sd.S: No.of seed per spike, SL (mm): Seed length (mm), SW: Seed width, ST (mm): Seed thickness, HW (gm): Hundred grain weight, AL: Awn length (cm), Yd: Yield (t/ha), and CV: cumulative variance %

The results of PCA suggested that key traits contributing to the variance are days to emergence, days to flowering, spike exertion, spike length, seed per spike, and spikelets per spike. These traits are critical for identifying genetic diversity and for improvement in wheat breeding. Similar inferences, i.e recognition of patterns in variability in traits via PCA, were obtained by several authors (Karkee et al 2023, Bhattarai et al 2025). Prioritization of these traits identified through PCA and CV can effectively enhance wheat performance and adaptability.

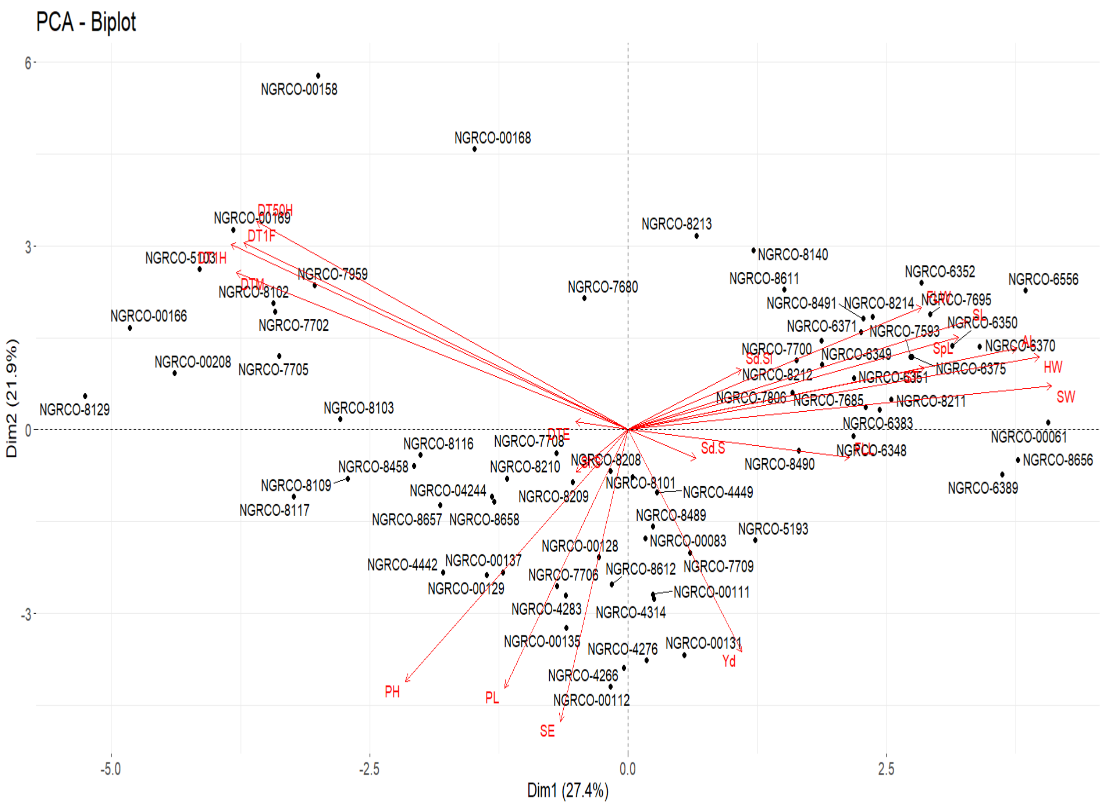

Figure 3. PCA Biplot of quantitative traits observed in wheat accessions at NAGRC, Khumaltar, Lalitpur, 2025

The PCA biplot in Figure 3. depicts the individual accessions distribution (black points) with trait vectors (red arrows). The arrows of each trait represent variables. Arrow direction, along with its length, shows contribution to variation by traits in either positive or negative direction of the principal components in the X-axis and Y-axis of each quadrant. On the top right quadrant of Figure 3, accessions like NGRCO6370, NGRCO6350, NGRCO7695, and NGRCO6556 represented high-yielding, large grain size quality, good spike, early, and elite type accessions. On the top left quadrant, accessions like NGRCO00168, NGRCO00169, NGRCO5103, and NGRCO8102 had high values for the traits like DTM, and DTH, indicating themselves as long duration types. On the bottom left quadrant, accessions like NRCO00129, NGRCO00135, NGRCO4266, NGRCO00112 implied themselves as late maturing, tall, low-yielding type. In the lower right quadrant, accessions in this quadrant, like NGRCO00131, NGRCO00111, NGRCO6348, and NGRCO8490 were high-yielding, large-seeded, early-type. Accessions like NGRCO00158 (long duration type but, unique phenology), NGRCO00168 (distinct for long duration), NGRCO00112 (late flowering and tall plant), NGRCO6348 (high yielding possibly short type) lied far from origin were genetically too distinct from other central accessions suggesting, they were genetically too different from each other and could be used to develop the new crop varieties either through direct selection or through hybridization. The correlation coefficient between any two attributes can be roughly calculated using the cosine angle created by their vectors.

Hierarchical Clustering

A dendrogram for good representation of the cluster was constructed by using the UPGMA (Average) clustering method based on average linkage and Euclidean distance across the 70 Landraces. The cluster analysis grouped the Landraces into four clusters for 20 quantitative traits (Figure 4). The optimal number of clusters was determined based on the elbow method. Cluster analysis grouped genotypes with greater morphological similarity, and the clusters did not necessarily include all genotypes collected from the same origin. Clusters 1, 2, 3, and 4 were represented by the blue, red, purple, and green colors. Clusters 1, 2, 3, and 4 constituted 24, 35, 8, and 3 wheat accessions, respectively.

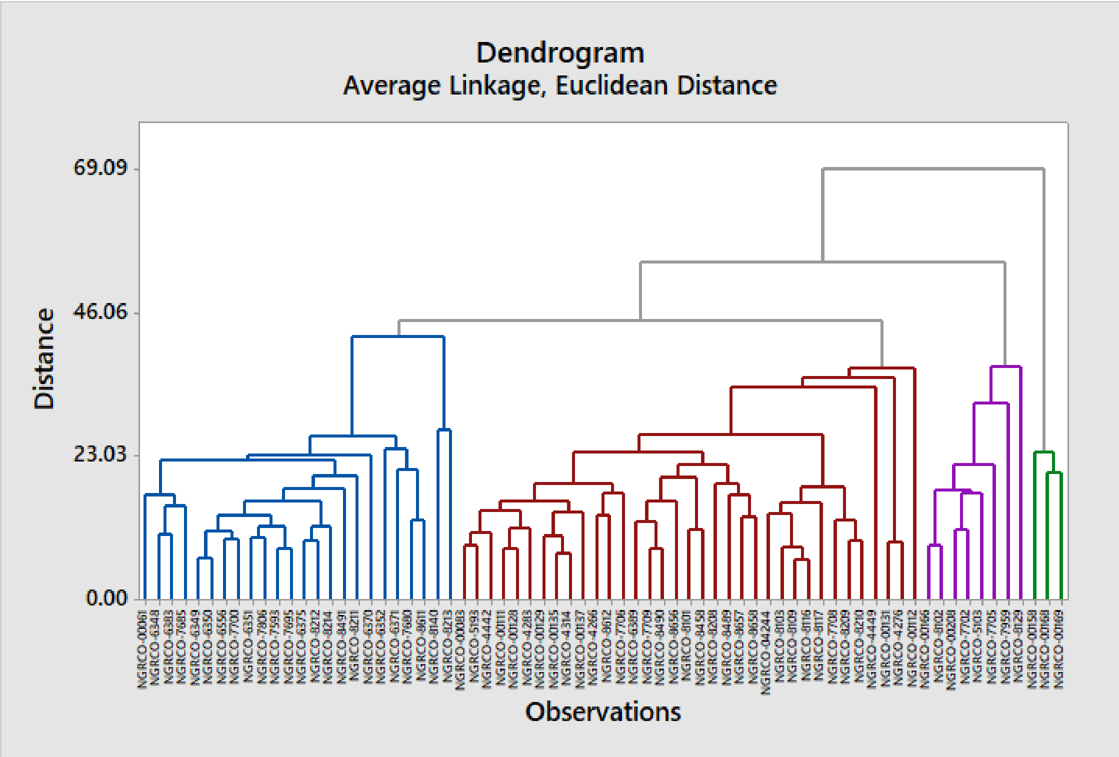

Figure 4. Cluster dendrogram of 20 quantitative traits observed in wheat accessions at NAGRC, Khumaltar, Lalitpur, 2025

Table 4. Cluster centroids of variables observed in wheat accessions at NAGRC, Khumaltar, Lalitpur, 2025

Variable	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Grand Centroid
Days to Emergence	9.92	10.17	11.00	10.25	10.13
Days to 1st heading	107.88	108.66	135.67	131.75	112.19
Days to 50% heading	115.13	113.34	141.33	139.38	118.13
Days to 1st flowering	115.96	115.94	137.67	135.13	119.07
Days to maturity	161.92	162.31	178.33	180.00	164.89
Flag leaf length	15.67	15.64	12.82	13.86	15.33
Flag leaf width	4.49	4.38	3.76	3.67	4.31
Plant height	88.34	121.51	69.93	118.08	107.53
Peduncle length	31.58	44.64	20.80	41.16	38.74
Spike exertion	15.20	30.50	5.87	20.72	23.08
Spike length	13.49	10.26	9.30	9.84	11.28
Seedlet per spike	9.88	9.74	7.93	10.45	9.79
Seed per spikelet	2.36	2.20	2.20	2.13	2.25
Seed per spike	40.50	41.01	36.00	36.23	40.07
Seed length	6.89	5.78	5.96	5.75	6.17
Seed width	3.41	3.12	3.19	2.85	3.19
Seed thickness	3.09	2.64	2.70	2.49	2.78
Hundred grain weight	4.50	3.57	3.42	3.42	3.86
Awn length	5.52	2.43	1.48	1.49	3.34
Yield	9.92	10.17	11.00	10.25	10.13

Cluster II was the largest cluster with 35 (50 %) accessions, cluster I consisted of 24 (35%) accessions, cluster III had 8 accessions, which comprised 11.42 % accessions, and cluster V was the smallest cluster with 3 (4.29%) accessions. Cluster I was superior in terms of morphological traits such as flag leaf length, flag leaf width, spike length, seed length, seed width, seed thickness, hundred grain weight, and awn length. Cluster-II had high mean for plant height, peduncle length, spike exertion, seed per spike, and yield. Cluster III had high mean for days to emergence, days to heading, and days to flowering. Cluster IV had high mean for spikelets per spike. The selected materials can be used as candidates for selective breeding operations that attempt to produce desirable features for the future. Crosses between the members of the intercluster are likely to provide an advantage for further improvement.

Correlation analysis among phenotypic traits

Correlation among 20 Quantitative traits is presented in Figure 5. Days to 50 % heading showed significantly high correlation with days to first heading (r = 0.90***), with days to first flowering (r = 0.89***), and with days to maturity (r = 0.84***). Days to first flowering had strong positive correlation with days to maturity (r = 0.88***). Days to maturity had moderate negative correlation with yield (r = -0.41***) and seed width (r = -0.41***), which might be due water stress. Days to 50 % heading showed moderately negative correlation with seed width (r = -0.40***), hundred grain weight (r = -0.31**), and also with a hundred grain weight. Plant height showed strong positive correlation (r = 0.80***) with spike exertion. While Plant height showed moderately negative correlation with awn length (r = -0.37**), seed width (r = -0.38**), and with hundred grain weight (r = -0.34**). Peduncle length had strong positive correlation with plant height (r = 0.88***) and with spike exertion (r = 0.87***). Flag leaf length showed positive correlation with flag leaf width (r = 0.57***), moderate positive correlation with Seed width (r = 0.31**), and hundred grain weight (r = 0.34**). For e.g. example, accession NGRCO6389, having the highest FLL (24.70) had high seed width (1.8). Also, it showed moderately negative correlation with days to heading and days to maturity. Flag leaf width also showed moderate positive correlation with hundred grain weight (r = 0.37**). Awn length showed strong positive correlation with spike length (r = 0.79***) and showed moderate positive correlation with hundred grain weight (r = 0.55***), with seed length (r = 0.52***), with seed thickness (r = 0.39***), with seed width (r = 0.48***), and with flag leaf width (r = 0.35**). While it showed moderately negative correlation with days to 1st heading (r = -0.35**), with days to 1st flowering (r = -0.35**), and with plant height (r = -0.37**). Seed length showed positive correlation (r = 0.73***) with a hundred-grain weight. Yield showed moderate positive correlation with spike exertion (r = 0.57***), and showed negative correlation with days to 50 % heading (r = -0.53***), days to flowering (r = -0.45***), and days to maturity (r = -0.41***). Bhattarai et al. (2025) found highly significant correlations among these agro-morphological traits, which supported these research findings.

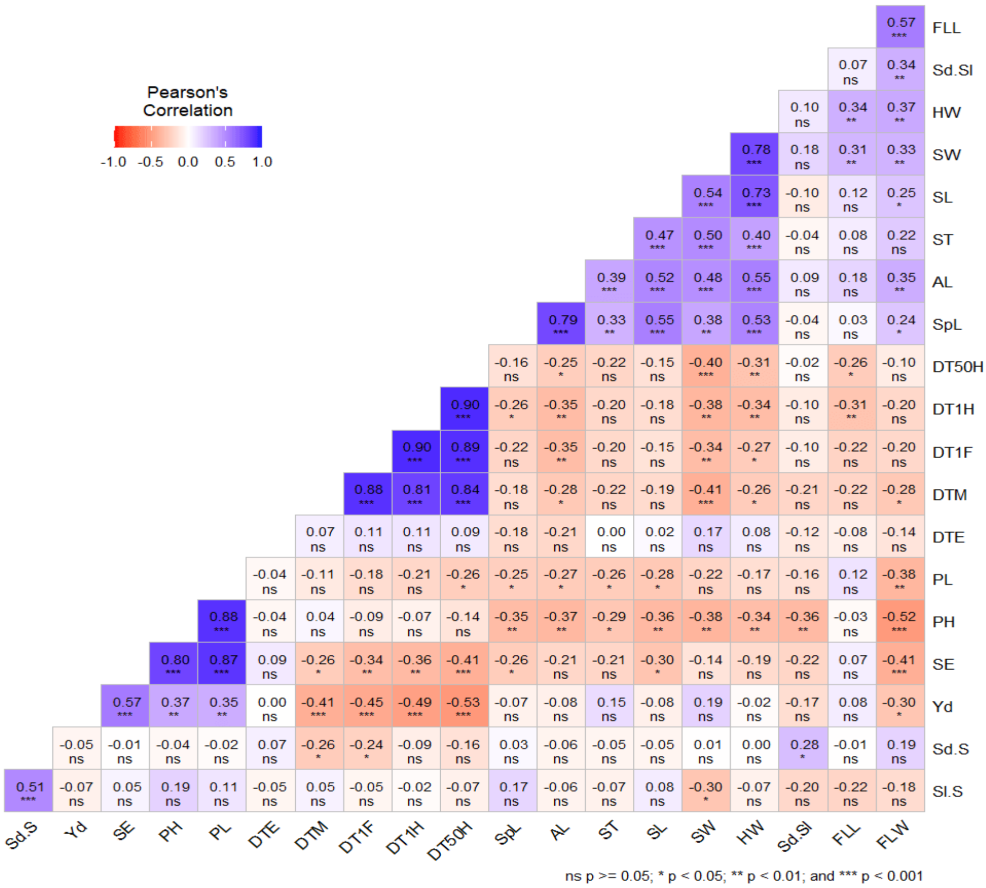

Figure 5. Karl Pearson correlation of quantitative traits of wheat landraces studied at Khumaltar, Lalitpur, Nepal, 2025

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), SpL: Spike length (cm), SE: Spike exertion (cm), Sl.S: No. of Spikelet per spike, Sd.Sl: No. of seed per spikelet, Sd.S: No. of seed per spike, SL (mm): Seed length (mm), SW (mm) : Seed width, ST: Seed thickness, HW (gm): Hundred grain weight, AL: Awn length (cm), and Yd: Yield (t/ha).

CONCLUSION

Significant and wide variation was revealed among qualitative and quantitative traits of wheat landraces, which indicated the existence of high opportunity for genetic improvement in wheat accessions through direct selection and conservation of germplasm for future utilization. Shannon-Weaver diversity indices (H') showed high to low levels of diversity for qualitative traits (0-1.12), while high to moderate levels of diversity were shown for quantitative traits. The results of PCA suggested that key traits contributing to these variances are days to emergence, days to flowering, spike exertion, spike length, seed per spike, and spikelets per spike. Cluster analysis further highlighted important strengths. Findings of this study suggested agro-morphological traits like days to emergence, days to heading, thousand-grain weight, days to flowering, short plant height, high seeds per spike, high seed thickness, seed length, seed width, and spikelets per spike should be prioritized during selection and breeding for improvement. In this study different promising lines for different traits like NGRCO00112 for early days to emergence and early days to heading, NGRCO8489 (53D) for early flowering, NGRCO8489, NGRCO8656, NGRCO8208 (158D)) for maturity, NGRCO00061(5.87 gm) for hundred grain weight, NGRCO00135(4.78 t/ha), NGRCO4276 (3.9 t/ha), NGRCO4266 (3.87 t/ha) for high yielding landraces were selected and are recommended for further multi-location and multi-year trial study. All things considered, this study reflects the landraces as potential candidates bearing initiatives to enhance wheat breeding programs.

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AUTHORS' CONTRIBUTION

M.B conceptualized and designed the whole study. A.S. performed the field experiment, A.S. and M.U. collected the data. A.S. performed the statistical analysis, compilation of the data, interpretation of the results, and drafting of the manuscript and M.B. helped in supervision and funding acquisition. All authors have read and approved the final manuscript.

CONFLICT OF INTEREST

The authors have no conflict of interest to disclose.

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