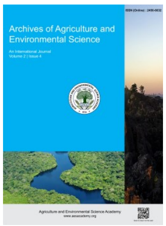
Archives of Agriculture and Environmental Science 9(2): 206-215 (2024)
https://doi.org/10.26832/24566632.2024.090202

e-ISSN: 2456-6632

This content is available online at AESA

Archives of Agriculture and Environmental Science

Journal homepage: journals.aesacademy.org/index.php/aaes



ORIGINAL RESEARCH ARTICLE

Performance evaluation of advanced durum wheat genotypes under irrigated condition at Bhairahawa, Nepal

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ARTICLE HISTORY

Received: 02 February 2024
Revised received: 28 March 2024
Accepted: 18 April 2024

Keywords

Cluster analysis
Correlation analysis
Durum wheat
Genotype evaluation
Principal component analysis

ABSTRACT

A field research was carried out at the National Wheat Research Program (NWRP) in Bhairahawa, Nepal in 2022 to investigate elite durum wheat genotypes and key traits contributing to grain yield. The experiment was performed in an alpha lattice design with two replications. Thirty distinct durum wheat genotypes were assessed, focusing on fourteen quantitative traits including days to booting, days to heading, days to maturity, plant height, spike length, peduncle length, number of tillers per square meter, number of spikes per square meter, number of grains per spike, grain weight per spike, thousand kernel weight, grain yield, biomass yield, chlorophyll content. The studied genotypes were grown under irrigated condition. Genotype NL1779 attained the highest grain yield of 3828 kg/ha, followed by NL1769 (3784 kg/ha), NL1772 (3726 kg/ha), NL1789 (3640 kg/ha) and NL1784 (3570 kg/ha). Principal components analysis revealed that eight traits were the major loadings on the first two principal components that describe 53.4% of the total morphological variance at irrigated condition. Cluster analysis grouped the different genotypes into four clusters, with each cluster showing variation in performance for different traits under irrigated conditions. Cluster III is characterized by genotypes exhibiting the highest grain yield, biomass yield, spike length, number of grains per spike, and number of spikes per square meter. Notably, the high-yielding genotypes NL1779, NL1769, NL1772, NL1789, NL1784, and NL1773 identified within this cluster could serve as potential candidates for inclusion in the national breeding program. These superior genotypes could be recommended for irrigated environment after further evaluation. Integrating them into national breeding programs offers an opportunity for genetic improvement, contributing to establishing a robust durum wheat production system in Nepal, meeting the growing demand for durum wheat products while promoting dietary diversity and sustainable agriculture.

Citation of this article: Pant, K. R., Pandey, D., Adhikari, U., Nainabasti, A., Chaudhary, S., Bastola, B. R., Yadav, R. P., Poudel, B. P., Bista, M., & Raut, S. K. (2024). Performance evaluation of advanced durum wheat genotypes under irrigated condition at Bhairahawa, Nepal. *Archives of Agriculture and Environmental Science*, *9*(3), 207-215, https://dx.doi.org/10.26832/24566632.2024.090202

INTRODUCTION

Wheat (*Triticum aestivum* L.) is a globally significant staple cereal crop, serving as a primary food source for millions worldwide (Khalid *et al*., 2022). Its paramount importance stems from its nutrient-rich grains, which are valuable sources of protein, essential minerals (copper, magnesium, zinc, iron, phosphorus), vitamins (riboflavin, thiamine, niacin, alpha-tocopherol), and carbohydrates (Garg *et al.*, 2021). In Nepal, following rice and maize, wheat is the third most crucial crop; however, in terms of human consumption, it holds the second position (Pandey *et al.*, 2017).

Nepal has released 54 wheat varieties out of them, only 2 are durum wheat varieties. There is very less area of durum wheat (~200-300ha) cultivated in Western Terai (Dang, Banke and Kailali) in Nepal but is in high demand for industrial purpose (NWRP, 2021). Beginning in 2000, the Nepal Agricultural Research Council (NARC) has introduced and initiated testing CIMMYT- develop durum wheat genotypes in different location in the country. Durum is developing into a promising crop and a more and more practical option to grow in near future (NWRP, 2021).

During the fiscal year 2021/22, wheat cultivation in Nepal spanned 716,978 hectares, with an average yield of 2.99 metric tons per hectare, contributing 5.6721% to the nation's agricultural GDP in 2022/23 (MoALD, 2023). Wheat comprises two main types: hexaploid bread wheat (*Triticum aestivum*), characterized by genomes A, B, and D, and tetraploid durum wheat (*Triticum durum*), containing genomes A and B (Khalid *et al.*, 2023). Durum wheat, an allotetraploid (2n = 4x = 28, AABB), is a crucial cereal crop primarily grown in the Mediterranean Basin, ranking second in importance after common bread wheat (Martınez-Moreno *et al.*, 2020; Marzario *et al.*, 2023; Nazco *et al.*, 2012; Paux *et al.*, 2012). It is the tenth most commonly grown cereal globally and plays a vital role in human diets, particularly in the Mediterranean region (Beres *et al.*, 2020).

Durum wheat is considered an exotic crop in Nepal, and its commercial production is limited due to factors such as lack of comprehensive understanding of end-use products, lack of favorable policies for farmers, and limited availability of high-yielding varieties. Consequently, bread wheat accounts for nearly the entire wheat cultivation in the country. However, with changing dietary preferences and increasing urbanization, the demand for durum wheat products in Nepal is rapidly rising (Adhikari *et al.*, 2018). It is utilized in various products, including pasta, bulgur, couscous, and diverse Mediterranean dishes like Gofio and Freekeh, as well as flatbreads (González-Ribot *et al.*, 2017). With a growing global trend towards healthier and diverse diets, the demand for durum wheat products is increasing due to their role in promoting well-rounded, nourishing dietary choices (Kadkol & Sissons, 2015). However, limited areas worldwide can produce durum wheat that meets the stringent quality standards required for end-use suitability (Beres *et al.*, 2020).

Durum wheat genotypes exhibit considerable variation in quantitative traits related to yield and yield-related traits, which are crucial for crop improvement through breeding and selection processes (Dukamo *et al.*, 2023). The success of crop improvement efforts largely depends on the magnitude of genetic variability available (Azad *et al.*, 2022; Kandel *et al.*, 2018) and the heritability of desirable traits (Sarker *et al.*, 2022). While researchers have proposed various methods like principal component analysis (PCA) and cluster analysis to assess genetic variability by studying morphological and growth attributes among genotypes (Azam *et al.*, 2023), there is a lack of comprehensive studies evaluating durum wheat genotypes for their traits, trait correlations, and selection of the best genotypes using PCA and cluster analysis in the context of Nepal. The aim of this study was to evaluate durum wheat genotypes for their traits, investigate the correlation between different traits, and select the best genotypes using principal component analysis (PCA) and cluster analysis. The findings can be exploited in future durum wheat breeding programs to establish a robust durum wheat production system in Nepal, addressing the growing demand for durum wheat products while promoting dietary diversity and sustainable agriculture.

Table 1. List of thirty durum wheat genotypes that were evaluated in the year 2022/23.

Number of Entries	Genotypes	Number of Entries	Genotypes
1	NL 1767	16	NL 1782
2	NL 1768	17	NL 1783
3	NL 1769	18	NL 1784
4	NL 1770	19	NL 1785
5	NL 1771	20	NL 1786
6	NL 1772	21	NL 1787
7	NL 1773	22	NL 1788
8	NL 1774	23	NL 1789
9	NL 1775	24	NL 1790
10	NL 1776	25	NL 1791
11	NL 1777	26	NL 1792
12	NL 1778	27	NL 1793
13	NL 1779	28	NL 1794
14	NL 1780	29	Khajura Durum 1(check)
15	NL 1781	30	Khajura Durum 2 (check)

MATERIALS AND METHODS

Plant materials and experimental site

The research was conducted during the 2022/23 cropping season under irrigated conditions at the varietal improvement block of the National Wheat Research Program (NWRP) in Bhairahawa, Nepal (27°31'49" N, 83°27'36" E, 112 m above sea level). The experimental site is characterized by a sub-tropical climate with an annual rainfall of 1725.3 mm and silt loam soil texture (Khadka *et al.*, 2015). Thirty durum wheat genotypes, including two standard check varieties, Khajura Durum 1 and Khajura Durum 2, developed by CIMMYT and NARC, were used as research materials (Table 1).

Experimental design and crop management

The experiment was laid out in an alpha lattice design with six blocks and five plots per block, replicated twice (Gomez and Gomez, 1984). Each plot measured 3 × 2 m^2 consisting of eight rows spaced 25 cm apart and 3 m in length. Sowing was done on December 5th, 2022, at a seed rate of 120 kg ha^{-1} by continuous seed drill method (Paudel *et al.*, 2022). Fertilizers were applied at the recommended rate of 150:50:50 kg N: P_2O_5: K_2O ha^{-1} (Bhatta *et al.*, 2020). Half of the nitrogen dose and the full doses of phosphorus and potassium were applied as basal doses during final land preparation, while the remaining half of the nitrogen dose was split into two equal top-dressings at the crown root initiation (CRI) stage (25 days after sowing) and the booting stage (60 days after sowing). Irrigation was provided at the CRI and booting stages, following standard practices for wheat cultivation. Plant protection measures and weeding were carried out.

Data collection and analysis

The following traits were phenotyped: days to booting (DTB), days to heading (DTH), days to maturity (DTM), spike length (SL), plant height (PH), chlorophyll content (SPAD), thousand kernel weight (TKW), number of tillers per square meter (NTPM), number of spikes per square meter (NSPM), peduncle length (PL), number of grains per spike (NGPS), grain weight per spike (GYPS), grain yield (kg ha^{-1}) (GY), and biomass yield (kg ha^{-1}) (BY). Data entry and processing were performed using Microsoft Office Excel 2007. Analysis of variance (ANOVA), correlation analysis, unweighted pair group method with arithmetic mean (UPGMA) clustering, principal component analysis (PCA), and calculation of means were conducted using R Studio software version 4.3.1. Statistical significance was determined at a 5% level of probability.

Table 2(a). Mean performance of thirty durum wheat genotypes for grain yield and yield attributing traits at Bhairahawa, Rupandehi (2022/23).

S.N.	Genotypes	DTB (days)	DTH (days)	DTM (days)	Spike Length (cm)	PH (cm)	No. of tiller/m^2
1	NL 1767	83	86	118	5.3	67	452
2	NL 1768	77	81	114	6.0	85	320
3	NL 1769	79	83	116	5.7	77	401
4	NL 1770	77	82	115	5.2	71	375
5	NL 1771	78	82	115	6.1	79	334
6	NL 1772	79	83	116	6.2	74	386
7	NL 1773	78	82	115	6.1	77	365
8	NL 1774	76	80	113	5.2	73	370
9	NL 1775	76	80	113	5.4	73	447
10	NL 1776	75	81	114	6.0	76	433
11	NL 1777	79	83	116	6.1	73	356
12	NL 1778	77	81	114	5.9	73	439
13	NL 1779	77	81	114	5.3	69	406
14	NL 1780	78	82	115	6.0	77	394
15	NL 1781	76	80	113	5.5	74	352
16	NL 1782	79	87	118	5.2	80	316
17	NL 1783	78	81	114	6.0	73	454
18	NL 1784	79	83	116	6.0	81	399
19	NL 1785	77	80	113	5.4	68	477
20	NL 1786	78	83	115	6.2	77	310
21	NL 1787	79	82	115	5.7	66	289
22	NL 1788	79	84	116	6.3	74	343
23	NL 1789	77	81	114	5.8	78	382
24	NL 1790	78	83	116	6.7	77	385
25	NL 1791	77	82	115	5.6	73	380
26	NL 1792	78	82	115	5.7	75	386
27	NL 1793	79	83	116	5.0	70	388
28	NL 1794	78	83	116	6.1	78	354
29	Khajura Durum 1(Check)	78	83	116	7.0	80	352
30	Khajura Durum2 (check)	76	80	113	5.9	75	359
	Grand Mean	77.6	82.1	114.95	5.83	74.84	380.11
	CV(%)	1.84	1.43	0.85	5.2	4.92	12.81
	LSD value	2.99	2.47	2.047	0.634	7.715	96.96
	P value	0.040	0.001	0.001	<0.001	0.011	0.080

Table 2(b). Mean performance of thirty durum wheat genotypes for grain yield and yield attributing traits at Bhairahawa, Rupandehi (2022/23).

S. No.	Genotypes	No. of spikes/m^2	SPAD Value	Peduncle length (cm)	No. of grains / spike	Grain weight/ spike	GY (kg/ha)	Biomass Yield (kg/ha)
1	NL 1767	369	39.3	31.9	39	1.8	2405	4684
2	NL 1768	314	42.8	37.8	48	1.6	2979	6210
3	NL 1769	397	43.4	31.2	55	1.4	3784	6694
4	NL 1770	371	44.8	34.9	46	1.6	3176	6081
5	NL 1771	306	45.4	35.8	35	1.3	2678	5645
6	NL 1772	381	45.9	32.6	45	2.1	3726	6532
7	NL 1773	356	44.5	33.5	49	1.3	3512	6493
8	NL 1774	361	38.6	35.3	43	1.8	2570	4973
9	NL 1775	444	44.1	34.8	46	1.6	3103	5644
10	NL 1776	421	39.3	32.1	44	1.6	3354	6284
11	NL 1777	351	47.8	32.5	50	1.7	2703	5260
12	NL 1778	427	43.0	35.3	51	1.7	3002	6312
13	NL 1779	398	44.2	30.6	41	1.6	3828	6751
14	NL 1780	381	44.0	32.9	56	1.4	2884	5487
15	NL 1781	376	37.0	32.9	46	1.5	2638	5436
16	NL 1782	309	43.3	28.0	42	1.7	3130	6459
17	NL 1783	446	41.0	30.0	39	2.0	3055	6201
18	NL 1784	397	43.3	30.8	50	1.8	3570	6769
19	NL 1785	449	35.7	33.8	42	1.6	2627	4996
20	NL 1786	293	42.9	33.6	43	1.4	3449	6255
21	NL 1787	279	41.3	26.8	38	1.6	1872	3777
22	NL 1788	335	42.4	34.6	46	1.9	3067	5721
23	NL 1789	379	37.8	35.5	51	1.8	3640	6093
24	NL 1790	376	41.2	32.5	47	1.5	2706	5348
25	NL 1791	360	45.6	33.5	58	1.5	3266	5924
26	NL 1792	376	44.6	31.3	41	1.3	3097	6085
27	NL 1793	379	47.2	29.4	36	1.6	2458	4841
28	NL 1794	346	39.7	33.1	58	1.7	3408	6670
29	Khajura Durum 1 (Check)	345	43.9	32.7	51	1.8	3440	6578
30	Khajura Durum 2 (check)	354	42.2	36.2	46	1.5	3098	5694
	Grand Mean	369.1	42.53	32.86	45.96	1.625	3074.2	5863.3
	CV(%)	11.94	6.43	4.46	11.06	8.47	7.46	8.79
	LSD value	92.33	5.72	3.072	10.64	0.287	480.03	1079.07
	P value	0.070	0.050	<0.01	0.010	<0.01	<0.001	0.003

Table 3. Mean value of traits for 4 clusters obtained from hierarchical cluster analysis.

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Grand Centroid
DTH	82.2	82.0	82.5	81.8	82.1
DTM	114.9	114.9	115.3	114.7	115.0
PH	68.8	76.1	76.8	75.4	74.3
SL	5.3	5.8	6.1	6.0	5.8
NSPM	367.4	369.6	374.2	365.3	369.1
NGPS	39.6	46.1	49.7	46.5	45.5
GWPS	1.7	1.6	1.7	1.6	1.6
TKW	32.1	35.2	34.6	32.5	33.6
GY	2386.4	3214.8	3609.7	2859.6	3017.6
BY	4654.0	6190.6	6641.0	5529.5	5753.8

Table 4. Number of clusters and genotypic details in each cluster.

S. No.	Clusters	No. of genotypes	Genotypes
1	Cluster I	5	NL 1787, NL 1774, NL 1785, NL 1767 and NL 1793
2	Clusters II	10	NL 1789, NL 1776, NL 1786, NL 1791, NL 1770, NL 1792, NL 1782, NL 1768, NL 1778 and NL 1783
3	Clusters III	7	NL 1772, NL 1769, NL 1779, NL 1773, NL 1794 and Khajura Durum1
4	Clusters IV	8	NL 1775, NL 1788, KhajuraDurum2, NL 1781, NL 1777, NL 1790, NL 1771 and NL 1780

RESULTS AND DISCUSSION

The present study was carried out for evaluating the 30 wheat genotypes for yield potential, character association, cluster analysis and principal component analysis and the results obtained were presented as below.

Analysis of variance

Significant variations were observed among the tested durum wheat genotypes for most of the assessed traits, except for SPAD, NTPM, and NSPM (Table 2). This finding is consistent with previous studies by Adhikari *et al.* (2018), Al-Sayaydeh *et al.* (2023), Nainabasti *et al.* (2024), Chamekh *et al.* (2017), Boussakouran *et al.* (2021), Mohammadi *et al.* (2019), Bányai *et al.* (2020), and Mansouri *et al.* (2018), who reported significant differences among durum wheat genotypes for various traits, including days to heading (DTH), days to maturity (DTM), flag leaf area (FLA), number of grains per spike (NGPS), spike length (SL), plant height (PH), peduncle length (PL), thousand kernel weight (TKW), SPAD, and grain yield (GY). The observed variability among genotypes for these traits suggests the potential for genetic improvement and trait integration through effective breeding strategies. Grain yield is a paramount trait in cereal crop evaluation, and in this study, the genotype NL 1779 exhibited the highest grain yield of 3828 kg ha^{-1}, closely followed by NL 1789 with 3640 kg ha^{-1}. Improving grain yield is often achieved by focusing on yield components, which are closely linked to grain yield (Razzaq *et al.*, 2013). One of the key yield components is grain weight per spike, as it directly impacts the overall grain yield per unit area. A higher grain weight per spike is desirable (Madan & Sethi, 2018), and in this study, the genotype NL 1772 exhibited the highest grain weight per spike of 2.1g. Larger grain weight is also advantageous for improved milling and flour extraction (Khan *et al.*, 2009), making genotypes with higher grain weight promising for developing genotypes with maximum flour yields. The grain weight per spike is influenced by the number of grains per spike, spike length, and number of spikes per square meter (Tahir *et al.*, 2009).

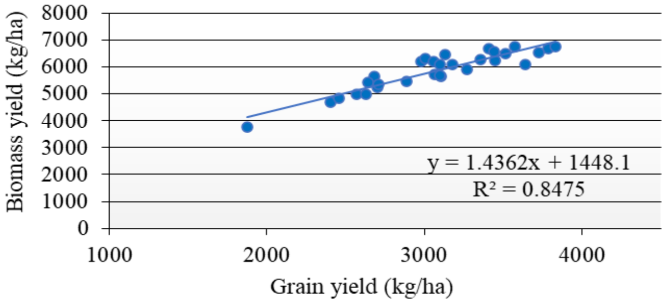

Figure 1. *Association between grain yield and biomass yield.*

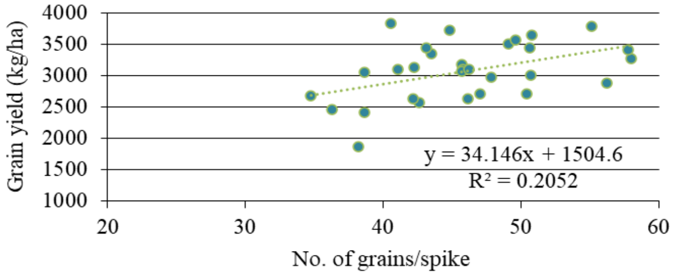

Figure 2. *Association between grain yield and number of grains per spike.*

In this study, the genotypes NL 1794 and NL 1791 exhibited the highest number of grains per spike (58), while the check variety Khajura Durum1 had the longest spike length (7 cm), followed by NL 1790 (6.7 cm). The genotype NL 1785 showed the highest number of spikes per square meter (449). Additionally, a greater number of tillers per square meter is generally desirable, as each tiller has the potential to develop into a productive stem bearing grain heads (Khaliq *et al.*, 2008). The genotype NL 1785 exhibited the highest number of tillers per square meter (447). Peduncle length is another important trait in wheat, as a shorter peduncle provides better support to the developing grain head, reducing the risk of lodging and improving crop stability under adverse weather conditions (Madan & Sethi, 2018). In this study, the genotype NL 1787 exhibited the shortest peduncle length (26.8 cm), while NL 1768 had the longest peduncle length (32.86 cm).

Plant height is a crucial trait in wheat breeding, as shorter plants are generally favored in modern breeding programs due to their improved resistance to lodging, more efficient resource utilization, and better adaptation to various environmental conditions (Mohammadi *et al.*, 2015). However, optimal plant height may vary depending on specific breeding objectives and environmental factors. In this study, the genotype NL 1787 exhibited the lowest plant height (66 cm), while NL 1768 had the tallest plant height (85 cm). Thousand kernel weight (TKW) is a valuable trait in durum wheat breeding programs, as larger kernels typically result in higher milling yields due to a greater ratio of endosperm to bran (Madan & Sethi, 2018; Mérida-García *et al.*, 2020). Additionally, higher TKW is associated with increased grain yield (Tahir *et al.*, 2009). In this study, the genotype NL 1779 achieved the highest TKW of 41.2 g. The SPAD value, an indicator of chlorophyll content and photosynthetic efficiency, is desirable for higher biomass production and ultimately higher grain yield. In this study, the genotype NL 1777 exhibited the highest SPAD value of 47.8, while NL 1785 had the lowest SPAD value of 35.7. Biomass yield is an important indicator of overall crop productivity and resource utilization efficiency. Higher biomass yield is generally desirable in wheat, as it suggests greater plant growth and potential for higher grain yield. In this study, the genotype NL 1784 achieved the highest biomass yield of 6769 kg ha^{-1}, followed by NL 1779 with 6751 kg ha^{-1}. Regarding the days to booting, heading, and maturity, shorter durations can be advantageous for avoiding potential abiotic and biotic stresses that could affect grain yield, unless specific circumstances or research objectives dictate otherwise (Mohammadi *et al.*, 2015; Mansouri *et al.*, 2018). In this study, the genotype NL 1776 reached booting stage earliest (75 days), while NL 1767 reached it later (83 days). The genotypes NL 1774, NL 1775, NL 1781, and the check variety Khajura Durum2 were the earliest to head (80 days), while NL 1782 showed late heading (87 days). The genotype NL 1785 and the check variety Khajura Durum2 reached maturity earliest (113 days), while NL 1767 matured later (118 days).

Table 5. Vector loadings and proportion of variance explained by the first five principal components (PC).

Traits	PC1	PC2	PC3	PC4	PC5
DTH	-0.172	0.568	0.302	-0.080	0.140
DTM	-0.190	0.552	0.316	-0.107	0.078
PH	-0.453	-0.016	-0.291	-0.145	-0.032
SL	-0.352	0.039	-0.252	-0.050	-0.655
NSPM	0.080	-0.448	0.471	0.163	-0.019
NGPS	-0.328	-0.219	0.201	-0.445	-0.260
GWPS	-0.050	0.086	0.432	0.545	-0.521
TKW	-0.173	0.151	-0.413	0.629	0.099
GY	-0.459	-0.235	0.176	0.141	0.310
BY	-0.498	-0.191	0.100	0.152	0.313
Loadings					
Eigen Value	3.04	2.30	1.37	1.32	0.87
Standard deviation	1.74	1.52	1.17	1.15	0.93
Proportion of Variance	0.30	0.23	0.14	0.13	0.09
Cumulative Proportion	0.30	0.53	0.67	0.80	0.89

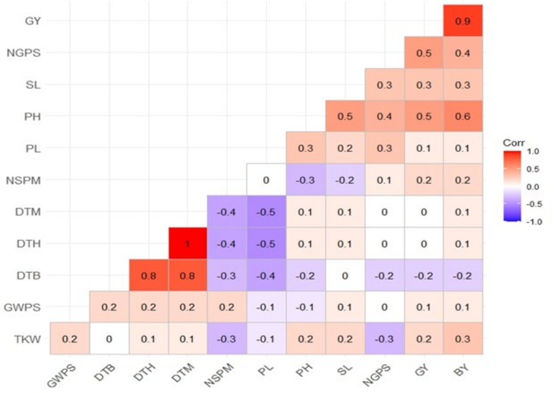

Figure 3. *Correlation matrix among different traits for 30 durum wheat genotypes.*

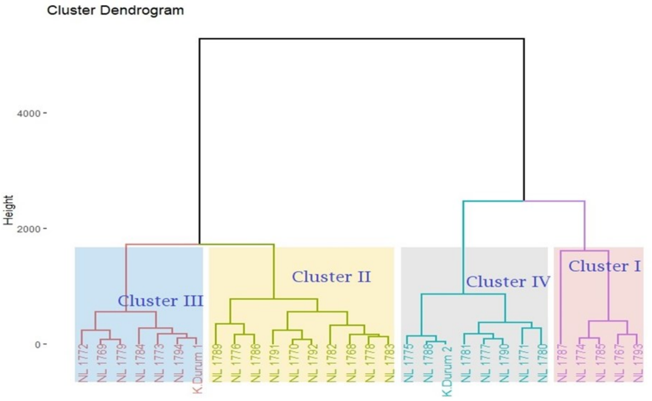

Figure 4. *Hierarchical clustering of 30 wheat genotypes.*

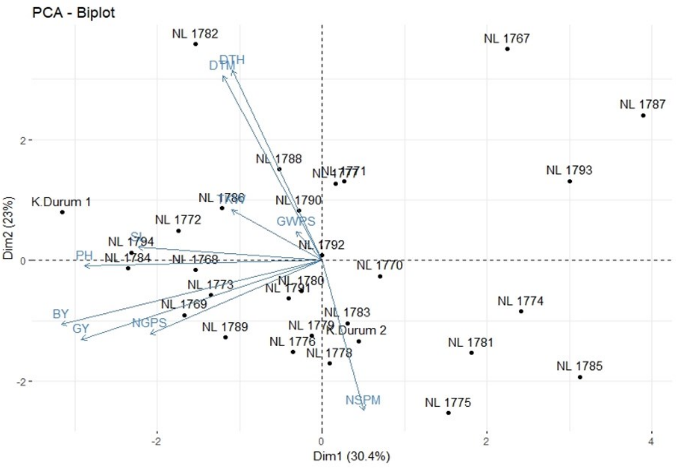

Figure 5. *Biplot between first and second principal components.*

Correlation analysis

Correlation analysis is a valuable tool for assessing the relationships and interdependencies between different traits. It assists plant breeders in understanding how the selection or improvement of one trait may influence other traits, enabling indirect selection strategies. Enhancing wheat grain yield can be achieved by focusing on traits that exhibit strong positive correlations with yield. In this study, several significant correlations were observed between the analyzed traits (Figure 3). Notably, grain yield exhibited highly significant positive correlations with biomass yield (0.92***), suggesting that genotypes with higher biomass production tended to yield higher grain yields as well. This finding aligns with the general understanding that increased biomass accumulation can contribute to enhanced grain yield potential. Furthermore, grain yield displayed significant positive correlations with the number of grains per spike (0.47**) and plant height (0.45*). These correlations indicate that genotypes with more grains per spike and taller plant stature tended to produce higher grain yields in the evaluated durum wheat genotypes. The positive association between grain yield and plant height is consistent with some previous reports (Mohammadi & Golkari, 2022; Laala *et al.*, 2021), although contrasting results have also been documented (Schulthess *et al.*, 2017; Shyam *et al.*, 2018), suggesting that the relationship may be influenced by environmental factors and genetic backgrounds. While grain yield exhibited non-significant positive correlations with traits such as the number of spikes per square meter (0.21), thousand kernel weight (0.19), and spike length (0.26), it showed a non-significant negative correlation with days to booting (-0.19). These weaker or non-significant correlations suggest that the direct selection for these traits may have a limited impact on improving grain yield in the studied durum wheat genotypes. The analysis also revealed other noteworthy correlations among various traits. For instance, biomass yield demonstrated a highly significant positive correlation with plant height (0.61**), indicating that taller genotypes tended to accumulate higher biomass. Plant height, in turn, exhibited highly significant positive correlations with spike length (0.52**) and a significant positive correlation with the number of grains per spike (0.41*).

Interestingly, thousand kernel weight showed non-significant positive correlations with spike length (0.23) but non-significant negative correlations with the number of spikes per square meter (-0.31) and the number of grains per spike (-0.30). These findings suggest potential trade-offs between kernel size and other yield components, which may need to be balanced in breeding programs. Moreover, days to booting exhibited highly significant positive correlations with days to heading (0.81***) and days to maturity (0.84***), as well as a significant negative correlation with peduncle length (-0.44*). However, it showed a non-significant positive correlation with grain weight per spike (0.22).

Cluster analysis

Cluster analysis was conducted on 30 genotypes of durum wheat using variables including plant height, spike length, number of spikes per square meter, number of grains per spike, grain weight per spike, thousand kernel weight, grain yield, and biomass yield. As a result, the genotypes were segregated into four clusters, as illustrated in Figure 4. Cluster I comprised 5 genotypes, accounting for 16.6% of the total genotypes, namely NL 1787, NL 1774, NL 1785, NL 1767, and NL 1793. This cluster encompassed genotypes characterized by the lowest values in terms of thousand kernel weight, grain yield, and biomass yield. Cluster II was composed of 10 genotypes, representing 33.33% of the total genotypes: NL 1789, NL 1776, NL 1786, NL 1791, NL 1770, NL 1792, NL 1782, NL 1768, NL 1778, and NL 1783. These genotypes exhibited the highest values in thousand kernel weight (TKW) and ranked second in terms of the number of spikes per square meter, grain yield, and biomass yield. Cluster III comprises 7 genotypes, accounting for 23.3% of the total genotypes: NL 1772, NL 1769, NL 1779, NL 1773, NL 1794, and KhajuraDurum1. This cluster is characterized by the highest values in grain yield, biomass yield, spike length, number of grains per spike, and number of spikes per square meter, and it ranks second in terms of thousand kernel weight. Cluster IV comprised 8 genotypes, representing 26.6% of the total genotypes: NL 1775, NL 1788, KhajuraDurum2, NL 1781, NL 1777, NL 1790, NL 1771, and NL 1780. This cluster encompasses genotypes exhibiting intermediate values across almost all traits, including plant height, spike length, number of spikes per square meter, number of grains per spike, grain weight per spike, thousand kernel weight, grain yield, and biomass yield.

Principle component analysis

PCA was use to enhance the distinct separation and categorization of diverse traits of durum wheat genotypes. The PCA analysis revealed that among five components (PC1, PC2, PC3, PC4, and PC5), PC5 explained a significant proportion of variation (0.89). Cumulative variance of 89.0% was shown by PC5 signifying their importance (Table 5). Within all PCs, the first PC (0.30) made the largest contribution to the total variance. The primary traits influencing the first PC included grain yield, biomass yield, plant height, spike length, and number of grains per spike. Likewise, for the second PC, Days to Heading (DTH), Days to Maturity (DTM), and number of spikes per square meter emerged as the major contributors. Thousand kernel weight (TKW), number of spikes per square meter, and grain weight per spike were the key factors contributing to diversity in the third PC. In the fourth PC, the maximum variation was attributed to TKW, followed by grain weight per spike. Spike length and grain weight per spike emerged as the major contributing traits for PC5. The biplot illustrates the correlation between 30 durum wheat genotypes and their component traits (Figure 5). Among the 30 genotypes, grain yield exhibited a positive relationship with both the number of grains per spike and biomass yield. The PCA1 and PCA2 axes, justify 53.4% (30.4% and 23%, respectively) of the total variation. The first component explained 53.4% of the variations and demonstrated strong correlations with BY, GY, NGPS, PH, SL. This component could be called the group of great performance under irrigated condition. The second component explained 23% of the variations, having a strong correlation with DTH, DTM, NSPM. NSPM has negative correlation with DTH and DTM. Therefore, selecting genotype with high PC1 and low PC2 is suitable. Among the genotypes, NL 1769, NL 1772, NL 1789 and NL 1784 exhibited high grain yield. These high-yielding genotypes also exhibited desirable traits like biomass yield, spike length, plant height, number of grains per spike, and number of spikes per meter square.

Conclusion

In conclusion, among the various genotypes evaluated, NL 1779 was the top-performing genotype in terms of yield, followed by NL 1769, NL 1772, NL 1789, and NL 1784. These high-yielding genotypes demonstrated favorable characteristics such as biomass yield, spike length, number of grains per spike, and number of spikes per square meter. Notably, cluster III comprised seven genotypes, namely NL 1769, NL 1772, NL 1773, NL 1779, NL 1784, NL 1794, and KhajuraDurum1, which exhibited superior traits related to grain yield, biomass yield, spike length, number of grains per spike, and number of spikes per square meter. As a result, these genotypes present promising candidates for integration into national breeding programs or for recommendation in irrigated regions after further evaluation.

Authors contribution: Conceptualization, KRP and DP; Methodology: KRP, DP, SC, BRB, RPY, BPP, SKR and MB; Software and validation: KRP; Formal analysis and investigation: KRP; Resources: KRP and DP; Data curation: KRP; Writing—original draft preparation: KRP, DP and UA; Writing—review and editing: KRP and AN; Visualization: KRP and AN; Supervision: KRP and DP; Project administration: KRP and DP; Funding acquisition: NWRP, NARC. All authors have read and agreed to the published version of the manuscript.

Conflicts of interest: The authors declare no conflict of interest.

REFERENCES

Adhikari, S., Rana, N., Ojha, B., Kharel, R., Chauhan, S., & Thapa, D. (2018). Study of Variability and Association of Yield Attributing Traits in Durum Wheat Genotypes. *Journal of Agriculture and Ecology Research International*, *14*(4), 1–12, https://doi.org/10.9734/jaeri/2018/42077

Al-Sayaydeh, R., Shtaya, M. J., Qubbaj, T., Al-Rifaee, M. K., Alabdallah, M. A., Migdadi, O., Gammoh, I. A., & Al-Abdallat, A. M. (2023). Performance and Stability Analysis of Selected Durum Wheat Genotypes Differing in Their Kernel Characteristics. *Plants*, *12*(14), 1–18.

Azad, A. K., Sarker, U., Ercisli, S., Assouguem, A., Ullah, R., Almeer, R., Sayed, A. A., & Peluso, I. (2022). Evaluation of Combining Ability and Heterosis of Popular Restorer and Male Sterile Lines for the Development of Superior Rice Hybrids. *Agronomy*, *12*(4), 1–23, https://doi.org/10.3390/agronomy12040965

Azam, M. G., Hossain, M. A., Sarker, U., Alam, A. K. M. M., Nair, R. M., Roychowdhury, R., Ercisli, S., & Golokhvast, K. S. (2023). Genetic Analyses of Mungbean [*Vigna radiata* (L.) Wilczek] Breeding Traits for Selecting Superior Genotype(s) Using Multivariate and Multi-Traits Indexing Approaches. *Plants*, *12* (10). https://doi.org/10.3390/plants12101984

Bányai, J., Kiss, T., Gizaw, S. A., Mayer, M., Spitkó, T., Tóth, V., Kuti, C., Mészáros, K., Láng, L., Karsai, I., & Vida, G. (2020). Identification of superior spring durum wheat genotypes under irrigated and rain-fed conditions. *Cereal Research Communications*, *48*(3), 355–364, https://doi.org/10.1007/s42976-020-00034-z

Beres, B. L., Rahmani, E., Clarke, J. M., Grassini, P., Pozniak, C. J., Geddes, C. M., Porker, K. D., May, W. E., & Ransom, J. K. (2020). A Systematic Review of Durum Wheat: Enhancing Production Systems by Exploring Genotype, Environment, and Management (G × E × M) Synergies. *Frontiers in Plant Science*, *11*(October). https://doi.org/10.3389/fpls.2020.568657

Bhatta, M., Regmi, A. P., Sah, S. N., & Shaheb, M. R. (2020). A guide for fertilizer recommendation for cereal crops in Nepal. Nepal Agricultural Research Council.

Boussakouran, A., El Yamani, M., Sakar, E. H., & Rharrabti, Y. (2021). Genetic Advance and Grain Yield Stability of Moroccan Durum Wheats Grown under Rainfed and Irrigated Conditions. *International Journal of Agronomy*. https://doi.org/10.1155/2021/5571501

Chamekh, Z., Karmous, C., Ayadi, S., Sahli, A., Belhaj Fraj, M., Yousfi, S., Rezgui, S., Ben Aissa, N., Serret, M. D., McCann, I., Trifa, Y., Amara, H., & Araus, J. L. (2017). Comparative performance of δ13C, ion accumulation and agronomic parameters for phenotyping durum wheat genotypes under various irrigation water salinities. *Annals of Applied Biology*, *170*(2), 229–239, https://doi.org/10.1111/aab.12332

CIMMYT. (2019). Wheat production. https://www.cimmyt.org/resources/wheat-production/

Dukamo, B. H., Gedebo, A., Tesfaye, B., & Degu, H. D. (2023). Genetic diversity of Ethiopian durum wheat (*T. turgidum* subsp. durum) landraces under water stressed and non stressed conditions. *Heliyon*, *9*(7), e18359. https://doi.org/10.1016/j.heliyon.2023.e18359

Garg, M., Sharma, A., Vats, S., Tiwari, V., Kumari, A., Mishra, V., & Krishania, M. (2021). Vitamins in Cereals: A Critical Review of Content, Health Effects, Processing Losses, Bioaccessibility, Fortification, and Biofortification Strategies for Their Improvement. *Frontiers in Nutrition*, *8*(6), 1–15, https://doi.org/10.3389/fnut.2021.586815

Gomez, K. A., & Gomez, A. A. (1984). Statistical procedures for agricultural research (2nd ed.). John Wiley and Sons.

González-Ribot, G., Opazo, M., Silva, P., & Acevedo, E. (2017). Traits explaining durum wheat (*Triticum turgidum* L. spp. durum) yield in dry chilean mediterranean environments. *Frontiers in Plant Science*, *8*(10), 1–11, https://doi.org/10.3389/fpls.2017.01781

Kadkol, G. P., & Sissons, M. (2015). Durum Wheat: Overview. In *Encyclopedia of Food Grains: Second Edition* (2nd ed., Vols. 1–4). Elsevier Ltd. https://doi.org/10.1016/B978-0-12-1

Kandel, B. P., Sharma, B. K., Sharma, S., & Shrestha, J. (2018). Genetic variability, heritability, and genetic advance estimates in early maize (*Zea mays* L,) genotypes in Nepal. *Agricultura*, *107*(3-4), 29-35, https://doi.org/10.30910/turkjans.421363394437-5.00024-3

Khadka, D., Lamichhane, S., Thapa, B., Rawal, N., Chalise, D. R., Vista, S. P., & Lakhe, L. (2015, March). Assessment of soil fertility status and preparation of their maps of National Wheat Research Program (NWRP), Bhairahawa, Nepal. In *Proceedings of the workshop, 24-25 March 2015*.

Khalid, A., Hameed, A., Shamim, S., & Ahmad, J. (2022). Divergence in Single Kernel Characteristics and Grain Nutritional Profiles of Wheat Genetic Resource and Association Among Traits. *Frontiers in Nutrition*, *8*(2), 1–13, https://doi.org/10.3389/fnut.2021.805446

Khalid, A., Hameed, A., & Tahir, M. F. (2023). Wheat quality: A review on chemical composition, nutritional attributes, grain anatomy, types, classification, and function of seed storage proteins in bread making quality. *Frontiers in Nutrition*, *10*(2), 1–14, https://doi.org/10.3389/fnut.2023.1053196

Khaliq, I., Irshad, A. and Arshad, M. 2008. Awn and flag leaf contribution towards grains yield in spring wheat (*Triticum aestivum* L.). Cereal *Research Communications*, *36*(1), 65-76.

Khan, M. R., Anjum, F.M., Zahoor, T., & Nawaz, H. (2009). Biochemical and technological characterization of Pakistani spring wheats. *Pakistan Journal of Agricultural Sciences*, *46*(4), 271-279.

Khan, S. A., & Hassan, G. (2017). Heritability and Correlation Studies of Yield and Yield Related Traits in Bread Wheat. *Sarhad Journal of Agriculture*, *33*(1), 103–107, https://doi.org/10.17582/journal.sja/2017.33.1.103.107

Laala, Z., Oulmi, A., Fellahi, Z. E. A., & Benmahammed, A. (2021). Studies on the nature of relationships between grain yield and yield-related traits in durum wheat (*Triticum durum* desf.) populations. *Revista Facultad Nacional de Agronomia Medellin*, *74*(3), 9631–9642, https://doi.org/10.15446/rfnam.v74n3.92488

Madan, S., & Sethi, S. K. (2018). Chemical Science Review and Letters Assessment of Yield Attributes of Durum Wheat (*Triticum Durum* L.) Genotypes under Irrigated Conditions. *Chemical Science Review and Letters*, *7*(25), 256–261.

Mansouri, A., Oudjehih, B., Benbelkacem, A., Fellahi, Z. E. A., & Bouzerzour, H. (2018). Variation and Relationships among Agronomic Traits in Durum Wheat [*Triticum turgidum* (L.) Thell. ssp. turgidum conv. durum (Desf.) MacKey] under South Mediterranean Growth Conditions: Stepwise and Path Analyses. *International Journal of Agronomy*, *2018*. https://doi.org/10.1155/2018/8191749

Martínez-Moreno, F., Solís, I., Noguero, D., Blanco, A., Özberk, İ., Nsarellah, N., & Soriano, J. M. (2020). Durum wheat in the Mediterranean Rim: Historical evolution and genetic resources. *Genetic Resources and Crop Evolution*, 67, 1415-1436, https://doi.org/10.1007/s10722-020-00913-8

Marzario, S., Sica, R., Taranto, F., Fania, F., Esposito, S., De Vita, P., Gioia, T., & Logozzo, G. (2023). Phenotypic evolution in durum wheat (Triticum durum Desf.) based on SNPs, morphological traits, UPOV descriptors and kernel-related traits. *Frontiers in Plant Science*, *14*(8), 1–20, https://doi.org/10.3389/fpls.2023.1206560

Mérida-García, R., Bentley, A. R., Gálvez, S., Dorado, G., Solís, I., Ammar, K., & Hernandez, P. (2020). Mapping agronomic and quality traits in elite durum wheat lines under differing water regimes. *Agronomy*, *10*(1), 1–23, https://doi.org/10.3390/agronomy10010144

MoALD. (2023). Statistical Information on Nepalese Agriculture 2078/79 (2021/22). *MoALD*, 269.

Mohammadi, R., & Amri, A. (2021). Agronomic Performance and Genotype × Moisture Conditions Interaction for Morpho-Physiological Traits in Durum Wheat. *Crop Breeding, Genetics and Genomics*, *3*(1), 1–25, https://doi.org/10.20900/cbgg20210002

Mohammadi, R., Etminan, A., & Shoshtari, L. (2019). Agro-physiological characterization of durum wheat genotypes under drought conditions. *Experimental Agriculture*, *55*(3), 484–499, https://doi.org/10.1017/S0014479718000133

Mohammadi, R., & Golkari, S. (2022). Genetic resources for enhancing drought tolerance from a mini-core collection of spring bread wheat (*Triticum aestivum* L.). *Acta Scientiarum - Agronomy*, *44*(1978), 1–15. https://doi.org/10.4025/actasciagron.v44i1.56129

Mohammadi, R., Sadeghzadeh, B., Ahmadi, H., Bahrami, N., & Amri, A. (2015). Field evaluation of durum wheat landraces for prevailing abiotic and biotic stresses in highland rainfed regions of Iran. *Crop Journal*, *3*(5), 423–433, https://doi.org/10.1016/j.cj.2015.03.008

Nazco, R., Villegas, D., Ammar, K., Peña, R. J., Moragues, M., & Royo., C. (2012). Can Mediterranean durum wheat landraces contribute to improved grain quality attributes in modern cultivars? *Euphytica*, *185*, 1–17, https://doi.org/10.1007/s10681-011-0588-6

Nainabasti, A., Subedi, B., Thapa, D. S., Bohora, K. B., Shah, M. K., & Pant, K. R.

(2024). Evaluation of elite spring wheat genotypes for grain yield and other agronomic attributes in hills of Sudurpaschim Province, Nepal. *Archives of Agriculture and Environmental Science*, *9*(1), 85–92. https://doi.org/10.26832/24566632.2024.0901013

NWRP. (2021). Annual Report 2077/78 (2020/21). National Wheat Research Program, NARC, Bhairahawa, Rupandehi, Nepal.

Pandey, G., Yadav, L., Tiwari, A., Khatri, H. B., Basnet, S., Bhattarai, K., Gyawali, B., Rawal, N., & Khatri, N. (2017). Analysis of Yield Attributing Characters of Different Genotypes of Wheat in Rupandehi, Nepal. *International Journal of Environment, Agriculture and Biotechnology*, *2*(5), 2374–2379. https://doi.org/10.22161/ijeab/2.5.13

Paudel, D. C., Paudel, G., Khatri-Chhetri, A., Bhatta, M., & Gurung, R. (2022). Mitigating simultaneous heat and drought stress in wheat by exploiting genetic variability for root traits in Western Nepal. *Agronomy*, 12(2), 472. https://doi.org/10.3390/agronomy12020472

Paux, E., Sourdille, P., Mackay, I., and Feuillet, C. (2012). Sequence-Based marker development in wheat: Advances and applications to breeding. *Biotechnology Advances*, *30*, 1071–1088, https://doi.org/10.1016/j.bioteChadv.2011.09.015

Razzaq, A., Ali, Q., Qayyum, A., Mahmood, I., Ahmad, M., & Rasheed, M. (2013). Physiological responses and drought resistance index of nine wheat (*Triticum aestivum* L.) cultivars under different moisture conditions. *Pakistan Journal of Botany*, *45*, 151–155.

Sarker, M. G., & Azam, M. Z. A. (2022).Talukder, Genetic variation in mineral profiles, yield contributing agronomic traits, and foliage yield of stem amaranth, *Genetika*, *54* (1), 91–108.

Schulthess, A. W., Reif, J. C., Ling, J., Plieske, J., Kollers, S., Ebmeyer, E., Korzun, V., Argillier, O., Stiewe, G., Ganal, M. W., Röder, M. S., & Jiang, Y. (2017). The roles of pleiotropy and close linkage as revealed by association mapping of yield and correlated traits of wheat (*Triticum aestivum* L.). *Journal of Experimental Botany*, *68*(15), 4089–4101, https://doi.org/10.1093/jxb/erx214

Shyam, C., P.K., C., N.K., R., Banjare, U., & Densena, M. (2018). Estimation of correlation coefficient study of some quantitative traits in wheat. *Annals of Plant Sciences*, *7*(2), 2078. https://doi.org/10.21746/aps.2018.7.2.17

Tahir, M., Tanveer, A., Hussain Shah, T., Fiaz, N., & Wasaya, A. (2009). Yield Response of Wheat (*Triticum aestivum* L.) to Boron Application at Different Growth Stages. *Pakistan Journal of Life and Social Sciences*, *7*(1), 39–42.