Research Article

Estimation of Genetic Parameters of Different Wheat Genotype Traits in Chitwan, Nepal

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This research was carried out to estimate the genetic parameters of fifty wheat genotypes received from the Agriculture Botany Division, Nepal Agriculture Research Council (NARC), Khumaltar, Lalitpur, in the winter season of 2014/2015 at Agriculture and Forestry University (AFU), Chitwan, Nepal. The experiment was performed in an alpha lattice design with two replications in five blocks in each replication and ten plots in each block. The analysis of variance showed highly significant differences among the genotypes for all the studied traits except spike length. This implies that, except for spike length, all other traits exhibited genetic variability. The phenotypic coefficient of variation (PCV) was generally higher than the genotypic coefficient of variation (GCV) for all characters. The difference between PCV and GCV was large in spike length followed by grain weight per spike, the number of grains per spike, grain yield, thousand-grain weight, and harvest index indicating that these traits are affected by the environment as well. Moderate to high heritability associated with a high genetic gain was observed for days to flag leaf appearance, panicle length, thousand-grain weight, grain yield, and harvest index indicating the involvement of additive gene action. Grain weight per spike, number of grains per spike, thousand-grain weight, biological yield, and harvest index were significantly correlated with grain yield indicating their important contribution to grain yield. WK 2525, WK 2437, and WK 2506 were three promising genotypes in terms of grain yield.

1. Introduction

Wheat (*Triticum aestivum* L.) is the staple food and the most widely grown cereal crop in the world with 717.2 million mt planted in 2013/2014 [1]. Wheat fulfills 21% of the total calories and 20% of the protein requirements of more than 4.5 billion people in 94 developing countries [2]. World wheat production is based almost entirely on two modern species: common or hexaploid bread wheat (*Triticum aestivum*, 2n = 6x = 42, AABBDD) and durum or tetraploid wheat (*T. turgidum* subsp. *durum*, 2n = 4x = 28, AABB). In Nepal, wheat is the third staple food after rice and maize in terms of production area, production, and productivity [3]. It is grown in the winter season in Nepal and is cultivated from the Terai (100masl) to a high mountain (2300 masl). At present, the area under wheat production in Nepal is

7,54,243 ha with a total production of 17,27,346 mt and productivity of 2.29 t ha^{-1} [3]. In Chitwan, wheat is cultivated on a total area of 8750 ha with a total production of 30,125 mt and productivity of 3.44 t ha^{-1} [3]. Mirza et al. [4] concluded that an improvement of 35 to 50% in wheat yield was achieved by the introduction of new high yielding cultivars in the country. It is the genetic makeup of a variety that is expressed by a favorable environment and produces different yields in different environments. Selections of improved and high yielding genotypes of different cereals with a wide range of adaptation to agroclimatic conditions are essential to increase yield per hectare.

Knowledge of the genetic variability present in existing crop species for the character under improvement is of paramount importance for the success of any plant breeding program. The observed variability is the result of the

combined action of genetic and environmental factors. Among these two factors, only genetic factors were heritable. Therefore, it is necessary to know the extent to which genetic factors contribute to the performance of a trait. Therefore, the estimation of genetic parameters is important. Heredity with genetic advance is more helpful in predicting gain under effective selection [5]. Thus, the estimation of genetic parameters such as heritability and genetic advance can provide essential knowledge that can be decisive in predicting the transfer of traits from parental plants to offspring. PCV and GCV are other important genetic parameters. This gives an idea of whether the trait is environmentally affected or not. If the values of PCV and GCV are closer to each other or their difference is very small, it suggests that the trait is mainly due to the genetic makeup of the genotype. The greater the difference between the values of PCV and GCV, the greater the influence of the environment on the performance of the genotype. It is a very important parameter that helps to determine the influence of the environment on the performance of the genotype. Heritability and genetic advance are other important selection parameters that help plant breeders in determining the characters for which selection would be performed. Keeping in view the above perspectives, the present investigation was taken up to find out to evaluate the genotypes for yield and yield components for their performance, to estimate and analyze the genetic parameters like heritability and genetic advance present for quantitative and yield attributing traits in the wheat genotypes, and to find out the correlation among various traits present in wheat genotypes.

2. Materials and Methods

2.1. Research Site.
The experiment was conducted at the research farm of the Agriculture and Forestry University, Nepal, from November 2014 to June 2015. The global positioning system (GPS) of the experimental site was 27.64728° N, 84.34775° E; 27.64715° N, 84.34779° E and at an altitude of 228 m above sea level. In the experimental field with sandy loam soil texture, the pH was 6.4. The weather data of the experiment site are shown in Figure 1.

2.2. Plant Materials.
The experimental material was collected from the Agri Botany Division NARC, Khumaltar. There were 45 advanced wheat genotypes including five local check varieties (WK 1204, Chyakhura #1, Danphe, Munal #1, and WK 1481) from NARC for the study. Genotypes used in the research along with their source genotypes are presented in Table 1:

2.3. Experimental Details.
There were 50 genotypes in the alpha lattice design in 2 replications with a plot size of $3\,m \times 1\,m$. Each replication comprised five blocks each consisting of ten plots. Each plot had 6 rows spaced 25 cm apart. Two deep ploughings followed by planking were done for field preparation. Well-rotted farmyard manure at a rate of $10\,t\,ha^{-1}$ was applied at the time of field preparation. The dose of chemical fertilizers applied was $100 : 60 : 40\,kg\,NPK$ per hectare. The basal dose of NPK was the half dose of nitrogen, the full dose of phosphorus, and potassium. The remaining dose of nitrogen was applied at the flowering and grain filling stage. Planting was performed on 3rd December 2014. Irrigation was provided at the crown root initiation (CRI), flowering, and grain filling stages. Manual weeding was performed twice after 30 and 60 days of sowing. Harvesting was performed on 4th April 2015. Each plot was harvested separately, threshed, well dried, and stored properly.

2.4. Data Collection.
Ten random plants per genotype per replication were used to record data. Observations were taken for the following quantitative traits: flag leaf area (cm), plant height (cm), peduncle length (cm), days to 50% flag leaf appearance, days to 50% booting, days to 50% heading, and days to 50% anthesis. Similarly, observations for yield attributing traits were taken for spike length (cm), the number of grains per spike, grain weight per spike (g), 1000 grain weight (g) days to physiological maturity, and grain yield (t ha^{-1}) after moisture adjustment at 14% was taken. The total weight of biomass from each plot was weighed as grams per plot and then converted into kg per hectare to calculate the biological yield. Harvest index was calculated by the formula shown in

$$harvest\ index = \frac{grain\ yield\left(t\ ha^{-1}\right)}{biological\ yield\left(t\ ha^{-1}\right)}. \tag{1}$$

2.5. Statistical Analysis.
Microsoft Office Excel 2010 software was used for data entry and processing. Analysis of variance (ANOVA) was performed using the MINITAB version 14. A linear correlation was computed using SPSS version 25. Genetic parameters were calculated using Microsoft Excel 2010. Clustering of genotypes was performed by using the MINITAB version 14.

2.6. Estimation of Genetic Parameters

2.6.1. Genotypic and Phenotypic Coefficient of Variation.
The genotypic and phenotypic components of variance were computed according to formulae given by Lush [6] and Choudhary and Prasad [7] for the observed characteristics.

Genotypic variance $(\sigma^2 g) = (TMSS – EMSS)/R$, error variance $= \sigma^2 e$, and phenotypic variance $(\sigma^2 p) = \sigma^2 g + \sigma^2 e$, where TMSS is the treatment mean sum of squares, EMSS is the error mean sum of squares, and R is the number of replications.

The genotypic and phenotypic coefficients of variation were computed according to Burton and Devane [8] and expressed as a percentage.

Genotypic coefficient of variation (GCV) $= (\sigma_g/\overline{X})$ x 100 and phenotypic coefficient of variation (PCV) $= (\sigma_p/\overline{X})$ x 100, where σ_g is the genotypic standard deviation, σ_p is the phenotypic standard deviation, and $\overline{X}$ is the general mean of character.
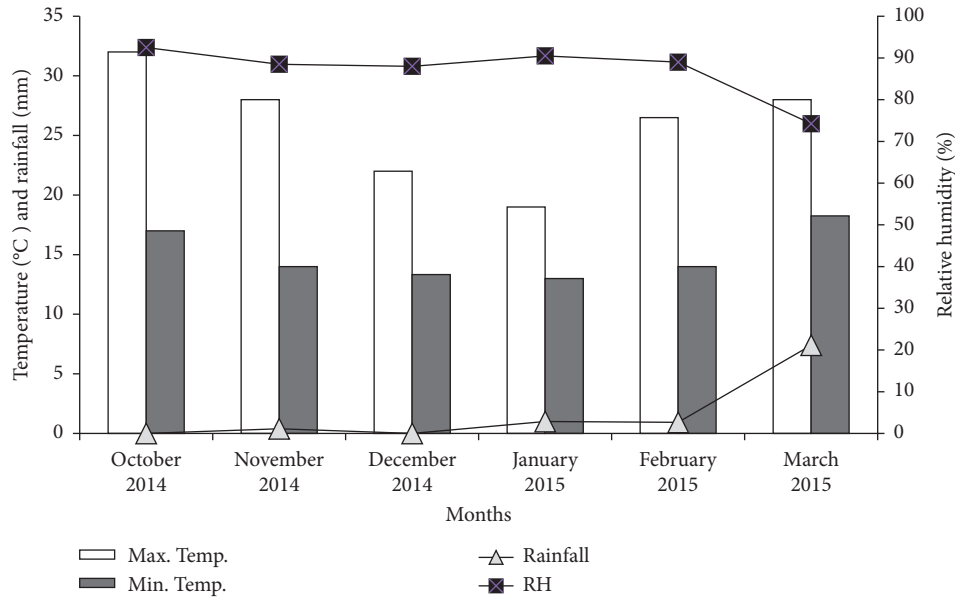
FIGURE 1: Weather data of the research site obtained from a nearby NMRP research station.

TABLE 1: Genotypes used in research along with their source genotype.

Entry	Source genotype	Genotype
1	2BWAVTR-1	WK 2208
2	2BWAVTR-2	WK 2248
3	2BWAVTR-6	WK 2272
4	2BWAVTR-9	WK 2278
5	IET-26	WK 2257
6	2BWAVTR-12	WK 2408
7	2BWAVTR-13	WK 2414
8	MPYT®-9	WK 2352
9	MPYT®-11	WK 2353
10	B.S.(check)	WK 1204
11	MPYT®-12	WK 2355
12	MPYT®-13	WK 2359
13	MPYT®-16	WK 2381
14	MPYT®-23	WK 2388
15	HRN-24	WK 2540
16	MPYT®-28	WK 2437
17	MPYT® - 29	WK 2438
18	IET-17	NL 1223
19	IET-19	WK 2218
20	B.S.(check)	Chyakhura#1
21	HRN-1	WK 2519
22	HRN-74	WK 2525
23	HRN-31	WK 2546
24	HRN-35	WK 2550
25	HRN-36	WK 2551
26	HRN-39	WK 2480
27	HRN-45	WK 2485
28	HRN-46	WK 2486
29	HRN-55	WK 2494
30	B.S.(check)	Danphe
31	HRN-56	WK 2495

TABLE 1: Continued.

Entry	Source genotype	Genotype
32	HRN-64	WK 2555
33	HRN-67	WK 2558
34	HRN-72	WK 2562
35	HRN-74	WK 2564
36	HRN-76	WK 2566
37	HRN-83	WK 2503
38	HRN-85	WK 2505
39	HRN-86	WK 2506
40	B.S.(check)	Munal#1
41	HRN-87	WK 2507
42	HRN-88	WK 2508
43	HRN-89	WK 2509
44	HRN-91	WK 2510
45	HRN-92	WK 2511
46	HRN-93	WK 2512
47	HRN-94	WK 2513
48	HRN-95	WK 2514
49	HRN-96	WK 2515
50	B.S.(check)	WK 1481

PCV and GCV values were categorized as low, moderate, and high values as indicated by Sivasubramanian and Menon [9] as follows: 0–10%: low, 10–20%: moderate, and >20: high.

2.6.2. Broad Sense heritability (h^2bs). Broad sense heritability was estimated as the ratio of genotypic variance to phenotypic variance and expressed as a percentage [10].

Heritability(h^2bs) = (Vg/Vp) x 100, where V_g is the genetic variance and V_p is the phenotypic variance.

The heritability percentage was categorized as low, moderate, and high as described by Robinson et al. [11] as follows: 0–30%: low, 30–60%: moderate, and >60%: high.

2.6.3. Genetic Advance. The extent of genetic advance to be expected by selecting 5% of the superior progeny was calculated using the following formula given by Robinson et al. [11].

GA = iσ_p h², where *i* is the efficacy of selection which is 2.06 at 5% selection intensity, σ_p is the phenotypic standard deviation, and h^2 is the heritability in a broad sense.

2.6.4. Genetic Advance as Percent of Mean (GAM). GAM = (GA/$\overline{\mathrm{X}}$) x 100, where GA is the genetic advance, and $\overline{\mathrm{X}}$ is the general mean of character.

GAM was categorized as low, moderate, and high as follows by Johnson et al. [12]: 0–10%: low, 10–20%: moderate, and 20 and above: high.

3. Results and Discussion

3.1. Phenological Traits. The mean number of days to flag leaf appearance was 63. The minimum number of days to flag leaf appearance was 50 DAS which was exhibited by WK 2495 whereas the maximum number of days to flag leaf appearance was exhibited by WK 2513 whose flag leaf appeared at 92 DAS. The mean number of days to booting was 69. The minimum day to booting was 57 DAS which was exhibited by WK 2495 whereas the maximum day to booting was exhibited by WK 2513 whose flag leaf appeared at 100 DAS. The mean number of days to heading was 75. The minimum day to heading was 65 DAS which was exhibited by WK 2495 whereas the maximum day to heading was exhibited by WK 2513 at 110 DAS. The mean number of days to anthesis was 80. The minimum day to anthesis was 71 DAS which was exhibited by WK 2495 whereas the maximum day to anthesis was exhibited by WK 2513 at 115 DAS. The mean number of days to maturity was 112. The minimum day to maturity was 101 DAS which was exhibited by WK 2353 whereas the maximum day to maturity was exhibited by WK 2513 at 138 DAS.

3.2. Growth Traits. The mean flag leaf area was 55.75 cm². The minimum flag leaf area was 26.33 cm² which was exhibited by WK 2505 whereas the maximum day to maturity was exhibited by WK 2515 at 103.64 cm². The mean plant height was 98.5 cm. WK 2540 was the shortest genotype with a plant height of 77.25 cm whereas WK 1481 was the tallest genotype with a plant height of 125.95 cm. The mean peduncle length was 40.814 cm. WK 2437 was the genotype with the shortest peduncle length, i.e., 31 cm, whereas WK 2278 was the genotype with the longest peduncle length of 54.3 cm.

3.3. Yield and Yield Attributes. The mean values of yield and yield attributing traits are presented in Table 2. The mean spike length was 9.91 cm. WK 2359 had the shortest spike

length with a spike length of 7.2 cm, whereas WK 2555 had the longest spike length of 17.9 cm. The mean number of grains per spike was 36. WK 2550 had the highest number of grains per spike with 53 grains per spike whereas WK 2513 had the lowest number of grains per spike with 10 grains per spike. The mean grain weight per spike was 7.67 g. WK 2512 had the highest grain weight per spike with 21.3 g whereas WK 2513 had the lowest grain weight per spike with 0.745 g. The mean thousand-grain weight was 40.886 g. WK 2512 had the highest thousand-grain weight which was 86.63 g whereas WK 2546 had the lowest thousand-grain weight which was 12.189 g. The mean biological yield was 6.54 t ha^{-1}. WK 2388 had the highest biological yield having 10.01 t ha^{-1} whereas WK 2485 had the lowest biological yield having 3.65 t ha^{-1}. The mean harvest index was 0.237. WK 2540 had the highest harvest index with 0.404 whereas WK 2513 had the lowest harvest index with 0.036. The mean grain yield was 1.54 t ha^{-1} which is lower than the national average of 2.29 t ha^{-1} [3]. WK 2525 gave the highest yield, i.e., 2.50 t ha^{-1}, whereas WK 2513 gave the lowest yield with 0.27 t ha^{-1}.

3.4. Estimation of Genetic Parameters

3.4.1. Phenotypic and Genotypic Coefficient of Variation. The highest values of GCV and PCV were obtained for the grain weight per spike (24.81% and 44.54%, respectively). The high difference between the PCV and GCV indicates that this trait is also highly influenced by environmental factors. There was a very small difference between PCV and GCV values among the traits such as days to flag leaf appearance, days to booting, days to heading, days to anthesis, and days to maturity indicating that these traits are highly under genetic control. Thus, these traits are highly controlled by the genetic makeup of the genotype. High PCV (38.52%) and GCV (20.18%) values were estimated for the flag leaf area. The difference between the PCV and GCV is pronounced which means that the flag leaf area is dependent on environmental factors. The difference between PCV and GCV for the trait plant height was 2.2 which means that the trait was not significantly affected by environmental factors. Similarly, the difference between PCV and GCV for the trait peduncle length was found to be 2.4 which means that the trait is mainly due to genetic factors and the environment does not play many roles in the expression of the trait.

Among the yield attributing traits, the difference between PCV and GCV was higher. This suggests that yield attributes are dependent on environmental factors and genetic factors are not sufficient for trait performance. The difference between the PCV and GCV is 14.4 for spike length, 19.7 for grain weight per spike, 10.9 for the number of grains per spike, 10.1 for 1000 grain weight, 7 for biological yield, 11.13 for grain yield, and 10.56 for harvest index. This suggests that yield and yield attributing characters are dependent on environmental factors as well.

3.4.2. Heritability and Genetic Advance as Percentage of Mean. Higher broad sense heritability reveals that a large portion of variation is heritable to the offspring. The highest

TABLE 2: Mean value for all characters of 50 wheat genotypes in Chitwan, Nepal, 2014/2015.

Genotype	DFLA	BD	HD	AD	MD	FLA (cm²)	PH (cm)	PL(cm)	SL (cm)	GWS(g)	NGS (g)	TGW (g)	HI (%)	BY (tha⁻¹)	GY (tha⁻¹)
WK 2208	63	70	74	78	113	41.4	118	43	9.9	5.8	29	38	0.20	7.4	1.4
WK 2248	64	71	72	80	111	85.6	113	44	9.6	9.9	42	47	0.17	7.6	1.3
WK 2272	60	66	74	80	112	60.8	90	41	9.3	7.9	36	45	0.32	6.4	2.1
WK 2278	63	71	75	80	113	61.1	116	54	8.8	6.9	34	41	0.16	5.3	0.8
WK 2257	66	70	74	79	111	46.7	84.	31	8.9	7.3	35	42	0.13	4.3	0.6
WK 2408	68	72	77	81	112	36.3	87	35	8.9	7.3	37	39	0.29	5.6	1.6
WK 2414	60	64	68	73	110	46.3	100	41	9.2	10.4	49	47	0.28	6.6	1.9
WK 2352	64	71	78	80	112	49.8	104	44	8.4	5.1	24	44	0.22	4.1	1.0
WK 2353	52	59	68	75	101	67.0	95	37	8.6	10.1	50	41	0.21	7.0	1.5
WK 1204	60	67	72	77	108	60.4	86	40	7.6	8.2	41	40	0.31	7.0	2.2
WK 2355	54	57	71	74	105	44.0	87	40.	9.3	6.6	38	35	0.28	6.5	1.8
WK 2359	56	65	69	75	111	42.4	111	52	7.2	7.4	33	45	0.21	7.7	1.6
WK 2381	61	67	73	78	111	49.4	92	37	9.5	7.3	38	39	0.37	6.3	2.3
WK 2388	89	95	104	108	136	30.4	112	34	13.1	1.8	41	13	0.04	10.0	0.4
WK 2540	59	63	71	75	107	58.6	77	34.	8.8	7.5	41	36	0.42	5.0	2.0
WK 2437	62	66	72	76	110	35.4	90	31	8.3	8.5	40	42	0.32	7.5	2.5
WK 2438	61	67	72	76	110	27.2	84	31	8.1	8.0	33	50	0.34	5.4	1.8
NL 1223	60	65	71	74	110	54.8	100	42	9.3	7.9	39	41	0.23	8.0	1.8
WK 2218	54	64	69	74	103	44.8	105	46	8.8	6.1	31	39	0.21	6.1	1.3
Chyakhura#1	66	70	76	81	111	42.0	93	44	10.5	4.5	21	44	0.20	6.6	1.4
WK 2519	64	69	74	79	112	37.7	92	36	9.3	6.2	33	38	0.25	7.5	1.9
WK 2525	62	69	74	79	112	47.3	84	33	8.9	8.3	43	39	0.35	7.2	2.5
WK 2546	65	70	77	80	115	36.9	110	45	8.0	1.0	17	12	0.10	6.9	0.7
WK 2550	53	57	68	74	110	80.9	97	41	9.6	11.7	53	45	0.23	6.0	1.4
WK 2551	57	67	73	78	109	57.3	109	48	10.0	10.7	53	41	0.28	7.2	2.0
WK 2480	59	67	71	76	111	35.1	95	42	8.0	4.3	23	38	0.19	5.3	1.0
WK 2485	62	70	74	77	110	34.7	110	43	12.2	5.9	37	32	0.16	3.7	0.6
WK 2486	67	71	76	81	106	45.3	102	43	11.9	7.2	34	42	0.25	6.9	1.8
WK 2494	71	76	80	87	115	53.9	101	38	11.3	5.7	34	34	0.14	4.9	0.7
Danphe	68	72	78	82	113	36.1	101	35	8.8	7.2	33	44	0.24	7.2	1.8
WK 2495	50	57	65	71	104	72.5	105	42	7.7	9.1	44	41	0.32	6.1	1.9
WK 2555	63	69	74	80	114	47.2	110	36	17.9	5.3	25	41	0.19	7.2	1.4
WK 2558	57	64	72	77	111	70.4	105	52	8.7	7.7	32	48	0.27	7.0	1.9
WK 2562	62	69	75	80	112	68.2	107	46	10.1	7.6	32	47	0.24	6.0	1.4
WK 2564	62	69	74	78	116	81.0	104	46	8.8	7.2	30	47	0.17	4.9	0.9
WK 2566	68	73	78	81	114	72.4	91	35	10.0	6.9	35	40	0.21	9.0	1.9
WK 2503	57	64	71	76	111	49.5	102	45	9.5	9.2	42	43	0.23	6.8	1.5
WK 2505	62	69	75	78	102	26.3	93	43	8.6	5.5	34	33	0.28	6.4	1.8
WK 2506	66	69	75	81	111	84.6	96	40	10.8	9.4	46	42	0.29	8.3	2.4
Munal#1	70	72	76	80	111	33.4	94	31	9.1	8.1	38	42	0.31	7.0	2.2
WK 2507	63	70	76	79	112	45.2	92	39	10.4	8.8	45	39	0.35	6.0	2.1
WK 2508	61	66	73	78	103	50.8	81	37	10.5	8.3	51	33	0.26	6.7	1.7
WK 2509	60	66	71	78	108	76.3	102	44	9.3	9.1	37	49	0.27	5.6	1.6
WK 2510	68	71	80	85	117	98.6	89	39	11.8	10.6	43	50	0.24	5.8	1.4
WK 2511	68	72	81	86	118	38.9	86	41	12.4	7.6	38	40	0.24	6.3	1.5
WK 2512	68	72	77	84	118	97.2	97	42	11.7	21.3	46	87	0.21	6.7	1.4
WK 2513	92	100	110	115	138	59.8	89	32	11.7	0.7	10	25	0.03	7.6	0.3
WK 2514	69	74	79	89	119	76.9	95	39	12.6	11.5	49	47	0.18	6.3	1.1
WK 2515	68	71	76	81	115	103.6	94	37	12.8	6.9	32	42	0.30	7.6	2.3
WK 1481	59.5	67	73.5	77	112	83.3	125	54	9.9	8.4	35	47	0.18	6.9	1.2
Mean	63	69	75	80	112	55.7	98	40.8	9.91	7.67	36	40.88	0.23	6.545	1.5
SEm	9.68	9.59	9.81	9.93	13.21	24.4	14.4	8.19	2.42	3.91	11.2	13.44	0.10	1.56	0.74
F test	∗∗	∗∗	∗∗	∗∗	∗	∗	∗∗	∗∗	ns	∗	∗∗	∗∗	∗∗	∗∗	∗∗
CV(%)	2.11	1.59	2.04	1.94	8.95	32.81	6.73	8.31	21.27	21.45	37.00	21.43	25.59	15.23	27.4

∗∗ Significant at 1% level, ∗significant at 5% level, ns = nonsignificant, SEm = standard error of mean, CV = coefficient of variance, DFLA = days to 50% flag leaf appearance, BD = days to 50% booting, HD = days to 50% heading, MD = days to 90% maturity, FLA = flag leaf area, PH = plant height (cm), PL = peduncle length (cm), SL = spike length (cm), GWS = grain weight per spike (g), NGS = no. of grains per spike, TGW = thousand-grain weight (g), BY = biological yield (t ha⁻¹), GY = grain yield (t ha⁻¹), HI = harvest index (%).

TABLE 3: Estimation of genetic parameters (PCV, GCV, h_{bs}^2, and GCV) for quantitative and yield attributing traits of wheat genotypes in Chitwan, Nepal, 2014/2015.

	PCV	GCV	h_{bs}^2	GAM
Flag leaf appearance	10.89	10.68	96.23	21.58
Days to booting	9.86	9.73	97.39	19.78
Days to heading	9.33	9.10	95.23	18.29
Days to anthesis	8.87	8.65	95.23	17.39
Days to maturity	5.71	5.46	91.41	10.75
Flag leaf area (cm^2)	38.52	20.19	27.47	21.80
Plant height (cm)	11.40	9.21	65.21	15.32
Peduncle length (cm)	15.36	12.92	70.77	22.40
Spike length (cm)	22.93	8.58	13.99	6.61
Grain weight per spike (g)	44.55	24.82	31.04	28.48
No. of grain per spike	26.61	15.75	35.02	19.20
Thousand grain weight (g)	27.76	17.65	40.40	23.10
Biological yield(t ha^{-1})	20.07	13.07	42.40	17.54
Grain yield (t ha^{-1})	39.21	27.94	50.79	41.02
Harvest index (%)	36.29	25.74	50.30	37.60

PCV = phenotypic coefficient of variation, GCV = genetic coefficient of variation, h_{bs}^2 = broad-sense heritability, GAM = genetic advance as a percentage of the mean.

broad sense heritability (97.388%) was observed for days to booting followed by days to flag leaf appearance (96.22%), days to anthesis (95.23%), and days to heading (95.23%) presented in Table 3. This indicates that these traits are highly heritable to offspring. Similar reports were obtained by Khan and Naqvi [13]. The heritability of these traits is very high (>90%) which means that these traits are highly heritable. Plant height and peduncle length had higher heritability values (65.21% and 70.7%, respectively). Similar reports were obtained for the length of the peduncle by Yahaya [14]. Flag leaf area had low heritability (27.4%). This indicates that plant height and peduncle length were heritable to the offspring but the flag leaf area is not much heritable to the offspring. Among the yield attributing characters, the grain yield and harvest index (50.79% and 50.29%, respectively) had higher heritability. All yield attributing traits, i.e., grain weight per spike, number of grains per spike, 1000 grain weight, biological yield, and harvest index, had moderate heritability (30–60%). Similar results were obtained for 1000 grain weight and biological yield by Maragheh [15]. This suggests that yield attributing characters are moderately heritable to the off-springs. Spike length (13.98%) had low heritability.

For an efficient selection, the knowledge of heritability alone is not sufficient, and heritability estimates along with the genetic advance are considered more useful [16]. High heritability with high genetic advance as a percentage of mean was observed for days to flag leaf appearance (21.58%) while days to booting (19.78%), days to heading (18.29%), days to anthesis (17.39%), and days to maturity (10.75%) had high heritability with moderate genetic advance as a percentage of the mean. This indicates that these traits could be improved through phenotypic selection. High heritability with high genetic advance as a percentage of the mean was observed for peduncle length (22.40%) which indicates that the selection for this trait is effective. Similar results were obtained by [17]. High heritability with moderate genetic advance as a percentage of the mean (15.32%) was seen for

the trait plant height. So, genetic improvement of these traits is effective through genetic selection. Khan and Naqvi [13] also obtained similar results under irrigated conditions.

Among the yield attributing traits, moderate heritability with high genetic advance as a percentage of the mean was seen for grain weight per spike (28.48%), 1000 grain weight (23.1%), grain yield (41.02%), and harvest index (37.6%). Similar reports have been reported by Khan and Naqvi [13] for harvest index. Moderate heritability with moderate genetic advance as a percentage of the mean was seen for the number of grains per spike (19.2%) and biological yield (17.54%). Similar findings have been reported by Laghari et al. [17] for the number of grains per spike. Low heritability with low genetic advance as a percentage of the mean was seen for spike length (6.61%) [18, 19], and also low to moderate heritability was found for spike length.

3.4.3. Correlation Coefficient Analysis. Grain yield was positively and highly significantly correlated with grain weight per spike, the number of grains per spike, 1000 grain weight, biological yield, and harvest index shown in Table 4. Among them, the most yield correlated traits were harvest index followed by the number of grains per spike, grain weight per spike, biological yield, and 1000 grain weight. Donmez et al. [20] also found similar relation of grain yield with both harvest index and biomass. Similar results were reported for grain per spike and grain weight by Singh and Singh [21]. Grain yield had a highly significant negative correlation with days to flag leaf appearance, days to booting, days to heading, days to anthesis, days to maturity, and grain yield and was negatively and significantly correlated with plant height. This means that these traits negatively influence the grain yield.

3.4.4. Cluster Analysis. All the 50 genotypes were clustered using 15 quantitative traits. The dendrogram as shown in Figure 2 revealed four clusters with a minimum of 31.86%

TABLE 4: Simple correlation coefficient of traits of wheat genotypes in Chitwan, Nepal, 2014/2015.

	FLAD	BD	HD	AD	MD	FLA	PH	PL	SL	GWS	NGS	TGW	BY	HI	GY
FLAD	1														
BD	0.95**	1													
HD	0.92**	0.94**	1												
AD	0.91**	0.93**	0.96**	1											
MD	0.82**	0.85**	0.86**	0.861**	1										
FLA	−0.07	−0.06	−0.06	−0.01	0.08	1									
PH	−0.07	0.05	−0.05	−0.04	0.09	0.10	1								
PL	0.38**	−0.27**	−0.30**	−0.27**	−0.20*	0.17	0.65**	1							
SL	0.34**	0.32**	0.32**	0.34**	0.36**	0.11	0.13	−0.22*	1						
GWS	−0.280**	−0.32**	−0.35**	−0.29**	−0.20*	0.34**	−0.04	0.07	0.07	1					
NGS	−0.3**	−0.38**	−0.38**	−0.34**	−0.34**	0.21*	−0.11	−0.05	0.05	0.74**	1				
TGW	−0.31**	−0.35**	−0.40**	−0.35**	−0.22*	0.31**	0.01	0.18	0.02	0.84**	0.34**	1			
BY	0.23	0.24	0.23*	0.24*	0.29**	0.08	0.22*	−0.08	0.2*	0.01	0.05	−0.12	1		
HI	−0.44	−0.49**	−0.49**	−0.50**	−0.48**	−0.07	−0.38**	−0.15	−0.17	0.34**	0.42**	0.29**	−0.09	1	
GY	−0.36**	−0.41**	−0.43**	−0.42**	−0.39**	0.001	−0.25**	−0.12	−0.07	0.35**	0.43**	0.28**	0.34**	0.8**	1

FLAD = days to flag leaf appearance, BD = days to 50% booting, HD = days to 50% heading, AD = days to 50% anthesis, MD = days to 90% maturity, FLA = flag leaf area (cm²), PH = plant height (cm), PL = peduncle length (cm), SL = spike length (cm), GWS = grain weight per spike (g), NGS = no. of grains per spike, TGW = thousand-grain weight (g), BY = biological Yield (t ha⁻¹), GY = grain yield (t ha⁻¹), HI = harvest Index (%), ** significant at 1% level, * significant at 5% level.
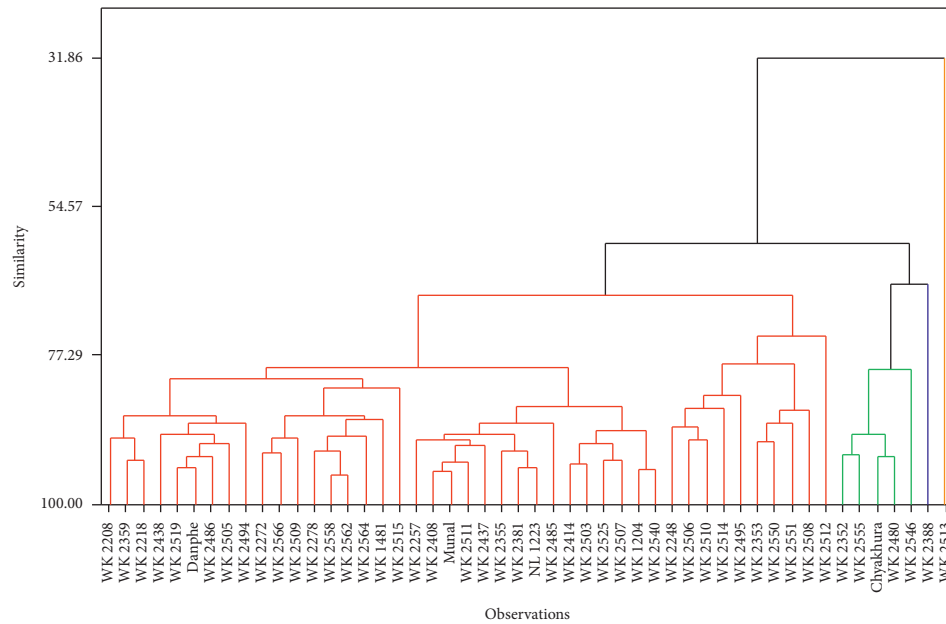
Figure 2: Dendrogram showing cluster analysis of 50 wheat genotypes.

Table 5: Distance between cluster centroids.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	0.000	87.1347	90.490	164.814
Cluster 2		0.0000	75.552	97.136
Cluster 3			0.0000	103.600
Cluster 4				0.0000

Table 6: Centroid of clustering of 50 wheat genotypes in Chitwan, Nepal, 2014/2015.

Variable	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Grand centroid
Flag leaf appearance	61.988	63.400	89.00	92.00	63.270
Days to booting	67.674	69.400	95.00	100.00	69.040
Days to heading	73.640	75.200	104.00	110.00	75.130
Days to anthesis	78.628	79.400	108.00	115.00	80.020
Days to maturity	110.674	112.600	136.00	138.00	111.920
Flag leaf area (cm^2)	57.820	42.238	30.46	59.85	55.755
Plant height (cm)	97.906	102.730	112.00	89.40	98.500
Peduncle length (cm)	40.985	42.400	34.40	31.95	40.814
Spike length (cm)	9.717	10.570	13.10	11.70	9.910
Grain weight per spike (g)	8.386	4.078	1.89	0.75	7.673
Grains per pike	194.326	109.200	146.00	50.00	181.960
Thousand grain weight (g)	42.722	35.904	12.84	14.92	40.886
Harvest index (%)	0.253	0.180	0.04	0.03	0.237
Biological yield (t ha^{-1})	6.505	6.020	10.00	7.60	6.548
Grain yield (t ha^{-1})	1.660	1.100	0.40	0.30	1.552

similarity level in UPGMA clustering. Wheat genotypes were classified into four cluster groups, namely, cluster 1, cluster 2, cluster 3, and cluster 4. The distance between the cluster's centroid was found the highest between clusters 1 and 4 and the lowest between clusters 2 and 4 presented in Table 5.

Cluster 1 consisted of 43 genotypes which represent 86% of total genotypes. Genotypes grouped in this cluster showed

the earliest appearance of flag leaf, booting, heading, anthesis, and maturity with the highest number of grains per spike, grain weight per spike, thousand-grain weight, biological yield, grain yield, and harvest index as shown in Table 6. Cluster 2 consisted of 5 genotypes including 10% of total genotypes. These genotypes are characterized by the longest peduncle. The genotypes categorized into clusters 3 and 4 consisted of only 1 genotype in each. Cluster 3 is

characterized by the highest plants, the longest spike, and the smallest flag leaf area while cluster 4 took the longest period for flag leaf appearance, booting, heading, anthesis, and maturity with the largest flag leaf area, the shortest plant height and peduncle length, and also the lowest grain yield and harvest index.

4. Conclusion

Based on quantitative traits, WK 2495 was considered the best variety because of its earliness in flag leaf appearance, booting, heading, and anthesis. WK 2513 was the least desired genotype due to its late character and it is the lowest yield. Regarding the yield attributes, WK 2512 had the highest 1000 grain weight and grain weight per spike. WK 2525 gave the highest yield due to the difference in the genetic makeup of the genotypes. Though WK 2388 gave the highest biomass yield, its yield was significantly low because of very low grain weight per spike.

From the study of genetic parameters, it was found that days to flag leaf appearance, days to booting, days to heading, days to anthesis, days to maturity, plant height, and peduncle length had high heritability with high to moderate genetic advance as a percentage of the mean indicating that these traits are effective for selection. Moderate heritability with high to moderate genetic advance as a percentage of the mean was observed for grain weight per spike, the number of grains per spike, 1000 grain weight, grain yield, biological yield, and harvest index indicating that these traits were prominent variables for selection for higher grain yield based on these traits. As revealed from correlation analysis, grain weight per spike, number of grains per spike, 1000 grain weight, biological yield, and harvest index were the most yield determinative traits. Hence, simultaneous selection of these traits might improve the grain yield of wheat.

Data Availability

The authors can also make data available on request through a data access committee, institutional review board, or the authors themselves. In this case, they should name who should be contacted to request the data (e.g., the ethics or data access committee) and provide appropriate contact detail. Data will be provided by the corresponding author upon request.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Acknowledgments

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