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ESTIMATION OF GENETIC PARAMETERS AND TRAIT ASSOCIATION IN WHEAT (*Triticum aestivum* L.) GENOTYPES

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ABSTRACT

Genetic diversity is important for effective selection and genetic improvement in breeding programs. A study was conducted at Rampur, Chitwan, to study genetic parameters and the association between yield and yield-attributing traits. Thirty-six wheat genotypes were evaluated in an alpha lattice design with two replications. Effective tillers showed the highest genotypic coefficient of variation (GCV) (25.87%) and phenotypic coefficient of variation (27.61%). The difference between PCV and GCV was minimal for the studied traits. Grain yield recorded the highest broad-sense heritability (95%). Grain yield was positively correlated with harvest index, flag leaf area, plant height, and biological yield at both the genotypic and phenotypic levels ($p \leq 0.05$). Future breeding programs should prioritize these traits to improve wheat yield potential.

Key words: *Genetic advance, selection, variation, trait association*

INTRODUCTION

Wheat (*Triticum aestivum L.* $2n = 6x = 42$, AABBDD) is a major cereal crop accounting for 28% of global cereal production (FAOSTAT, 2021). It ranks as the third major cereal crop after rice and maize in Nepal. It is cultivated over 697,766 ha, producing 2.10 Mt at 3.01 t/ha (MoALD, 2024). Wheat production in Nepal is limited by inadequate irrigation, limited improved varieties, erratic rainfall, and temperature fluctuation (Devkota & Phuyal, 2016; Kandel et al., 2024). Wheat demand is expected to rise by 890 thousand metric tons by 2030 (Prasad et al., 2011). Although the cultivation area has increased over the past three years, the productivity has remained constant (MoALD, 2023). Compared to neighboring countries, China, Bangladesh, Pakistan, and India, Nepal's wheat productivity remains low (Adhikari et al., 2021). This highlights the need for genetic improvement and yield enhancement to bridge the productivity gap.

Yield improvement depends on genetic variability, heritability, and association between yield-related traits and grain yield (Sharada et al., 2024). Genetic variability is fundamental in breeding programs, to select superior genotypes with desirable traits for hybridization programs (Kumar et al., 2014; Tiwari et al., 2019). The greater the genetic diversity, the higher the likelihood of selecting a genotype with desired traits. The relative magnitude of GCV and PCV reflects the extent of genetic diversity in breeding populations (Ene et al., 2016). Genotypic coefficient of variation, heritability, and genetic advance help to distinguish heritable and non-heritable components of genetic diversity within a population (Bhushan et al., 2013). This information helps breeders make effective decisions during selection.

Grain yield is a complex polygenic trait influenced by genetic factors and environmental interactions (Kulsum et al., 2022). Thus, selection based on yield-attributing traits is a more reliable approach than direct selection for yield (Bhandari et al., 2024; Bhutto et al., 2016). Trait-based selection selects genotypes based on independent attributes, enhancing the chance of developing high-yielding wheat varieties (Tshikunde et al., 2019). Similarly, correlation analysis assesses the direction and relative strength of yield with yield-attributing traits (Shrestha et al., 2023). Several studies have used these approaches to dissect genetic variability and trait association with yield. Poudel et al. (2021) reported high heritability for booting and heading days, while Upadhyay et al. (2019) reported high heritability for grain yield and thousand seed weight. Similarly, Regmi et al. (2021) reported a positive correlation of grains per spike, thousand seed weight with grain yield, while Thapa et al. (2022) reported a positive association between plant height and a negative association of chlorophyll content with grain yield. However, these findings often vary across different environments, genotypes, and trait combinations. Therefore, the present study was conducted to evaluate thirty-six wheat genotypes under the agro-climatic conditions of Chitwan, Nepal, with the objective of (i) assessing genetic variability and (ii) examining the association between yield and yield-attributing traits. The findings of this study aim to support effective trait selection in wheat yield improvement programs in Nepal.

MATERIALS AND METHODS

Plant materials

This research utilized a collection of thirty-six genotypes obtained from the National Wheat Research Program (NWRP), Bhairahawa, Nepal. Among them, two were check varieties (Vijaya and Banganga). The complete list of wheat genotypes used in this research is presented in Table 1.

Table 1: List of genotypes used for the field experiment

S.N.	Genotypes	Collected from	S.N.	Genotypes	Collected from
1	BL 5346	NWRP, Bhairahawa	19	NL 1858	NWRP, Bhairahawa
2	BL 5351	NWRP, Bhairahawa	20	NL 1860	NWRP, Bhairahawa
3	BL 5369	NWRP, Bhairahawa	21	NL 1861	NWRP, Bhairahawa
4	BL 5373	NWRP, Bhairahawa	22	NL 1862	NWRP, Bhairahawa
5	BL 5402	NWRP, Bhairahawa	23	NL 1863	NWRP, Bhairahawa
6	NL 1845	NWRP, Bhairahawa	24	NL 1864	NWRP, Bhairahawa
7	NL 1846	NWRP, Bhairahawa	25	NL 1865	NWRP, Bhairahawa
8	NL 1847	NWRP, Bhairahawa	26	NL 1866	NWRP, Bhairahawa
9	NL 1848	NWRP, Bhairahawa	27	NL 1867	NWRP, Bhairahawa
10	NL 1849	NWRP, Bhairahawa	28	NL 1868	NWRP, Bhairahawa
11	NL 1850	NWRP, Bhairahawa	29	NL 1869	NWRP, Bhairahawa
12	NL 1851	NWRP, Bhairahawa	30	NL 1870	NWRP, Bhairahawa
13	NL 1852	NWRP, Bhairahawa	31	NL 1871	NWRP, Bhairahawa
14	NL 1853	NWRP, Bhairahawa	32	NL 1872	NWRP, Bhairahawa
15	NL 1854	NWRP, Bhairahawa	33	NL 1873	NWRP, Bhairahawa
16	NL 1855	NWRP, Bhairahawa	34	NL 1859	NWRP, Bhairahawa
17	NL 1856	NWRP, Bhairahawa	35	Vijaya(check)	NWRP, Bhairahawa
18	NL 1857	NWRP, Bhairahawa	36	Banganga (check)	NWRP, Bhairahawa

Research site and climatic observation

The study was carried out from November 2023 to April 2024 in Rampur, Chitwan, Nepal (27.65° N and 84.34° E). The research field is located in the inner Terai region, 187 meters above sea level. Agroclimatic data for the research period were obtained from the NASA Power Project's Data Access Viewer (DAV) (https://power.larc.nasa.gov/data-access-viewer/). Figure 1 illustrates the maximum-minimum temperature and total rainfall recorded during the crop growth period (November 2023 to April 2024).

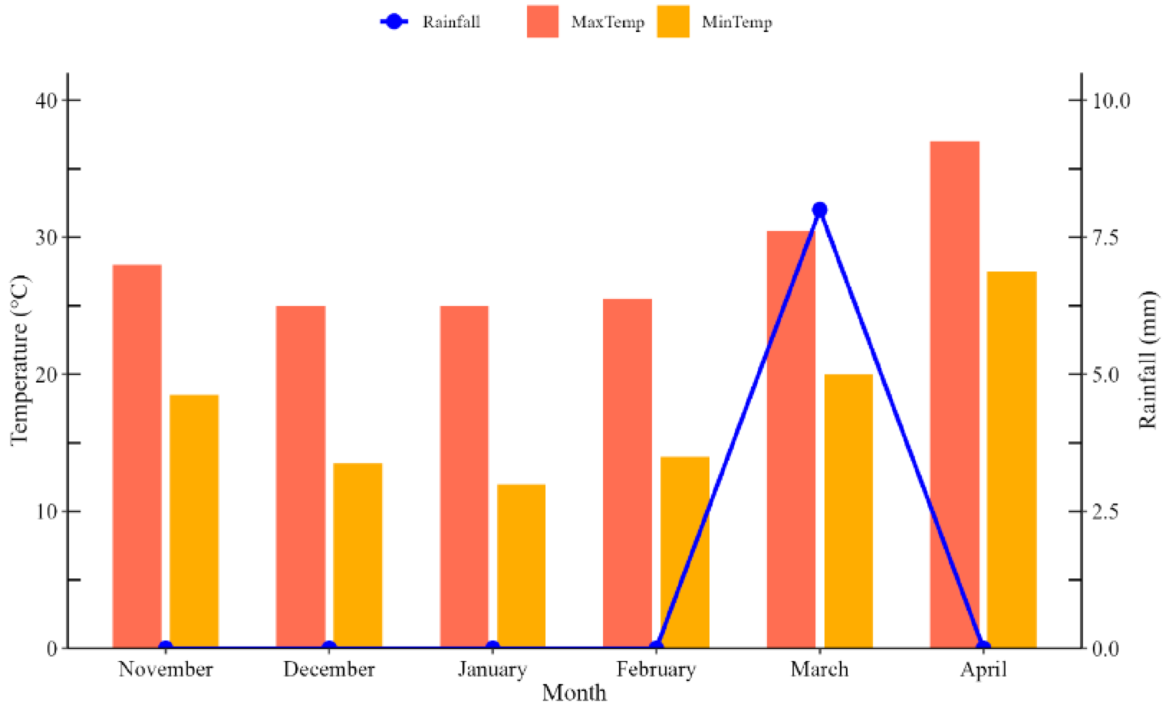

Figure 1: Monthly maximum and minimum temperatures and total rainfall, during the research period at the experimental site.

Research design and agronomic practices

The experiment was conducted using an alpha lattice design with two replications, comprising six blocks, each containing six genotypes. Each plot measured 6 m² and consisted of 8 rows of 3 meters in length. The row-to-row distance was 25 cm. Line sowing was performed on November 12, 2023, at the rate of 100 kg/ha. Primary tillage was conducted using a tractor 15 days before sowing, followed by two light plowings. Compost manure (5 t/ha) and the recommended fertilizer dose of 60:30:30 kg NPK per hectare were applied. Half dose of nitrogen, full dose of phosphorus, and potassium were applied as a basal dose during field preparation, and the remaining Nitrogen was top-dressed at 45 and 90 DAS. Weeding was performed twice at 45 and 70 days after sowing. The crop was grown under rainfed conditions without external irrigation. The standard package of practices for wheat cultivation was ensured throughout the research period.

Data collection

Data were recorded from ten randomly selected plants per plot at the appropriate growth stage. The complete list of 14 studied quantitative traits and the method of assessment are presented in Table 2.

Table 2: List of studied traits and method of assessment

Trait	Code	Assessment
Plant height (cm)	PH	Measured from base of the plant to the tip of the spike, excluding awns.
Total tillers (n)	TT	Counted all tillers at maturity.
Effective tillers (n)	ET	Productive tillers bearing spikes were counted at maturity.
Flag leaf area (cm²)	FLA	FLA = leaf length × leaf width × 0.75, where 0.75 represents the correction factor.
Number of florets (n)	NF	Counted manually from randomly selected spikes and averaged.
Awn length (cm)	AL	Measured from the base to the tip of the awn.
Peduncle length (cm)	PL	Measured from the top of the last internode to the base of the spike.
Spike length (cm)	SL	Measured from the base of the spike to the tip of the uppermost floret.
Number of spikelets per spike (n)	NSPS	Counted manually from spikes and averaged.
Number of spikes per square meter (n)	NSPMS	Spikes counted within a one-square-meter area.
Number of grains per spike (n)	NGPS	Manually counted from selected spikes and averaged.
Grain yield (t/ha)	GY	Total grain weight per plot at 12% moisture content was recorded and converted into tons per hectare.
Biological yield (t/ha)	BY	Total above-ground biomass weight per plot was recorded and expressed in tons per hectare.
Harvest index (%)	HI	Ratio of grain yield to biological yield and expressed as a percentage.

Statistical analysis

Data entry and processing were conducted using Microsoft Office Excel 2016. Estimation of genetic parameters, and correlation analysis were conducted using specified formulas with the "variability" package (https://cran.r-project.org/package=variability) in R-Studio version 4.3.1 (https://rstudio.com/). The formula used to estimate genetic parameters, and correlation analysis is listed below.

Phenotypic variance (σ_p^2), genotypic variance (σ_g^2), broad sense heritability (h^2_b) and genetic advance (GA) were calculated by the formula provided by Allard (1999) and Johnson et al. (1955).

a) Genotypic variance (σ_g^2)= $\frac{\text{GMS} - \text{EMS}}{\text{r}}$ (eqn 1)

b) Phenotypic variance (σ_p^2)= EMS +σ_g^2 (eqn 2)

where GMS is genotypic mean square, EMS is error mean square, and r is the number of replications.

c) Broad sense heritability was expressed in percentage and calculated using equation 3.

Broad sense heritability (h^2_b) = $\frac{\sigma_g^2}{\sigma_p^2}$ *100% (eqn 3)

Where, σ_g^2 represents genotypic variance and σ_p^2 represents phenotypic variance.

Heritability was categorized as low (below 30%), medium (30-60%), and high (above 60%).

d) Genetic advance (GA) = h^2_b. K. σ_P (eqn 4)

Where, σ_P=phenotypic standard deviation and K= selection differential (2.06 at 5% at selection intensity)

Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) were computed using the formula provided by Burton & De Vane (1953).

Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\sigma_p^2}}{\bar{x}}$ x 100% (eqn 5)

Similarly, Genotypic coefficient of variation (GCV)= $\frac{\sqrt{\sigma_g^2}}{\bar{x}}$ x 100% (eqn 6)

where $\bar{x}$ = Population means, σ_g^2 =genotypic variance, σ_p^2= phenotypic variance

GCV and PCV values were classified into three categories: low (<10%), moderate (10-20%), and high (>20%), as described by Sivasubramaniam & Madhava Menon (1973).

Genetic advance as percentage of mean (GAM) was calculated as suggested by Comstock & Robinson (1952).

GAM = $\frac{GA}{\bar{x}}$ x 100% (eqn 7)

where $\bar{x}$ = Population means and GA = genetic advance.

Genotypic and phenotypic correlation was calculated as suggested by Faysal et al. (2022).

$r_g = \frac{\mathrm{Covg\ X.Y}}{\sqrt{\sigma_g^2 X.\sigma_P^2 Y.}}$ (eqn 8)

$r_p = \frac{\mathrm{Covp\ X.Y}}{\sqrt{\sigma_p^2 X.\sigma_g^2 Y.}}$ (eqn 9)

where, Cov_g X.Y represents genotypic covariance of x and y traits, Cov_p X.Y represents phenotypic covariance of x and y traits, σ_g^2X = genotypic variance for trait X, σ_p^2Y= phenotypic variance for trait Y.

RESULTS AND DISCUSSION

Estimation of Variability Components

The extent of variation is influenced by the scale of measurement. Thus, coefficient of variation (CV%), being unitless, is more effective to compare variability across breeding populations (Ahsan et al., 2015). In this study, the highest GCV was observed in ET (25.87%), followed by TT (25.20%) and GY (15.70%). HI, FLA, PL and AL exhibited moderate GCV and the remaining traits showed a low GCV (Table 3). The highest PCV was observed in ET (27.61%), followed by TT (25.93%). Similarly, medium PCV was observed in FLA, followed by BY, HI, GY, NGPS, PL, AL and NF, whereas low PCV was observed in PH, SL, NSPS and NSPMS (Table 3). The relatively high GCV and PCV observed in ET, TT, FLA, GY and HI indicate considerable genetic variation among the studied genotypes. Conversely, low estimates of GCV and PCV observed in PH, SL and NSPMS indicate limited diversity. For such traits, induced mutations or hybridization should be done to introduce new alleles and improve these traits. In general, higher PCV compared to corresponding GCV for all the studied traits is due to environmental influence on trait expression (Tripathi et al., 2011).

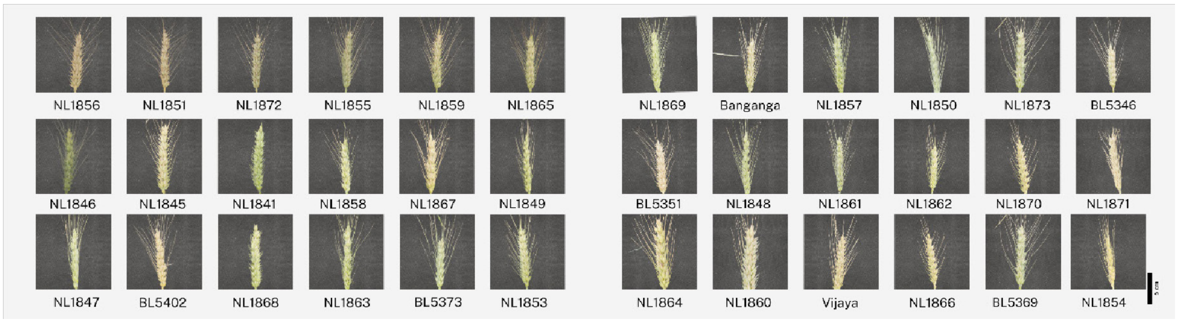

Figure 2: Variation in spike length and awn length among the studied wheat genotypes

Table 3: Estimation of genetic parameters, heritability and expected genetic advance

Traits	Mean	GCV (%)	PCV (%)	h^2_b (%)	GA	GAM (%)
PH	97.38	7.25	8.75	68	12.05	12.37
TT	2.36	25.2	25.93	94	1.19	50.45
ET	2.01	25.87	27.61	87	1.07	49.92
FLA	25.17	12.29	19.86	38	3.94	15.67
AL	7.01	11.7	13.33	76	1.48	21.14
NF	55.41	6.51	11.09	34	4.36	7.87
PL	37.59	11.72	12.75	84	8.34	22.19
SL	9.53	5.13	7.17	51	0.72	7.57
NSPS	16.96	4.59	8.29	30	0.89	5.24
NGPS	46.47	8.29	12.75	42	5.16	11.12
NSPMS	9.47	5.54	8.27	44	0.72	7.65
BY	9.57	6.8	19.29	12	0.47	4.94
HI	34.52	12.93	17.74	53	6.7	19.43
GY	3.5	15.7	16.1	95	1.1	31.55

Note: GA= Genetic advance, GAM (%) = Genetic advance as percentage of mean, GCV= genotypic coefficient of variation, PCV= phenotypic coefficient of variation, GV= genotypic variance, PV = phenotypic variation, h^2_b*= broad sense heritability, PH=plant height, TT= total number of tillers, ET= total number of effective tillers, FLA= flag leaf area, AL= awn length, NF= number of florets, PL= peduncle length, SL= spike length, NSPS= number of spikelet per spike, NFPS= number of florets per spike, NGPS= number of grains per spike, BY= biological yield, HI= harvest index and GY= grain yield.*

Broad sense heritability and genetic advance are two interrelated concepts. They help to understand the nature of gene action in the expression of various polygenic traits (Johnson et al., 1955). In this study, heritability ranged from 12 to 95% (Table 3). High heritability was observed in GY (95%), followed by TT (94%), ET (87%), PL (84%), and AL (76%). Similarly, moderate heritability was recorded in HI, NSPMS, NGPS, NF, and FLA, while BY showed the lowest heritability. GAM helps to determine the expected improvement in a particular trait resulting from selection. GAM ranged from 50.45% to 5.25% in our study. The highest GAM was observed for TT (50.45%), ET (49.92%), GY (31.55%), PL (22.19%)

and AL (21.14%). Medium GAM was observed in HI, FLA, PH, and NGPS and low GAM was noted in BY, NSPMS, NSPS, SL, and NF (Table 3). High heritability coupled with high GAM for ET, TT, GY, and PL suggests that these traits are controlled by additive gene action (Desheva & Cholakov, 2014; Khokhar et al., 2010). This supports their potential for selection in breeding programs. Conversely, low heritability and low GAM observed in NSPS and BY indicate that these traits are highly influenced by environmental factors. Heterosis breeding and progeny testing may be more effective for improving these traits (Adhikari et al., 2018). However, this was different from the previous report of Verma et al. (2019), who reported high heritability with low GAM for PH and ET. This might be due to the genetic and agro-ecological differences.

Correlation Analysis

Grain yield, being a complex polygenic trait, is governed by both genetic and environmental factors (Attri et al., 2021). Traits positively correlated with GY are important and should be prioritized for selection. In this study, HI, FLA, PH, PL and BY exhibited a significant positive correlation with GY at both phenotypic and genotypic levels ($p < 0.05$) (Table 4). This is consistent with previous findings (Baye et al., 2020; Singh et al., 2023). These traits contribute directly to yield and should be prioritized in breeding programs. Flag leaf area is the most photosynthetically active during grain filling and contributes 45–58% of the total photosynthate to grain yield (Khaliq et al., 2008). Thus, genotypes with large FLA are desirable as they improve light interception and contribute to grain yield. Harvest index reflects dry matter allocation to grain and positively influences yield (Xi et al., 2024). Longer peduncle length enhances the accumulation of water-soluble carbohydrates under water deficit conditions (Ntawuguranayo et al., 2024). As a result, genotypes with longer PL could be beneficial in rainfed areas. However, excessive peduncle length influences plant architecture and stability and increases lodging risk (Shah et al., 2019).

Table 4: Phenotypic and genotypic correlation among the studied traits

Trait	PH	TT	ET	FLA	AL	NF	PL	SL	NSPS	NGPS	NSPMS	BY	HI	GY
PH		0.16	0.16	0.45**	0.18	−0.75**	0.83**	−0.22	−0.80**	−0.57**	−0.21	0.08	0.08	0.33*
TT	0.1		0.96**	0.29	0.32	0.19	0.09	0.31	0.07	0.12	0.44**	0.73**	−0.04	0.1
ET	0.2	0.87**		0.43**	0.28	−0.07	0.18	0.13	−0.15	−0.08	0.29	0.50**	−0.04	0.19
FLA	0.31**	0.16	0.22		0.91**	−0.56**	0.51**	0.28	−0.39*	−0.53**	0.22	0.59**	0.1	0.53**
AL	0.26*	0.24*	0.24*	0.46**		−0.47**	0.27	0.13	−0.50**	−0.41*	0.22	0.23	−0.09	−0.02
NF	−0.27**	0.05	−0.01	0.05	−0.24*		−0.93**	0.62**	0.92**	0.92*	0.66**	−0.48**	−0.12	0.21
PL	0.75**	0.06	0.18	0.43**	0.28**	−0.38**		−0.28	−0.64**	−0.58**	−0.35*	−0.23	0.26	0.35*
SL	0.01	0.16	0.1	0.30**	0.25**	0.41**	−0.06		0.76**	0.37*	0.98**	0.43**	−0.24	0.29
NSPS	−0.80**	−0.02	−0.08	−0.17	−0.15*	0.54**	−0.30**	0.46**		0.64**	0.59**	−0.72**	0.05	0.24
NGPS	−0.23**	0.04	−0.01	0.09	−0.30**	0.85**	−0.26*	0.27*	0.36**		0.34*	−0.48**	0.19	0.29
NSPMS	0.05	0.27*	0.23**	0.21	0.27*	0.22	−0.85*	0.85**	0.35**	0.35**		0.47**	−0.40*	0.25
BY	0.28*	0.15	0.23**	0.30*	0.2	0.32**	0.18	0.41**	0.21	0.07	0.38**		−1.18**	0.60**
HI	0.13	−0.03	0.01	0.11	−0.10	0.06	−0.22	−0.14	−0.01	0.15	−0.20	−0.32**		0.44**
GY	0.33**	0.08	0.2	0.34**	−0.02	0.21	0.36**	0.24*	0.17	0.22	0.2	0.32**	0.37**	

*Note: Below diagonal phenotypic correlation coefficient and above diagonal genotypic correlation coefficient. PH=plant height, TT= total number of tillers, ET= total number of effective tillers, FLA= flag leaf area, AL= awn length, NF= number of florets, PL= peduncle length, SL= spike length, NSPS= number of spikelets per spike, NFPS= number of florets per spike, NGPS= number of grains per spike, BY= biological yield, HI= harvest index, GY= grain yield. * & ** indicate significance at 5% and 1% level of probability, respectively.*

In this study, NGPS and SL were positively correlated with GY only at phenotypic level. In contrast, TT, ET, NSPS, and NSPMS showed positive but non-significant associations at both phenotypic and genotypic levels. NF was the only trait that exhibited equal genotypic and phenotypic coefficients. Traits with a high phenotypic correlation coefficient are more influenced by environmental factors.

Overall, this study provides a reference for the selection of key yield-attributing traits in wheat genotypes. However, multi-locational and multi-year trials with these genotypes are recommended to validate these results under different agro-climatic conditions, supporting wheat improvement programs in Nepal.CONCLUSION

The present study revealed wide variations across the studied traits among wheat genotypes and offers scope for selection or hybridization to achieve genetic gains. The study of genetic parameters showed that effective tillers, total tillers, grain yield, and peduncle length had high heritability coupled with high genetic advance. Harvest index, spike length, effective tillers, and biological yield showed a strong positive association with grain yield at both genotypic and phenotypic levels. Future wheat breeding programs should prioritize developing wheat genotypes with effective tillers, higher grains per spike, and improved harvest index to maximize yield potential.

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REFERENCES

Adhikari, B. N., Joshi, B. P., Shrestha, J., & Bhatta, N. R. (2018). Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (*Oryza sativa* L.). *Journal of Agriculture and Natural Resources*, 1(1), 149–160. https://doi.org/10.3126/janr.v1i1.22230

Adhikari, S. P., Ghimire, Y. N., Timsina, K. P., Subedi, S., & Kharel, M. (2021). Technical efficiency of wheat growing farmers of Nepal. *Journal of Agriculture and Natural Resources*, 4(2), 246–254. https://doi.org/10.3126/janr.v4i2.33857

Ahsan, M. Z., Majidano, M. S., Bhutto, H., Soomro, A. W., Panhwar, F. H., Channa, A. R., & Sial, K. B. (2015). Genetic variability, coefficient of variance, heritability and genetic advance of some *Gossypium hirsutum* L. accessions. *Journal of Agricultural Science*, 7(2), 147–157. https://doi.org/10.5539/jas.v7n2p147

Allard, R. W. (1999). Principles of plant breeding. John Wiley & Sons.

Attri, H., Dey, T., Singh, B., & Kour, A. (2021). Genetic estimation of grain yield and its attributes in three wheat (*Triticum aestivum* L.) crosses using six parameter model. *Journal of Genetics*, 100, 47.

Baye, A., Berihun, B., Bantayehu, M., & Derebe, B. (2020). Genotypic and phenotypic correlation and path coefficient analysis for yield and yield-related traits in advanced bread wheat (*Triticum aestivum* L.) lines. *Cogent Food & Agriculture*, 6(1), 1752603. https://doi.org/10.1080/23311932.2020.1752603

Bhandari, R., Paudel, H., Nyaupane, S., & Poudel, M. R. (2024). Climate resilient breeding for high yields and stable wheat (*Triticum aestivum* L.) lines under irrigated and abiotic stress environments. *Plant Stress*, 11, 100352. https://doi.org/10.1016/j.stress.2024.100352

Bhushan, B., Bharti, S., Ojha, A., Pandey, M., Gourav, S. S., Tyagi, B. S., & Singh, G. (2013). Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. *Journal of Cereal Research*, 5(1), 1–7.

Bhutto, A. H., Rajpar, A. A., Kalhoro, S. A., Ali, A., Kalhoro, F. A., Ahmed, M., Raza, S., & Kalhoro, N. A. (2016). Correlation and regression analysis for yield traits in wheat (*Triticum aestivum* L.) genotypes. *Natural Science*, 8(3), 96–104. https://doi.org/10.4236/ns.2016.83013

Burton, G. W., & DeVane, E. H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, 45, 478–481.

Comstock, R. E., & Robinson, H. F. (1952). Genetic parameters, their estimation and significance. Proceedings of the 6th International Grassland Congress, 1, 284–291.

Desheva, G., & Cholakov, T. (2014). Variability, heritability and genetic progress for some yield components in common winter wheat genotypes (*Triticum aestivum* L.). *Genetics and Plant Physiology*, 4(3–4), 191–200.

Devkota, N., & Phuyal, R. K. (2016). Climatic impact on wheat production in Terai of Nepal. *Journal of Development and Administrative Studies*, 23(1–2), 1–22. https://doi.org/10.3126/jodas.v23i1-2.15445

Ene, C. O., Ogbonna, P. E., Agbo, C. U., & Chukwudi, U. P. (2016). Studies of phenotypic and genotypic variation in sixteen cucumber genotypes. *Chilean Journal of Agricultural Research*, 76(3), 307–313. https://doi.org/10.4067/S0718-58392016000300007

FAOSTAT. (2021). *World food and agriculture – Statistical yearbook 2021*. FAO. https://doi.org/10.4060/cb4477en

Faysal, A. S. M., Ali, L., Azam, M. G., Sarker, U., Ercisli, S., Golokhvast, K. S., & Marc, R. A. (2022). Genetic variability, character association, and path coefficient analysis in transplant Aman rice genotypes (*Oryza sativa* L.). *Plants*, 11(21), 2952. https://doi.org/10.3390/plants11212952

Haydar, F., Ahamed, M., Siddique, A., Uddin, G., Biswas, K., & Alam, M. (2019). Estimation of genetic variability, heritability and correlation for some quantitative traits in wheat (*Triticum aestivum* L.). *Journal of Bio-Science*, 28, 81–86. https://doi.org/10.3329/jbs.v28i0.44713

Ilyas Khokhar, M., Hussain, M., Zulkiffal, M., Sabir, W., Mahmood, S., Waqas Jamil, M., & Anwar, J. (2010). Studies on genetic variability and inter-relationship among the different traits in wheat (*Triticum aestivum* L.). *Krmiva*, 52(2), 77–84.

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47, 314–318.

Kandel, P., Shrestha, A., Sai, R., Koirala, P., Subedi, P., & Baral, S. (2024). Status of adoption of wheat (*Triticum aestivum* L.) production technology in wheat zone, Rupandehi, Nepal. *Russian Journal of Agricultural and Socio-Economic Sciences*, 155(11), 1184–1192.

Khaliq, I., Irshad, A., & Ahsan, M. (2008). Awns and flag leaf contribution towards grain yield in spring wheat (*Triticum aestivum* L.). *Cereal Research Communications*, 36(1), 65–76. https://doi.org/10.1556/CRC.36.2008.1.7

Kulsum, U., Sarker, U., & Rasul, M. (2022). Genetic variability, heritability and interrelationship in salt-tolerant lines of T. Aman rice (*Oryza sativa* L.). *Genetika*, 54(2), 761–776. https://doi.org/10.2298/GENSR2202761K

Kumar, Y., Lamba, R. A. S., Singh, B., & Kumar, V. (2014). Genetic variability, correlation and path analysis in wheat varieties under late sown conditions. *Annals of Agri Bio Research*, 19(4), 724–727.

MoALD. (2023). Statistical information on Nepalese agriculture 2078/79 (2021/22). Ministry of Agriculture and Livestock Development.

MoALD. (2024). Statistical information on Nepalese agriculture 2079/80 (2022/23). Ministry of Agriculture and Livestock Development.

Ntawuguranayo, S., Zilberberg, M., Nashef, K., Bonfil, D. J., Bainsla, N. K., Piñera-Chavez, F. J., Reynolds, M. P., Peleg, Z., & Ben-David, R. (2024). Stem traits promote wheat climate-resilience. *Frontiers in Plant Science*, 15, 1388881. https://doi.org/10.3389/fpls.2024.1388881

Poudel, M. R., Poudel, P. B., Puri, R. R., & Paudel, H. K. (2021). Variability, correlation and path coefficient analysis for agro-morphological traits in wheat genotypes (*Triticum aestivum* L.) under normal and heat stress conditions. *International Journal of Applied Sciences and Biotechnology*, 9(1), 65–74. https://doi.org/10.3126/ijasbt.v9i1.35985

Prasad, S. K., Pullabhotla, H., & Ganesh-Kumar, A. (2011). Supply and demand for cereals in Nepal, 2010–2030. IFPRI Discussion Paper.

Sakamoto, T., Morinaka, Y., Ohnishi, T., Sunohara, H., Fujioka, S., Ueguchi-Tanaka, M., Mizutani, M., Sakata, K., Takatsuto, S., Yoshida, S., Tanaka, H., Kitano, H., & Matsuoka, M. (2006). Erect leaves caused by brassinosteroid deficiency increase biomass production and grain yield in rice. *Nature Biotechnology*, 24(1), 105–109. https://doi.org/10.1038/nbt1173

Shah, L., Yahya, M., Shah, S. M. A., Nadeem, M., Ali, A., Ali, A., Wang, J., Riaz, M. W., Rehman, S., Wu, W., Khan, R. M., Abbas, A., Riaz, A., Anis, G. B., Si, H., Jiang, H., & Ma, C. (2019). Improving lodging resistance: Using wheat and rice as classical examples. *International Journal of Molecular Sciences*, 20(17), 4211. https://doi.org/10.3390/ijms20174211

Sharada, H. B., Kumar, S. L., Lakshmi, D., Basavaraj, C. D., & Shankar, K. M. (2024). Trait association and genetic variability study in rice MAGIC lines for yield-related traits. *Journal of Advances in Biology & Biotechnology*, 27(12), 673–680. https://doi.org/10.9734/jabb/2024/v27i121815

Shrestha, S., Niraula, D., Regmi, S., Basnet, S., Chhetri, S. T., & Kandel, B. P. (2023). Performance evaluation and genetic parameters estimation of multi-company maize hybrids in Lamahi Dang, Nepal. *Heliyon*, 9(3), e14552. https://doi.org/10.1016/j.heliyon.2023.e14552

Singh, P. K., Singh, L., Singh, S. V., Nath, S., Yadav, V., Mishra, A., & Kuswaha, C. (2023). Estimation of genetic variability, correlation and path analysis for yield and some yield contributing traits in bread wheat (*Triticum aestivum* L.). *International Journal of Environment and Climate Change*, 13(11), 2429–2440. https://doi.org/10.9734/ijecc/2023/v13i113409

Sivasubramaniam, S., & Madhava Menon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*, 60, 1093–1096.

Taheri, S., Saba, J., Shekari, F., & Abdullah, T. L. (2011). Effects of drought stress condition on the yield of spring wheat (*Triticum aestivum*). *African Journal of Biotechnology*, 10(80), 18339–18348.

Thapa, A., Jaisi, S., & Poudel, M. R. (2022). Genetic variability and association among yield and yield components of wheat genotypes (*Triticum aestivum* L.). *Big Data in Agriculture*, 4(1), 1–7. https://doi.org/10.26480/bda.01.2022.01.07

Tiwari, D. N., Tripathi, S. R., Tripathi, M. P., Khatri, N., & Bastola, B. R. (2019). Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. *Advances in Agriculture*, 2019, 1–9. https://doi.org/10.1155/2019/5975901

Tripathi, S. N., Marker, S., Pandey, P., Jaiswal, K. K., & Tiwari, D. K. (2011). Relationship between some morphological and physiological traits with grain yield in bread wheat (*Triticum aestivum* L. em. Thell.). *Trends in Applied Sciences Research*, 6(9), 1037–1045.

Tshikunde, N. M., Mashilo, J., Shimelis, H., & Odindo, A. (2019). Agronomic and physiological traits, and associated quantitative trait loci (QTL) affecting yield response in wheat (*Triticum aestivum* L.): A review. *Frontiers in Plant Science*, 10, 1428. https://doi.org/10.3389/fpls.2019.01428

Upadhyay, K., Adhikari, N. R., C, G. B. K., & Sharma, S. (2019). Genetic variability and cluster analysis of wheat (*Triticum aestivum* L.) genotypes in foot hill of Nepal. *Archives of Agriculture and Environmental Science*, 4(3), 350–355. https://doi.org/10.26832/24566632.2019.0403013

Verma, P., Saini, P., Singh, V., & Yashveer, S. (2019). Genetic variability of wheat (*Triticum aestivum* L.) genotypes for agro-morphological traits and their correlation and path analysis. *Journal of Pharmacognosy and Phytochemistry*, 8(4), 2290–2294.

Xi, Y., Du, Y.-L., Wang, D., Ren, J.-Y., Luo, W.-Y., Peng, Q., Fang, W.-Y., & Li, F.-M. (2024). Wheat genetic progress in biomass allocation and yield components: A global perspective. *Field Crops Research*, 318, 109617. https://doi.org/10.1016/j.fcr.2024.109617