



## RESEARCH ARTICLE

## GENETIC VARIABILITY AND ASSOCIATION AMONG YIELD AND YIELD COMPONENTS OF WHEAT GENOTYPES (*Triticum Aestivum* L.)

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## ABSTRACT

The demand for wheat will be increased 60 % compared to existing by 2050 and the wheat productivity of Nepal is lower than world's average productivity. Therefore, it is important to increase the yield potentiality of wheat. This research was conducted for the estimation of variability and association among yield and yield components of wheat. The experimental field was designed in alpha lattice design with 20 diverse wheat genotypes considering 12 important traits. In variability analysis, thousand kernel weight (TKW) had maximum values for the genotypic coefficient of variance (GCV) (11.83%) and phenotypic coefficient of variance (PCV) (12.14%) indicating the presence of high variation in TKW. The number of spikes/m<sup>2</sup> (NSPM) and grain yield (GY) showed higher values for heritability (82.62% and 58.95%) and GA (73.36 and 456.25). These traits have additive gene action and are less affected by the environmental condition. Plant height (PH) had significant positive correlation with GY (0.346) and chlorophyll showed highly significant negative correlation with GY (-0.448). NSPM and PH had a maximum positive direct effect (0.375 and 0.347), chlorophyll content had maximum negative direct effect (-0.234) and days to heading (DTH) and days to anthesis (DTA) showed a positive indirect effect on GY. The selection of genotypes with higher values of PH and NSPM along with moderate or low chlorophyll content is a prerequisite for attaining a higher yield in wheat. Genotypes having longer DTH, DTA and days to maturity (DTM) should be considered during selection of genotypes to obtain higher yield.

## KEYWORDS

Phenotype, Heritability, Genetic advance, Correlation and Path analysis

## 1. INTRODUCTION

Wheat (*Triticum aestivum*) is an important cereal food crop of the world and is the world's most favored staple food (Akter and Islam, 2017). It is nutritious food containing 60-70% starch, 6-26% protein, 2.7% fibers, 2.1% minerals, 2.1% fat and vitamins (Kumar et al., 2011). It is used as food for humans (consumed by 2.5 billion people all over the world) and feeds for an animal. Wheat grain is easy to store, transport and can be processed into various types of food (Poudel et al., 2017). In a world, it is in the first rank in terms of both production (765.76 million tonnes) and production area (215.9 million hectares) and the productivity of wheat in the world is 3.54 tonnes/hectare (FAOSTATA, 2019). Until 2050, the demand for wheat is expected to increase by 60 % than in the present year (FAOSTATA, 2018). In Nepal, wheat is the third most important staple food crop after rice and maize with 0.7 million hectares of production area and 2 million tons total production (MOALD 2018/19). Wheat productivity is 2.85 tons/hectare in Nepal which is lower than the world's productivity (3.54 tonnes/ha) (FAOSTATA 2019). The causes behind the low production of wheat in Nepal are lack of high yielding genotype, climate change, global warming, lack of inputs and irrigation, soil fertility degradation and biotic/abiotic stresses like drought, heat stress and various diseases (Upadhyay 2017; Poudel et al., 2020; Sharma et al. 2020).

Being a complex quantitative character, grain yield is greatly influenced by external environmental conditions. It is associated with various yield attributing characters such as chlorophyll content, number of grains per spike, number of spikelets per spikes, thousand kernel weight, etc.

Therefore, the only genotypic selection isn't effective and selection should be based on the performance of yield components and morpho-physiological characters (Khan 2014; Ali et al., 2009; Khaliq et al., 2004). The presence of higher variability among wheat genotypes provides more opportunity to the breeders for improvement of genotypes via a selection program. To obtain a genetically superior individual selection of genotypes should be done with adequate phenotypic variation and high heritability (Nukasani et al., 2013). Selection of traits with the estimate of heritability and genetic advance altogether gives a precise result for genetic gain (Adhikari et al., 2018).

The correlation coefficient is the measure of the degree of symmetrical association between two variables or characters which helps us in understanding the nature and magnitude of association among yield and yield components and provides an opportunity for indirect selection. Genotypic and phenotypic correlations quantify the degree of association of various morpho-physiological characters with economic productivity (Baye et al., 2020). The correlation coefficient is used to study the magnitude and direction of different components in the main character (Da Silva et al., 2009). Path coefficient analysis provides more information about the relationship between grain yield and yield attributing characters than correlation (Arshad et al., 2006). It is useful to find direct and indirect effects of one variable to another variable and to interpret cause and effect relationships among the traits (Dewey and Lu, 1959). In plant breeding, path coefficient analysis is helpful for the plant breeder to select useful traits for improving crop yield (Milligan et al., 2003).

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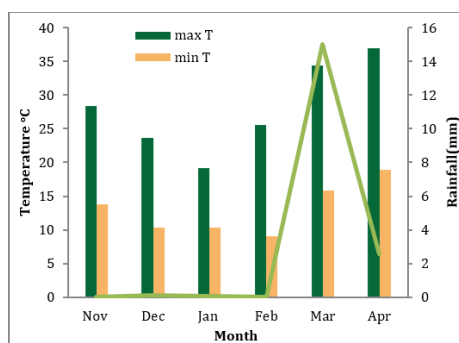
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Some researchers identified the positive correlation of some morphological characters with grain yield such as plant height, numbers of spikes/m<sup>2</sup>, number of spikelets per spike, number of grains per spike, chlorophyll content, days to anthesis, spike weight, spike length, thousand kernel weight, days to heading and plant height (Mohammad et al. 2002; Mecha et al. 2017; Dutamo et al. 2015; Singh et al. 2012; Ayer et al. 2017; Ojha et al. 2018b; Sokoto et al. 2012; Akram et al. 2008; Ojha et al. 2018b). Spike weight, spike length, thousand kernel weight, number of spikes/m<sup>2</sup>, number of grains per spike and days to anthesis had a direct positive effect on grain yield and plant height, chlorophyll content and days to heading had the negative direct effect of on grain yield (Singh et al., 2012; Ojha et al., 2018b). This research was conducted to study genetic variability and the relationship between yield and yield components of diverse wheat genotypes that will be useful for the selection of wheat genotypes with the yield attributing characters that support higher grain yield.

## 2. MATERIALS AND METHODS

### 2.1 Description of the research area

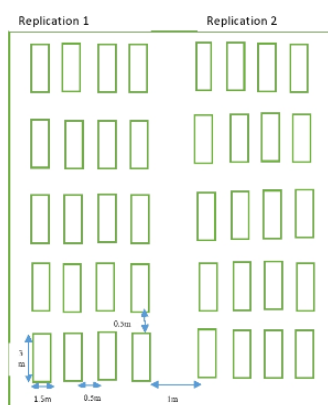
The research was conducted at the Institute of Agriculture and Animal Science, Paklihawa Campus, Bhairahawa, Nepal. The research site is located at 79 meters above the sea level and geographic location is 27°30' North and 83°27' east. The climate is a humid and sub-tropical type with hot summers and cold winters and total rainfall is 1725.3 mm. According to climatic data obtained from the Department of Hydrology and Meteorology, the maximum temperature during the crop period was 38 °C in April and the minimum temperature was 8.8 °C in January. There was little rainfall in March (15mm) and April and no rainfall in other months.



**Figure 1:** Mean monthly maximum temperature, minimum temperature and rainfall of experimental site during the wheat growing season (Source: Department of Hydrology and Meteorology)

### 2.2 Experimental materials and design

The experimental material consisted of 20 wheat genotypes obtained from National Wheat Research Program (NWRP), Bhairahawa among them Bhirkuti and Gautam are commercial varieties used as a standard check. The research was conducted from 28<sup>th</sup> November 2020 to 7<sup>th</sup> April 2021. The experimental design was an alpha lattice design with 2 replications and 5 blocks per replication (Figure 2). The size of the plot was 3m<sup>2</sup> and was spaced by 50cm. The space between the two replication was 1m. Seeds were sown by line sowing method and spacing between two rows was 25 cm. The seed rate of 100kg/ha was used and recommended dose of fertilizer 100:50:30 Kg NPK/ha was used (MOALD 2018/19). Irrigation was given at Crown root initiation stage, booting stage, heading stage, flowering stage, milking stage and soft dough stage. Weeding was done two times at 45 DAS and 70 DAS for both conditions (MOALD 2018/19).



**Figure 2:** Field layout of the experimental field in an alpha lattice design.

S.N	Genotypes*	Source
1.	Bhirkuti	NWRP, Bhairahawa
2.	BL 4407	NWRP, Bhairahawa
3.	BL 4669	NWRP, Bhairahawa
4.	BL 4919	NWRP, Bhairahawa
5.	Gautam	NWRP, Bhairahawa
6.	NL 1179	NWRP, Bhairahawa
7.	NL 1346	NWRP, Bhairahawa
8.	NL 1350	NWRP, Bhairahawa
9.	NL 1368	NWRP, Bhairahawa
10.	NL 1369	NWRP, Bhairahawa
11.	NL 1376	NWRP, Bhairahawa
12.	NL 1381	NWRP, Bhairahawa
13.	NL 1384	NWRP, Bhairahawa
14.	NL 1386	NWRP, Bhairahawa
15.	NL 1387	NWRP, Bhairahawa
16.	NL 1404	NWRP, Bhairahawa
17.	NL 1412	NWRP, Bhairahawa
18.	NL 1413	NWRP, Bhairahawa
19.	NL 1417	NWRP, Bhairahawa
20.	NL 1420	NWRP, Bhairahawa

### 2.3 Data recorded

Twelve different phenological and morphological data were recorded from randomly selected 10 sample plants per plot excluding border plants.

#### 2.3.1 Days to heading

The heading is the emergence of a spike from flag leaf. When 50% of selected plants were at a stage of heading then days of heading were recorded.

#### 2.3.2 Days to anthesis

Anthesis is the opening of a flower. It was recorded when flowers were opened in 50% of selected plants.

#### 2.3.3 Days to maturity

When 75% of plants on plots were matured i.e., yellowing and drying of the whole plant then days to maturity were recorded.

#### 2.3.4 Plant height

It was measured by scale from the land surface to the tip of the spike.

#### 2.3.5 Spike length

It was measured by scale from the base to the tip of the spike.

#### 2.3.6 Spike weight

Spike weight was recorded by weighing 10 spikes of randomly selected plants.

#### 2.3.7 Chlorophyll content

It was measured by a SPAD meter. The first measurement was taken before heading, the second measurement after 1 week of the first measurement and the last time after one week of the second measurement. Then measured value was averaged and chlorophyll of genotype was recorded.

#### 2.3.8 Number of spikelets per spike

It was recorded by counting the spikelet of selected 10 sample plants and thereby averaging the value.

#### 2.3.9 Number of grains per spike

It was recorded by counting the total number of grains of sampled plants and thereby averaging the value.

#### 2.3.10 Number of spike/m<sup>2</sup>

Spike number from two areas of the single plot each of 1 m<sup>2</sup> was counted and such obtained number were averaged and recorded a number of spike per m<sup>2</sup>.

### 2.3.11 Grain yield

Grain obtained from two areas of a single plot each of 1 m<sup>2</sup> were weighed separately. Then thus obtained values were averaged and converted into kg/ha.

### 2.3.12 Thousand kernel weights

A thousand kernels were counted randomly from the bulk of grain obtained from a single plot and weight was taken with weighing balance.

## 2.4 Statistical analysis

Data entry and processing were done by Microsoft Office Excel 2010. Analysis of Variance was done by using R3.5.0 a software package for alpha lattice design by ADEL-R (CIMMYT, Mexico). Correlation and path coefficient analysis was done by using SPSS and Microsoft office excel. Estimation of variance components, genetic advance and genetic advance as % of the mean Phenotypic and genotypic coefficients of variance were estimated by the formula given (Burton and De Vane, 1953).

$$GCV = \frac{\sqrt{\sigma_g^2}}{\mu} \times 100$$

$$PCV = \frac{\sqrt{\sigma_p^2}}{\mu} \times 100$$

Where, GCV = genotypic coefficient of variance, PCV = phenotypic coefficient of variance,  $\sigma_g^2$  = genotypic variance,  $\sigma_p^2$  = phenotypic variance,  $\mu$  = mean of the characters.

Broad sense heritability (H<sup>2</sup>) and expected genetic advance (GA) were calculated by the formula suggested (Allard, 1960).

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

$$GA = K \times \sigma_p \times H^2$$

Where, K = selection differential (2.06 for 5% at selection intensity) and  $\sigma_p$  = phenotypic standard deviation.

## 3. RESULTS

### 3.1 Analysis of variance

The mean sum of the square of different characters obtained is shown in table 2. The result revealed that there were significant differences among the genotypes indicating that there is variation among the genotypes which provides further opportunities for wheat improvement programs. Table no. 2 showed highly significant difference among the genotypes for days to heading, days to maturity, chlorophyll content, plant height, spike length, number of spikelet per spike, thousand kernel weight and number of spikes/m<sup>2</sup> while days to anthesis, grain yield and number of grains per spike shows the non-significance difference among genotypes. There were no grain yield differences among wheat genotypes. There are significant differences for replication in case of DTH, DTM, TKW and Chlorophyll

content and non-significant difference among the genotypes in favor of DTA, PH, SL, SW, NSPS, NGPS and GY.

Table 2: Mean sum of the square of 12 important characters including the yield of wheat genotypes				
Traits	Replication (df=1)	Treatment (df=19)	Block (df=4)	Error (df=15)
DTH	75.62**	11.88**	0.50	2.45
DTA	40.00	117.44NS	118.56	117.78
DTM	72.90**	9.73**	3.71	2.48
Chlorophyll content	38.02*	44.69**	2.21	8.57
PH	3.02	23.76**	2.90	5.33
SL	0.10	0.65**	0.10	0.10
SW	0.90	4.71NS	1.58	2.25
NSPS	0.02	1.89**	0.65	0.39
NGPS	2.50	12.21NS	2.18	5.78
GY	80192.02	72345.69NS	164338.40	88977.93
TKW	9.02*	23.59**	3.40	1.52
NSPM	60.02	2467.01**	896.08	735.27

\*=significant at 0.05% level of significance, \*\*=significant at 0.01% level of significance, NS = non-significant.

Note: DTH= days to heading, DTA= days to anthesis, DTM= days to maturity, PH= plant height, SL= spike length, SW= spike weight, NSPS= number of spikelet per spike, NGPS= number of grain per spike, GY= grain yield, TKW= thousand kernel weight, NSPM = number of spikes/m<sup>2</sup>.

\* The genotypes used are promising so that there is no significant difference in grain yield among genotypes.

### 3.2 Variability, heritability and genetic advance

The genetic coefficient of variance ranged from 0.56% to 11.83%. Thousand kernel weight (TKW) showed maximum value for GCV (11.83%) and other characters showed low GCV. PCV was ranged from 0.69% to 12.14%. TKW showed maximum value for PCV (12.14%), SW, GY and NSPM showed moderate PCV (10.78%, 10.27% and 10.79%) and other characters showed low PCV. The values of heritability were classified as low (less than 30%), moderate (30-60%) and high (more than 60%). TKW showed a maximum value of heritability (94.96%) and chlorophyll showed the minimum value of heritability (35.26%). DTH, DTA, DTM, PH, SL, NGPS, TKW and NSPM showed high value of heritability and chlorophyll, SW, NSPS and GY showed a moderate value of heritability.

**Table 3:** Genotypic coefficient of variance, phenotypic coefficient of variance, broad-sense heritability, genetic advance and genetic advance as % of the mean for 12 characters.

Characters	$\sigma_g^2$	$\sigma_p^2$	Mean	GCV	PCV	H <sup>2</sup>	GA	GAM
DTH	3.31	4.23	82.48	2.21	2.49	78.30	3.32	4.02
DTA	3.56	4.56	88.3	2.14	2.42	78.02	3.42	3.89
DTM	0.45	0.69	119.95	0.56	0.69	65.70	1.12	0.94
Chlorophyll	1.84	5.22	42.03	3.23	5.44	35.26	1.66	3.95
PH	20.00	26.00	89.18	5.01	5.72	76.88	8.08	9.06
SL	0.27	0.38	10.375	5.00	5.99	69.91	0.89	8.62
SW	1.53	4.31	19.25	6.43	10.78	35.47	1.52	7.88
NSPS	0.57	1.11	16.38	4.61	6.43	51.58	1.12	6.83
NGPS	10.95	16.65	41.95	7.89	9.73	65.78	5.53	13.18
GY	83212.66	141158.03	3659.68	7.88	10.27	58.95	456.25	12.47
TKW	14.68	15.46	32.4	11.83	12.14	94.96	7.69	23.74
NSPM	1534.81	1857.67	399.3	9.61	10.79	82.62	73.36	18.37

Note:  $\sigma_g^2$ = genotypic variance,  $\sigma_p^2$ = phenotypic variance, GCV= genotypic coefficient of variance, PCV= phenotypic coefficient of variance, H<sup>2</sup>= broad-sense heritability, GA= genetic advance and GAM= genetic advance as % of the mean.

GY showed a maximum value of GA (456.25) followed by NSPM (73.36), PH (8.08) and TKW (7.69). SL showed a minimum value of GA (0.89). GA was grouped as low (less than 10), moderate (10-20) and high (more than 20). High values of GA were found for GY and NSPM and other remaining

characters showed a low value of GA. A high value of GA as % of mean was observed for TKW (23.74%), moderate values for NSPM (18.37%), NGPS (13.18%) and GY (12.47%) and other characters showed low values.

### 3.3 Correlation among characters at the phenotypic level

The correlation coefficient of 12 characters was evaluated under this study (Table 4). PH showed maximum positive and significant correlation with GY (0.346) and chlorophyll showed a highly significant negative correlation with GY (-0.448). DTH, DTA, DTM, SL, NSPM and TKW had shown a positive but non-significant correlation with GY. While SW, NSPS and NGPS showed negative and non-significant correlations. DTH showed a positive and highly significant correlation with DTA (0.897) and DTM (0.638). It showed a positive and significant correlation with NSPM and a negative and significant correlation with PH and TKW. It showed a non-significant correlation with other characters. The DTA showed highly positive significance with DTH (0.897) and DTM (0.663), positive and significant relationship with NSPM, negative but significant relationship with TKW and non-significant correlation with other characters. The DTM showed positive and non-significant correlation with NSPM, chlorophyll content, SW, NSPS and GY, negative and non-significant relationship with PH, SL and TKW.

Chlorophyll content showed positive and significant correlation with NGPS (0.364), positive and non-significant correlation with DTH, DTA, DTM, SW and NSPS, negative and highly significant correlation with PH (-0.413) and GY (-0.448) and negative but non-significant correlation with SL and TKW. PH showed positive and highly significant correlation with SL (0.584), SW (0.437) and TKW (0.513), positive and significant correlation with GY (0.346), negative and highly significant correlation with chlorophyll content (-0.413), negative and significant correlation with days to heading (-0.399) and a number of spikes/m<sup>2</sup> (-0.340) and non-significant correlation with other characters. SL showed positive and highly significant correlation with PH (0.584), SW (0.639) and TKW (0.669), negative and highly significant correlation with NSPS (-0.442) and non-significant correlation with other characters.

SW showed positive and highly significant correlation with PH (0.437), SL

(0.639), NSPS (0.429) and NGPS (0.526), positive and significant relation with TKW (0.356) and non-significant correlation with others. NSPS showed a positive and highly significant correlation with SW (0.429) and NGPS (0.648) and a non-significant correlation with other characters. NGPS showed a positive and highly significant correlation with SW (0.520) and NSPS (0.648), positive and significant correlation with chlorophyll content (0.364), positive and non-significant correlation with DTM, PH, SL and NSPM. It showed a negative and non-significant correlation with DTH, DTA, TKW and GY.

NSPM showed positive and significant correlation with DTH (0.344) and DTA (0.339), negative and highly significant correlation with SL (-0.442), SW (-0.423) and TKW (-0.645), negative and significant correlation with PH (-0.340) and non-significant correlation with others. TKW showed positive and highly significant correlation with PH (0.513) and SL (0.669), positive and significant correlation with SW (0.356), negative and highly significant with NSPM (-0.645), negative and significant correlation with DTH (-0.320), DTA (-0.319) and non-significant correlation with other characters.

### 3.4 Path coefficient analysis at the phenotypic level

#### 3.4.1 Direct effect

The number of spikes/m<sup>2</sup> showed a maximum positive direct effect (0.375) on grain yield followed by plant height (0.3479) (Table 5). Chlorophyll content showed a maximum negative direct effect (-0.234) on grain yield followed by NSPS (-0.222) and NGPS (-0.208). Days to heading, days to anthesis, days to maturity and spike weight showed a direct positive effect on grain yield with values of 0.195, 0.009, 0.244 and 0.266 respectively whereas chlorophyll content, spike length, NSPS and NGPS showed negative direct effect (-0.234, -0.129, -0.222 and -0.208 respectively) on grain yield.

**Table 4: Correlation between different characters at the phenotypic level**

	DTH	DTA	DTM	Chlorophyll	PH	SL	SW	NSPS	NGPS	NSPM	GY	TKW
DTH	1											
DTA	0.897**	1										
DTM	0.638**	0.663**	1									
Chlorophyll	0.074	0.053	0.110	1								
PH	-0.399*	-0.306	-0.119	-0.413**	1							
SL	-0.274	-0.203	-0.067	-0.250	0.584**	1						
SW	-0.211	-0.155	0.011	0.133	0.437**	0.639**	1					
NSPS	-0.080	-0.086	0.015	0.118	0.125	0.242	0.429**	1				
NGPS	-0.095	-0.118	0.091	0.364*	0.086	0.055	0.520**	0.648**	1			
NSPM	0.344*	0.339*	0.221	-0.089	-0.340*	-0.442**	-0.423**	0.027	0.060	1		
GY	0.034	0.096	0.160	-0.448**	0.346*	0.107	-0.020	-0.207	-0.231	0.209	1	
TRW	-0.320*	-0.319*	-0.129	-0.244	0.513**	0.669**	0.356*	-0.155	-0.292	-0.645**	0.134	1

\*\*= significant at 1% level of significance, \*= significant at 5% level of significance.

Note: DTH= days to heading, DTA= days to anthesis, DTM= days to maturity, PH= plant height, SL= spike length, SW= spike weight, NSPS= number of spikelet per spike, NGPS= number of grain per spike, GY= grain yield, TKW= thousand kernel weight, NSPM = Numbers of spike/m<sup>2</sup>.

#### 3.4.2 Indirect effect

Days to heading and days to anthesis showed a low positive indirect effect on grain yield via a number of spikes/m<sup>2</sup> with values 0.129 and 0.127. Plant height and spike length showed a low negative indirect effect on grain yield through a number of spikes/m<sup>2</sup> with values -0.127 and -0.165

respectively, spike weight showed a low indirect negative effect on grain yield through NGPS (-0.108) and a number of spikes/m<sup>2</sup> (-0.158), NSPS showed a low negative indirect effect on grain yield via NGPS (-0.134), NGPS showed a low indirect negative effect on grain yield through NSPS (-0.144) and a number of spikes/m<sup>2</sup> showed low negative indirect effect on grain yield via plant height (-0.118).

**Table 5: Path analysis between grain yield and other characters at the phenotypic level.**

	DTH	DTA	DTM	Chlorophyll	PH	SL	SW	NSPS	NGPS	NSPM
DTH	<b>0.195</b>	0.175	0.124	0.014	-0.078	-0.053	-0.041	-0.015	-0.018	0.067
DTA	0.008	<b>0.009</b>	0.006	0.000	-0.002	-0.001	-0.001	-0.000	-0.001	0.003
DTM	0.155	0.162	<b>0.244</b>	0.026	-0.029	-0.016	0.002	0.003	0.022	0.054
Chlorophyll	-0.017	-0.012	-0.025	<b>-0.234</b>	0.096	0.058	-0.031	-0.027	-0.085	0.020
PH	-0.138	-0.106	-0.041	-0.143	<b>0.347</b>	0.203	0.152	0.043	0.029	-0.118
SL	0.035	0.026	0.008	0.032	-0.075	<b>-0.129</b>	-0.082	-0.031	-0.007	0.057
SW	-0.056	-0.041	0.002	0.035	0.116	0.170	<b>0.266</b>	0.114	0.138	-0.112
NSPS	0.017	0.019	-0.003	-0.026	-0.027	-0.053	-0.095	<b>-0.222</b>	-0.144	-0.006
NGPS	0.019	0.024	-0.018	-0.075	-0.017	-0.011	-0.108	-0.134	<b>-0.208</b>	-0.012
NSPM	0.129	0.127	0.082	-0.033	-0.127	-0.165	-0.158	0.010	0.022	<b>0.375</b>
Correlation	0.034	0.096	0.160	-0.448**	0.346*	0.107	-0.020	-0.207	-0.231	0.209
Residual value	0.5743									



*Note:* Diagonal values show direct effect and off diagonal or column values show indirect effect in grain yield. DTH= days to heading, DTA= days to anthesis, DTM= days to maturity, PH= plant height, SL= spike length, SW= spike weight, NSPS= number of spikelet per spike, NGPS= number of grain per spike, GY= grain yield, TKW= thousand kernel weight, NSPM=number of spikes/m<sup>2</sup>. (High = 0.30-0.99, Moderate = 0.20-0.29, Low = 0.10-0.19)

#### 4. DISCUSSION

Higher values of PCV were found than the values of GCV which indicate the presence of environmental effect (Kumar et al., 2019). DTH, DTA, DTM, PH and SL were showed closely associated GCV and PCV which mean that environment had little effect in these characters whereas SW, NSPS, NGPS, GY, TKW and NSPM showed greater differences between PCV and GCV values which indicated that higher effect of environment on these characters. These results are in line with the finding (Poudel et al., 2021). TKW showed maximum values for both GCV and PCV (11.83% and 12.14%) indicating the presence of high variability in this character and genotype can be reflected by phenotype and there is more effectiveness in a selection based on its phenotypic performance of the character. Moderate values of PCV were obtained for SW, GY, TKW and NSPM. Similar results were also obtained (Meles et al., 2017).

TKW showed a maximum value of heritability (94.96%) followed by NSPM (82.26%). DTH, DTA, DTM, PH, SL and NGPS showed high heritability which indicated less effect of environment in these characters and selection of these characters based on phenotypic performance will give effective results. Some researchers also found similar results (Poudel et al., 2021). The selection of characters based on the high value of heritability only did not give a precise result. NSPM showed high heritability (82.62%) along with a high value of GA (73.36) which indicated that additive gene effect is predominant for this character. Whereas TKW showed a low value for GA (7.69) and selection of this character was not appropriate although this had high heritability. Selection of NSPM and GY with moderate heritability (58.95%) and high value of GA (456.25) is beneficial over other characters. Porte et al. (2021) also found high heritability and low value of GA.

If there is a positive association among characters then an increase in one character causes an increase in another character and if there is a negative correlation among the characters then an increment in one character will cause a decrease in another character. PH showed the highest positive and significant correlation with GY (0.346) this result was similar to the finding of (Poudel et al., 2021). Chlorophyll showed a highly significant negative correlation with grain yield (-0.448) which is the same as the result obtained by (Ojha et al., 2018a). The positive association of DTH, DTA, DTM, SL, NSPM and TKW with GY was due to linkages among the genes related to these characters or pleiotropic gene effect. High GY may be resulted from the higher assimilation of photosynthesis due to increased PH (Meles et al., 2017). DTH showed a positive and highly significant correlation with DTA (0.897) and DTM (0.638). Some researchers also reported a positive significant association of DTH with DTA and DTM (Ayer et al., 2017; Ahmed et al., 2018). It showed a positive and significant correlation with NSPM, which is similar to the finding of also found a negative and significant correlation of days to heading with TKW (Mecha et al., 2017; Baye et al., 2020). A highly positive significant correlation of DTA with DTH and DTM was also reported also found a negative and significant correlation of DTA with TKW (Maurya et al., 2020; Ayer et al., 2017).

Chlorophyll content showed a negative and highly significant correlation with GY (0.448). A group researchers also found a similar association (Abdulhamid et al., 2017). In other study also researchers found a positive and highly significant correlation of PH with SL (0.584), SW (0.437) and TKW (0.513), a positive and significant correlation with GY and a negative and highly significant correlation with chlorophyll content (0.413) (Maurya et al., 2020). A positive and highly significant association of SL with PH (0.584), SW (0.639) and TKW (0.669) was observed which was similar to the finding (Sokoto et al., 2012). Some researchers also reported a negative and highly significant association of SL with NSPM (-0.442) (Singh et al., 2012). SW showed positive and highly significant correlation with PH (0.437), SL (0.639), NSPS (0.429) and NGPS (0.526), positive and significant relation with TKW, negative and highly significant correlation with NSPM (-0.423). These findings are in line with the finding (Singh et al., 2012). Rajput also reported a positive and significant correlation of SW with thousand kernel weight (Rajput, 2018).

NSPS showed a positive and highly significant correlation with SW (0.429) and NGPS (0.648). Some researchers reported positive correlation of NSPS with PH and SL and a negative correlation with TKW (Meles et al., 2017; Mecha et al., 2017). A group researcher also found a positive correlation of NSPS with NSPM and a negative correlation with GY (Abdelhamid et al.,

2017). NGPS showed a positive and highly significant correlation with SW (0.520), NSPS (0.648) and negative association with TKW. A group researchers also found a highly significant positive correlation of NGPS with SW, NSPS and a negative correlation with TKW (Djuric et al., 2018). Some researcher also reported a positive correlation of NSPS with DTM, NSPS, GY and a negative correlation with PH which was the same as the present results (Bhushan et al., 2013). TKW showed a negative correlation with DTH, DTM, NSPS and NGPS and a positive correlation with GY. These findings are in line with the finding (Fouad, 2018; Bhushan et al., 2013; Mecha et al., 2017). A decrease in TKW with an increase in NSPS and NGPS may be due to an increase in competition for nutrition among kernels (Baye et al., 2020).

The higher direct effect of NSPM and PH on GY was obtained which suggests that there were little or no indirect effects of these traits on GY. The positive correlation of NSPM (0.209) and PH (0.346) on GY was due to the direct effect of these traits and we can use these characters in the selection of wheat genotypes for improving GY. The direct positive effect of PH in GY yield was also reported and the direct positive effect of NSPM on GY with a positive correlation was also found by (Maurya et al. 2020; Arya et al. 2017; Poudel et al., 2021). DTH and DTA showed a low positive direct effect on GY with a correlation coefficient of 0.034 and 0.096. The positive correlation on GY was due to the indirect effect of NSPM via DTH (0.123) and DTA (0.127). In other study, researchers also reported d. DTM showed a positive correlation coefficient (0.160) with GY and the reason behind it was a moderate direct effect of DTM on grain yield. These characters should be considered for improving grain yield. A group researchers also found a positive direct effect of DTM on grain yield (Meles et al., 2017).

SW showed a direct moderate effect on GY (0.266) and was negatively associated with GY (-0.020). The negative association of SW with GY was due to the indirect negative effect of NSPM (-0.158) and NGPS (-0.108) through SW. The direct positive effect of SW on grain yield was also observed (Singh et al., 2012; Nasri et al., 2014). Chlorophyll content showed a highly negative significant correlation coefficient with grain yield. This association was due to the moderate negative direct effect of chlorophyll content (-0.234) and the negative indirect effect of PH (-0.143) through chlorophyll content on GY. A group researcher also confirmed the negative direct effect of chlorophyll on GY (Khanal et al., 2020). SL showed a positive association with GY (0.107) but had a negative low direct effect on GY.

The positive association with GY was due to the indirect positive effect of SW (0.170) via SL. Khan and Dar also reported a negative direct effect and positive correlation of SL with grain yield (Khan and Dar, 2010). NSPS and NGPS were negatively associated with grain yield (-0.207 and -0.231 respectively). This negative association was due to the negative indirect effect of these traits on grain yield. These traits contribute to grain yield indirectly through a number of spikes/m<sup>2</sup>. A group researcher also reported a negative direct effect of NGPS and NSPS on grain yield (Singh et al., 2012; Khan and Dar, 2010). The residual value of the present study was 0.5743, which indicated that 42.57% variability in grain yield was expressed by the characters in the path analysis and the remaining 57.43% needs additional characterization for the future breeding program.

#### 5. CONCLUSION

Analysis of variance showed significant differences among wheat genotypes. TKW showed maximum values for both PCV and GCV indicating the presence of high variation for TKW than other characters. PCV had higher values than GCV which was due to environmental effects. TKW showed high values for both heritability and GA and GY showed moderate value for heritability and high value for GA so the selection of these characters is beneficial over other characters. PH showed a significant positive association with GY and chlorophyll content showed a highly negative significant association with GY. NSPM and PH showed a maximum direct positive effect on GY and chlorophyll content showed moderate positive direct effect with highly negative significant correlation with grain yield. PH and NSPM should be emphasized in the selection program of wheat genotype for improving the grain yield of wheat. DTH, DTA and DTM also should be considered in the selection of wheat genotypes. Therefore, the selection of wheat genotypes with high PH and NSPM along with moderate or low chlorophyll content is a prerequisite for attaining high yield in wheat.

#### AUTHOR'S CONTRIBUTION

All authors have contributed equally to the preparation of this manuscript.

#### CONFLICT OF INTEREST

The authors' have no conflict of interest with the present publication.

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