

Research Article**VARIABILITY, HERITABILITY AND CORRELATION STUDIES ON GRAIN YIELD AND RELATED TRAITS IN SPRING WHEAT GENOTYPES**

B. R. Ojha*, A. Ojha, and R. Chaudhary
Agriculture and Forestry University, Rampur, Chitwan

*Corresponding author: brojha@afu.edu.np

ABSTRACT

A field research was done at the research station of AFU, Rampur, Chitwan during the wheat growing season of 2018/19 to study the genetic variability, heritability, genetic advance, and correlation of grain yield and yield attributing traits in wheat. Eight wheat genotypes were tested using Completely Randomized Block Design with three replications under rainfed condition. Observations were taken for grain yield, spike length, number of tillers per m², test weight, number of grains per spike, and grain weight per spike. The analysis of variance revealed significant differences among the tested wheat genotypes for all the characters, except number of tillers per m². 8thHPYT409 had the highest number of effective tillers per m² (399), number of grains per spike (54), grain weight per spike (2.32 g), test weight (406 g) and grain yield per plot (2.51 kg). Number of grains per spike had the highest broad sense heritability (0.72) along with high genetic advance (22%) which can be considered the good estimate for effective selection of the trait. Moderate heritability (0.54) and highest genetic advance (31%) was estimated for grain yield per plot. Number of grains per spike had highly significant positive correlation with grain weight per spike and yield per plot, suggesting number of grains per spike has positive influence on yield ($r = 0.59^{**}$).

Key words: Yield attributing traits, correlation, spike, genetic advance

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the leading cereal crops in the world in terms of both area and production. Worldwide, it is grown on nearly 218 million hectares, with a production of 771 million tons (FAO, 2017). The area under cultivation, production, and productivity of wheat in Nepal are 740,150 ha, 1,856,191 t and 2.51 t/ha, respectively (MoAD, 2018). Agriculture contributes about 29.31% to national GDP and so wheat has a major role besides rice and maize in food production. However, wheat production needs to grow at rapid rate to meet the rising demand, mainly due to increase in population and changing environment. Hence, improvement of wheat productivity will always be one of the important breeding objectives.

The nature of variability present in the gene pool for any important character determines the success of genetic improvement. Therefore, an insight into the magnitude of variability present in the gene pool of a crop species is of utmost importance to a plant breeder for starting a judicious plant breeding program (Farshadfar et al., 2013). It is also important to divide total variation in to heritable and non-heritable components with the aid of genetic parameters e.g., genotypic and phenotypic coefficient of variation, heritability and genetic advance. Heritability, a measure of phenotypic variance attributable to genetic causes; provides information about the extent to which a particular character can be transmitted to the successive generations. High heritability estimates along with high genetic advance indicates that the selection for a character would be more effective due to the presence of additive gene action (Johnson et al., 1955). Grain yield is the end result of many complex morphological and physiological processes occurring during the growth and development of the crop. It is a polygenic trait governed by so many polygenes with low heritability. Therefore, knowledge of the association between grain yield and different yield attributing traits can help breeders to improve the efficiency of selection. Selection based on yield components is deemed to be more effective rather than yield alone (Shamsuddin & Ali, 1989). Thus, it is important to determine the relationships among the desired traits using correlation analysis. Therefore, the objective of the study was to estimate variability, heritability, genetic advance and association of yield and its attributing traits for the improvement of wheat grain yield.

MATERIAL AND METHODS

The experiment was conducted at the research farm of AFU, Rampur during the wheat growing season (November 2018 to April 2019) in completely randomized block design with three replications. The total area of each plot was 1.5 m x 2 m. The row spacing was maintained 25 cm and each plot had six rows of each genotype. Seeds were sown in November 22, 2018. Eight wheat genotypes collected from Nepal Agriculture Research Council, Khumaltar were tested. Standard agronomic and plant protection practices were followed. The data were recorded for grain yield per plot, spike length, number of tillers per m², test weight, number of grains per spike and grain weight per spike and analyzed for heritability estimation and correlation test. Both genotypic and phenotypic

coefficient of variation were computed according to Burton and Devane (1953) and expressed as percentage.

$$\text{Genotypic coefficient of variation (GCV)} = \left(\frac{\sigma_g}{\bar{x}}\right) \times 100 \left(\frac{\sigma_g}{\bar{x}}\right) \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \left(\frac{\sigma_p}{\bar{x}}\right) \times 100 \left(\frac{\sigma_p}{\bar{x}}\right) \times 100$$

where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

\bar{x} = General mean of the trait

The broad sense heritability was estimated as the ratio of genotypic variance (V_g) to the phenotypic variance (V_p), and expressed in percentage (Hanson et al., 1956).

$$\text{Broad sense heritability } (h_{bs}^2) = \left(\frac{V_g}{V_p}\right) \times 100 \left(\frac{V_g}{V_p}\right) \times 100$$

Likewise, the extent of genetic advance to be expected by selecting about five percent of the genotypes was calculated by using the following formula given by Robinson, Comstock and Harvey (1949).

$$GA = i \cdot \sigma_p \cdot h_{bs}^2 \cdot i \cdot \sigma_p \cdot h_{bs}^2$$

where,

i = Efficacy of selection which is 2.06 at 5% selection intensity

σ_p = Phenotypic standard deviation

h_{bs}^2 = Broad Sense Heritability

Data entry and processing was carried out using Microsoft Office Excel 2010 software and mean and standard deviations for all quantitative traits were computed. Analysis of variance and correlation were calculated using GenStat 15 software.

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences ($p \leq 0.01$) among wheat genotypes for grain yield per plot and number of grains per spike; and significant differences ($p \leq 0.05$) for grain weight per spike, test weight and spike length. Mean values of yield and yield attributing traits of eight spring wheat genotypes is presented in Table (1). Pearson correlation coefficients among the traits are presented in Table (2). An LSD test at 5 % level of significance was performed to evaluate the yield per plot (kg), effective tillers per m^2 , spike length (cm), number of grains per spike, grain weight per spike (g) and test weight (g). Phenotypic and genotypic coefficient of variation, heritability and genetic advance as percentage of mean were estimated and presented in Table (3).

Grain yield and attributing traits and correlation between them

Grain yield: The mean grain yield per plot was 1.99 kg and it ranged from 1.17 – 2.51 kg (Table 1). 8thHPYT409 had the highest grain yield followed by 8thHPYT406 (2.46 kg) and 8thHPYT402 (2.34 kg) whereas the lowest yield was recorded in 8thHPYT404. There was highly significant genotypic difference among genotypes, indicating an array of variation existed for grain yield. This result indicates that variation among genotypes was due to their different genetic makeup. Grain yield had significant positive correlation with number of grains per spike ($r = 0.59^{**}$), effective tillers per m^2 ($r = 0.44^*$) and grain weight per spike ($r = 0.49^*$) (Table 2). This result suggests that yield can be increased by increasing effective tillers per m^2 , grain weight per spike, and number of grains per spike. This finding supported to the previous findings reported by Poudel *et al* (2015b); Ojha (2010); Ojha (2011); Ojha & Ojha (2012); Baral (2011) and Neupane (2009) with the facts that grain yield was increased with an increase in number of grains per spike. Likewise, this finding matches to the result of previous finding reported by Ojha (2012), as the authors explained that grain yield increased due to increase in the number of effective tillers per m^2 .

Number of effective tillers per m^2 :

Number of effective tillers per m^2 among genotypes remained statistically similar. The mean number of effective tillers per m^2 was 364 and varied from 344 (8thHPYT401) to 399 (8thHPYT409) (Table 1). Positive correlation was observed with all yield and yield attributing traits. Significant positive correlation was found with yield per plot ($r = 0.44^*$) (Table 2). This finding was similar to the finding reported by other researchers (Ojha, 2012; Sharma, 1993).

Grain weight per spike: A significant difference was observed for grain weight per spike among genotypes. The mean grain weight per spike (g) was 2.065 and varied from 1.767 (8thHPYT403) to 2.323 (8thHPYT409)

(Table 1). Genotypes 8thHPYT409 and 8thHPYT406 had better performance, but poor performance was noted in 8thHPYT403 and 8thHPYT404. There was a positive correlation with all yield and yield attributing traits. Significant positive correlation was noted with yield per plot ($r = 0.49^*$) and test weight ($r = 0.45^*$), but a highly positive correlation existed with number of grains per spike ($r = 0.56^{**}$) (Table 2). This result suggests that yield can be increased by increasing grain weight per spike, and similarly, increasing the number of grains per spike increases the grain weight per spike. This finding was in agreement with the findings reported by several researchers (Poudel *et al.*, 2015b; Thapa *et al.*, 2009; Baral, 2011).

Number of grains per spike: A highly significant difference was found for number of grains per spike among genotypes. The mean number of grains per spike was 47, and varied from 33 (8thHPYT404) to 54 (8thHPYT409) (Table 1). 8thHPYT409 had the maximum number of grains per spike whereas 8thHPYT404 had the least. Positive correlation was noted with all yield and yield attributing traits. Highly significant positive correlation existed with grain weight per spike ($r = 0.56^{**}$) and yield per plot ($r = 0.59^{**}$) (Table 2). This results matches well to the findings of previous researches (Poudel *et al.*, 2015b; Ojha, 2010; Ojha, 2012; Thapa *et al.*, 2009; Baral, 2011), as the authors reported that the number of grains per spike increased the grain weight per spike and grain yield. Likewise, positive correlation was found between number of grains per spike and spike length.

Spike length: There was a significant difference between the genotypes for spike length. The mean spike length was 10.35 cm and it varied from 8.97 cm (8thHPYT403) to 11.60 cm (8thHPYT407) (Table 1). Positive correlation was observed with all yield and yield attributing traits. Increase in spike length increased the number of grains per spike ($r = 0.28$) and grain weight per spike ($r = 0.28$). Similarly grain yield was also increased with an increase in spike length ($r = 0.13$) (Table 2). This result suggests that yield can be increased by increasing spike length, and similarly, increasing the spike length increases the number of grains per spike, and ultimately increases the grain weight per spike. This finding matches to the findings of previous researches (Ojha, 2010; Ojha, 2012; Ojha & Ojha, 2012; Thapa *et al.*, 2009; Baral, 2011; Shahi *et al.*, 2015) where the authors reported that the number of grains per spike increased the grain weight per spike and grain yield. Likewise, positive correlation was observed between spike length and test weight (Table 2).

Test weight: A significant difference was observed for test weight among genotypes. The mean test weight was 398.2 g and varied from 387.3 g (8thHPYT403) to 406 g (8thHPYT409) (Table 1). Positive correlation was observed with all yield and yield attributing traits. Significant positive correlation was observed with grain weight per spike ($r = 0.45^*$) and strong positive correlation was found with yield per plot ($r = 0.22$). This result suggests that yield can be increased by increasing test weight. This finding was similar to the findings reported by several researchers (Bhattarai *et al.*, 2017; Poudel *et al.*, 2015a; Poudel *et al.*, 2015b; Ojha, 2010; Ojha, 2012; Ojha & Ojha, 2012; Ojha, 2014; Thapa *et al.*, 2009; Baral, 2011, Shahi *et al.*, 2015).

Table 1. Mean grain yield and yield attributing traits of eight spring wheat genotypes

Genotypes	Grain yield and yield attributing traits					
	ET	GWS	NGS	SL	TW	YLP
8 th HPYT401	344	1.99 ^{ab}	48 ^{ab}	11 ^{ab}	391 ^b	2.129 ^{ab}
8 th HPYT402	373	2.11 ^{ab}	47 ^{ab}	9.3 ^{ab}	397.3 ^{ab}	2.346 ^{ab}
8 th HPYT403	364	1.767 ^b	48 ^{ab}	8.97 ^b	387.3 ^b	1.803 ^{bc}
8 th HPYT404	348	1.837 ^b	33 ^c	10.07 ^{ab}	396.7 ^{ab}	1.176 ^c
8 th HPYT406	382	2.317 ^a	45 ^b	10.27 ^{ab}	404.7 ^a	2.462 ^a
8 th HPYT407	352	2.09 ^{ab}	51 ^{ab}	11.6 ^a	405.3 ^a	1.713 ^{bc}
8 th HPYT409	399	2.323 ^a	54 ^a	10.8 ^{ab}	406 ^a	2.51 ^a
8 th HPYT410	350	2.083 ^{ab}	48 ^{ab}	10.77 ^{ab}	397 ^{ab}	1.805 ^{bc}
Mean	364	2.065	47	10.35	398.2	1.993
SEM	33.7	0.124	2.09	0.848	3.7	0.213
F test	ns	*	**	*	*	**
LSD(0.05)	102.3	0.376	6.344	2.57	11.24	0.6457
CV (%)	15	10.4	7.8	14.2	1.6	18.5

Note: ET = Number of effective tillers per m², SL = Spike length (cm), NGS = Number of grains per spike, GWS = Grain weight per spike (g), TW = Test weight (g), and YLP = Grain yield per plot (kg). Significant in 5% level, **Significant in 1% level.

Table 2. Pearson correlation coefficients among grain yield and yield attributing traits

	ET	SL	NGS	GWS	TW
SL	0.246				
	0.247				
NGS	0.275	0.278			
	0.193	0.188			
GWS	0.308	0.275	0.558**		
	0.143	0.193	0.005		
TW	0.122	0.177	0.088	0.449*	
	0.571	0.407	0.682	0.028	
YLP	0.444*	0.132	0.585**	0.490*	
			0.224		
	0.030	0.540	0.003	0.015	
			0.293		

Cell Contents: Pearson correlation coefficient
P-value

Phenotypic and genotypic coefficient of variation

A difference in PCV and GCV values were estimated (Table 3) which indicates the variability was not only due to genotypes, but also due to influence of environment. Among yield and yield governing traits, the highest value of both GCV and PCV was obtained for yield. Moderate PCV was observed in effective tillers per m², number of grains per spike, spike length, and grain weight per spike, and lowest GCV and PCV was observed in test weight (Table 3). Low GCV was found for effective tillers per m², spike length, grain weight per spike, and test weight. The GCV ranged from 1.44 (test weight) to 20.07 grain yield and PCV ranged from 2.16 (test weight) to 27.60 (grain yield) (Table 3).

Heritability and genetic advance as percentage of mean

Number of grains per spike had the highest heritability (0.72) followed by moderate heritability for yield (0.54), test weight (0.45) and grain yield per spike (0.35) indicating presence of heritable variation among genotypes for these traits. This finding was found similar to the previous findings (Nandawal *et al.*, 2000; Shahi *et al.*, 2015) as the authors reported high heritability values for plot yield and thousand grain weight. High and moderate heritability value for these traits indicated that the observed variation was mainly under genetic control and was less influenced by environment. The lowest heritability was noted for spike length (0.03) followed by effective tillers per m² (0.29) (Table 3). This finding did not support to the previous findings by Thakur *et al.*, 1999 as the authors reported that high heritability was found for spike length. The genetic advance as percentage of mean at 5 % selection intensity exhibited substantial differences for yield and yield governing traits (Table 3). The yield showed the highest genetic advance as percentage of mean (30.88%) followed by number of grains per spike (22%). The lowest genetic advance as percentage of mean was recorded for spike length (0.83%). Low genetic advance as percentage of mean was observed for spike length, test weight, effective tillers per m² and grain weight per spike (Table 3).

The number of grains per spike had high heritability and genetic advance as percentage of mean and hence might be considered to be governed by additive genes and was less influenced by environment. Thus direct selection can be done through this character for further improvement of genotypes. Moderate heritability with low genetic advance as percentage of mean was found for grain weight per spike and test weight. Therefore, these two traits were regulated by non-additive gene action and presence of high genotype x environment interaction. Heritability, if exhibited due to the favorable influence of environment, rather than the genotype, simple selection will not be practicable. This implies that the breeder can go for selection over several successive generations following hybridization to isolate desirable transgressive segregants.

Table 3. Estimates of Coefficient of Variation, Heritability and Genetic advance of different traits in spring wheat

Traits	GCV	PCV	PCV – GCV	H _{bs}	GA	GAM
ET	7.57	14.15	6.57	0.29	30.40	8.35
GWS	7.75	13.08	5.33	0.35	0.19	9.36
NGS	12.56	14.77	2.21	0.72	10.25	21.99
SL	2.42	14.40	11.98	0.03	0.09	0.83
TW	1.44	2.16	0.72	0.45	7.92	1.99
YLP	20.07	27.60	7.53	0.54	0.62	30.88

Note: GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, H_{bs} = heritability in broad sense, GA = genetic advance and GAM = GA as percent of mean.

CONCLUSION

Genotypes used in this study differ significantly for number of grains per spike, and yield per plot. Similarly, significant differences were also observed for grain weight per spike, spike length and test weight. Positive and strong association between different traits was also observed between number of grains per spike and grain weight per spike; number of grains per spike and yield per plot whereas significant positive correlation was found for effective tillers per m² and yield per plot; test weight and grain weight per spike, and yield per plot and grain weight per spike. These facts suggest that yield can be increased by increasing effective tillers per m², grain weight per spike and number of grains per spike. The results also explained positive influence of these traits to the final grain yield. Likewise, these traits also had high level of genotypic variability; broad sense heritability along with better genetic advance, except grain weight per spike. Hence, these traits can be considered as the good estimates for effective selection of high yielding genotypes.

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