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Genetic Variability of Wheat (*Triticum aestivum* L.) in Different Agro-climatic Zone of Western Himalayan Region of Pakistan

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ABSTRACT

Background: *Triticum aestivum* L. (Wheat) is vital grain crop used globally as a staple food. The increasing population is posing a great challenge for agriculture sector especially to secure the availability of wheat. In Pakistan, from the last few years' wheat productivity has improved but it is still far less than other countries. Its low productivity is attributed to various factors like weeds, pests, diseases, soil fertility and moisture. To overcome these obstacles, there is a dire need to assess the genetic variability of wheat by rapid and reliable methods. Observations for nine morphological traits were noted and analysis was done at 0.05 probability level.

Methods: To study the genetic variability in wheat (*Triticum aestivum* L.) genotypes a field experiment was done during 2017 and 2018 at two different locations Rara and Danna of Muzaffarabad. Hundred wheat genotypes were investigated by using simple lattice design with 4 replications. Analysis of the observations for nine morphological traits was carried out at 0.05 probability.

Result: High values for phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were noted for grain yield (16.44 and 17.07%) and (14.75 and 15.94%) at both locations, separately. High heritability were obtained for plant height (98.80%) harvest index (96.84), thousand grain weight (95.47), spike length (94.91) and grain yield (92.80) at Rara and plant height (98.09), thousand grain weight (95.66), harvest index (93.32) and number of grain (91.28) at Danna. High genetic advance values were noted for number of tiller (53.45 and 42.89) at both locations. It is concluded from this research that estimation of the variability, heritability and genetic advance in the wheat genotypes (*Triticum aestivum* L.) is important in the plant breeding, because it might be used for improvement of novel varieties by breeders of wheat at relevant location.

Key words: Genetic advance, Genetic variability, Genotypic coefficient of variation, Heritability, Phenotypic coefficient of variation, *Triticum aestivum*.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is essential grain crop in the world and it has the widest distribution among cereals. It is a virtuous source of minerals, protein, vitamins (Thiamin, Riboflavin), sugar and fats. Main components of wheat are protein (7 to18%), ash (1.5 to 2%), fat (1.5 to 2%), crude fiber (2 to 2.5%) and moisture contents (8 to 18%) Mughal (2019).

In developing and developed countries 16% and 26% of total dietary calories, derived from wheat (Ortiz *et al*., 2008). It is cultivated to accomplish the demands of food for consumptions of population in Pakistan and other countries of world, the ongoing progress in demands of population an extensive rise in its productivity (Islam *et al*., 2012). It is among the three world's major cereal trade earners, other two being maize and rice (Abdellatif and Abouzeid, 2011).

Pakistan is an agrarian country and its economy generally depends on agriculture. Pakistan is the eighth important producer of wheat, for almost 3.17% of the wheat output in the world from 3.72% of the area under its cultivation (Shuaib *et al*., 2010). Overall cultivated area in Pakistan for wheat is 8.83 million hectares with the production of 25.16 million tons (PARC, 2019).

Genetic variability is the variation in traits among individuals of a population. It is very important because, without variability, it becomes difficult for a population to acclimatize to environmental changes and it plays a very vital role in any crop breeding programme. Genetic parameters PCV and GCV is not simply beneficial for associating the comparative quantity of phenotypic and genotypic variations between diverse traits but also very valuable to evaluate the choice for enhancement by selection. Heritability (H) estimates give a vision into the amount of genetic regulator to express a specific attribute and phenotypic consistency in expecting its value of breeding (Ndukauba *et al*., 2015).

Wheat breeders usually evaluate heritability using genetic advance values as only heritability is not an actual indicator of the quantity of genetic variability. The major parameters for the selections include heritability and genetic advance. Moreover, assessing genetic development is

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suitable as a tool selection while measuring through heritability estimation (Johnson *et al*., 1955). The genetic advances function as information for preservative gene action whereas low values are revealing non-additive gene action. Although much of the work have been conducted in Pakistan regarding wheat cultivation but still there are a few studies that reported the cultivation of wheat in harsh environmental conditions of Kashmir region. Thus present study was conducted to find out variations in heritability, genetic components and genetic advance in wheat (*Triticum aestivum* L.) varieties grown in two different agro climatic zones of AJK.

MATERIALS AND METHODS

Experimental materials

Seeds of hundred genotype of wheat were taken from National Agriculture Research Council (NARC) Islamabad, Pakistan. Plants were grown in field under standard agricultural practices. The genotypes details along with their pedigrees are given in Table 1.

Experimental design

Hundred genotypes of wheat were planted at two locations, Rara and Danna during 2017 and 2018 by using simple lattice design with 4 replications. Altitude of Rara is 719 meters latitude is 34°17.455 N and longitude is 73°28.836 E whereas altitude of Danna is 1329 meters latitude is 34°20′59.99″N and longitude is 73°27′59.99″E. Plot size of 5 m × 5 m with 30 cm inter row spacing and 20 cm intra row spacing. Sowing was done by hand drilling. For recording the biometrical observations ten plants were select at random from each experimental plot in each replication.

Analysis of variance (ANOVA)

Combined analysis of variance (ANOVA) was practiced for statistical analysis and significant variations at $P<5\%$ (0.05) by using R software version 3.0.

Genetic Variability, heritability and genetic advance

For analysis, the mean values were used for genetic studies to find out the (GCV) and (PCV) giving to Singh and Chaudhury (1985).

$$\text{GCV}\ (\%) = \delta^2 g/X \times 100$$
$$\text{PCV}\ (\%) = \delta^2 p/X \times 100$$

Where,

GCV= Genotypic co-efficient of variation.

PCV= Phenotypic co-efficient of variation.

X= Sample mean.

Heritability was assessed by the formula proposed by Singh and Chaudhary (1985).

$$H^2\ (\%) = \delta^2 g\ /\delta^2 p \times 100$$

Where

H= Heritability in broad sense.

To estimate the genetic advance for different characters under selection the following formula as proposed by Johnson *et al*. (1955).

$$\text{G.A} = \delta^2 g\ /\delta^2 p \times (\delta^2\ p)^{0.5} \times K$$

Where

G.A.= Genetic advance.

$\delta^2 g$= Genotypic variance of the trait.

$\delta^2 p$= Phenotypic variance of the trait.

K= Selection differential. value of K at 5 per cent selection intensity being 2.06.

Genetic advance in percentage of mean was calculated by the following formula purposed by Comstock and Robinson (1952).

Genetic advance in percentage of mean =

$$\frac{\text{Genetic advance}}{X} \times 100$$

RESULTS AND DISCUSSION

Analysis of variance of morphological characters

Analysis of variance was conceded on various morphological traits for studying the variation over locations and years. The analysis of variance for the data recorded on various traits *viz*. plant height, number of tillers, spike length, number of spike per spikelet, number of grains, thousand grain weights, grain yield, biological yield and harvest index are shown in the Table 2. These results display the differences of climatic conditions prevailing at two locations. Based on the combined analysis of variance, the mean squares of year for all characters were highly significant ($P<0.001$) whereas significant ($P<0.05$) for biological yield and number of spikelet per spike. For location, the analysis of variance revealed highly significant ($P<0.001$) effects for all the characters except harvest index representing the alterations in growth conditions revealed at the two locations. Significant trend was followed by genotypes for all the traits by showing significant differences among them. Significant genetic variation of genotypes recommended that the genotypes were genetically varied and could be a worthy chance for breeders to select genotypes for trait of concern. Numerous investigators reported significant differences between studied genotypes of wheat (Birhanu *et al*., 2016).

The interactions between year and genotypes for plant height, tillers numbers, spike length, biological yield, grain yield and harvest index were highly significant while thousand grain weights and number of spikelet per spike were non-significant as there were difference in responses among genotypes during growing years. Similar results were obtained by Mehari *et al*. (2015) and Kaya and Turkoz (2016). The location and genotype interaction was significant for plant height, spike length, grain yield, harvest index and biological yield. Whereas tillers number, number of spikelet per spike, number of grain, thousand grain weight showed non-significant difference indicating difference in performance of genotype of wheat through the two locations. The difference in genotypes response to the different conditions of environment determines to recognize well performing genotypes for a specific environment. The analysis of variance showed significant variation between genotypes for all the investigated characters. Gharib *et al*. (2021) also reported significant difference among studied

Table 1: List of genotypes along with their pedigrees.

Genotypes	Pedigrees
PAK-81	CM33027-F-15M-500Y-0M-76B-OY-OPAK
PIRSABAK-13	PTSS02B00132T-0TOPY-0B-0Y-0B-38Y-0M-0SY-0ID
NARC-11	CMSS00Y01881T-050M-030Y-030M-030WGY-33M-0Y-01D
ASS-11	PBD 795-23A-1A- 0A
MILLAT-2011	CHENAB2000/INQ-91
AHSAN-16	
ZINCOL-2016	CMSS07Y01302T-099Y-19M-0Y-2B-0Y-0ID
PUNJAB-11	AMSEL/ATTILA//INQ-91/PEW'S
PIRSABAK-15	CMSS97M03689T -040Y-030M- 020Y- 030M -015Y-030M- 3Y-1M -0Y
BORLAUG 2016	PTSS02B00015S-0Y-0B-0Y-0B-1Y-0M-0SY-0ID
HPYT-03	CMSS97M03912T-040Y-020Y-030M-020Y-040M-4Y-2M-0Y
HPYT-04	CMSA06M00195T-099Y-099Y-9M-0Y-7B 0Y
HPYT-05	CMSS08Y01129T-099M-099Y-3M-0Y-5M-0Y
HPYT-06	CMSS11B01191T-099TOPY-099M-099Y-3M-0WGY
HPYT-07	CMSS11B01191T-099TOPY-099M-099Y-30M-0WGY
HPYT-08	CMSS11B01191T-099TOPY-099M-099Y-31M-0WGY
HPYT-09	CMSS11B01204T-099TOPY-099M-099Y-8M-0WGY
HPYT-10	CMSS11B01210T-099TOPY-099M-099Y-9M-0WGY
HPYT-37	CMSS11B01084S-099M-099Y-42M-0WGY
HPYT-48	CMSS11B01152S-099M-099Y-6M-0WGY
NR-449	CMSA04M00552S-040ZTP0Y-040ZTM-040SY-19ZTM-03Y-0B
NR-488	CMSS08Y01129T-099M-099Y-15M-0Y-1M-0Y
NR-499	CMSS08Y00871T-099TOPM-099Y-099M-099NJ-7WGY-0B
NR-505	CMSS07B00512T-099TOPY-099M-099Y-099M-12WGY-0B
NR-519	CMSS07Y00124S-0B-099Y-099M-099Y-16M-0WGY
NR-520	PTSA08M00051S-050ZTM-050Y-19ZTM-010Y-0B
NR- 521	CMSS09Y00815T-099TOPM-099Y-099M-099Y-16WGY-0B
NR- 522	CMSS09B00277S-099ZTM-099NJ-099NJ-19WGY-0B
NR- 523	CMSA10Y00587S-050Y-050ZTM-12WGY-0B
NR- 524	PTSA08M00046S-050ZTM-050Y-50ZTM-010Y-0B-020Y-0MXI
NUWYT-03	1447/PASTOR//KRICHAUFF/3/PAURAQ
NUWYT-04	WBLL1/FRET2//PASTOR*2/3/MURGA
NUWYT-05	W462/VEEK/LOEL/3/PEG//MRL/BUC
NUWYT-06	KS82W418/SPN/3/CHEM/AESQ//2*OPATA/4/FRET2
NUWYT-07	MILAB/KAUZ//PRINIA/3/BAV92/4/2*SOKOL
NUWYT-08	BECARD/KACHU
NUWYT-09	SNLG/3/EMB16/CBRD//CBRD/4/KA/NAC//TRCH
NUWYT-10	WBLL1/4/BOW/NKT//CBRD/3/CBRD/5/WBLL1*2/TUKURU
NUWYT-37	TWS12464(CHEN/AEGILOPSSQU ARROSA(TAUS)//BCN/3/AV92
NUWYT-48	BEC ARD/QUAIU#1
WYCYT-02	PTSS09GHB00019S-0SHB-099Y-099B-9Y-0Y-020Y-0MXI
WYCYT-03	PTSS09GHB00024S-0SHB-099Y-099B-10Y-0Y-020Y-0MXI
WYCYT-04	PTSS09GHB00024S-0SHB-099Y-099B-18Y-0Y-020Y-0MXI
WYCYT-05	PTSS09GHB00014S-0SHB-099Y-8Y-020Y-0MXI
WYCYT-06	PTSS11SHB00014S-099B-099Y-099B-21Y-099Y-0MXI
WYCYT-07	PTSS11SHB00014S-099B-099Y-099B-22Y-099Y-0MXI
WYCYT-08	PTSS11SHB00014S-099B-099Y-099B-38Y-099Y-0MXI
WYCYT-09	PTSS11SHB00014S-099B-099Y-099B-51Y-099Y-0MXI
WYCYT-10	PTSS11SHB00014S-099B-099Y-099B-55Y-099Y-0MXI
WYCYT-25	PTSS02Y00021S-099B-099Y-099B-099Y-213B-0Y
ESWYT-2	CMSS97M03912T-040Y-020Y-030M-020Y-040M-4Y-2M-0Y-082Y
ESWYT-3	CMSS06Y00946T-099TOPM-099Y-099ZTM-099Y-099M-8WGY-0B
ESWYT-4	CMSS07Y00066S-0B-099Y-099M-099Y-38M-0WGY
ESWYT-5	CMSS07Y01083T-099TOPM-099Y-099M-099Y-40M-0WGY
ESWYT-6	CMSS08B00763T-099TOPY-099M-099NJ-29WGY-0B-4B-0WGY
ESWYT-7	CMSS10Y00023S-099Y-099M-099NJ-099NJ-4WGY-0B
ESWYT-8	CMSS10Y00327S-099Y-099M-099NJ-099NJ-6WGY-0B
ESWYT-9	CMSS10Y00372S-099Y-099M-099NJ-099NJ-15WGY-0B
ESWYT-10	CMSS10Y00373S-099Y-099M-099NJ-099NJ-24WGY-0B
ESWYT-11	CMSS10Y00375S-099Y-099M-099NJ-099NJ-38WGY-0B
ESWYT-12	CMSS10Y00472S-099Y-099M-099NJ-099NJ-7WGY-0B

Table 1: Continue...

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ESWYT-13	CMSS10Y00474S-099Y-099M-099NJ-099NJ-17WGY-0B
ESWYT-14	CMSS10Y00903T-099TOPM-099Y-099M-099NJ-099NJ-10WGY-0B
ESWYT-15	CMSS10Y00933T-099TOPM-099Y-099M-099NJ-099NJ-22WGY-0B
ESWYT-16	CMSS10B00295S-099M-099NJ-099NJ-11WGY-0B
ESWYT-17	CMSS10B00326S-099M-0SY-45M-0WGY
ESWYT-18	CMSS10B00407S-099M-099NJ-099NJ-23WGY-0B
ESWYT-19	CMSS10B00474S-099M-099NJ-099NJ-19WGY-0B
ESWYT-20	CMSS10B00824T-099TOPY-099M-099NJ-099NJ-19WGY-0B
ESWYT-21	CMSS10B00855T-099TOPY-099M-099NJ-099NJ-5WGY-0B
ESWYT-22	CMSS10B00895T-099TOPY-099M-0SY-23M-0WGY
ESWYT-23	CMSS10B01009T-099TOPY-099M-099NJ-099NJ-21WGY-0B
ESWYT-24	CMSS10B01010T-099TOPY-099M-099NJ-099NJ-4WGY-0B
ESWYT-25	CMSS10B01019T-099TOPY-099M-099NJ-099NJ-7WGY-0B
ESWYT-30	CMSS10B01023T-099TOPY-099M-099NJ-099NJ-34WGY-0B
SAWYT-3	CMSA07M00445S-040ZTM-040ZTY-22ZTM-010Y-01B-0Y
SAWYT-4	CMSS06Y00878T-099TOPM-099Y-099ZTM-099Y-099M-18WGY-0B
SAWYT-5	CMSS06B00154S-0Y-099ZTM-099Y-099M-2WGY-0B
SAWYT-6	CMSS10Y00033S-099Y-099M-099NJ-099NJ-1WGY-0B
SAWYT-7	CMSS10Y00035S-099Y-099M-099NJ-099NJ-13WGY-0B
SAWYT-8	CMSS10Y00052S-099Y-099M-099NJ-099NJ-36WGY-0B
SAWYT-9	CMSS10Y00235S-099Y-099M-099NJ-099NJ-20WGY-0B
SAWYT-10	CMSS10Y00375S-099Y-099M-099NJ-099NJ-22WGY-0B
SAWYT-11	CMSS10Y00985T-099TOPM-099Y-099M-099NJ-099NJ-7WGY-0B
SAWYT-12	CMSS10Y01063T-099TOPM-099Y-099M-099NJ-099NJ-6WGY-0B
SAWYT-13	CMSS10Y01085T-099TOPM-099Y-099M-099NJ-099NJ-10WGY-0B
SAWYT-14	CMSS10Y01193T-099TOPM-099Y-099M-099NJ-099NJ-26WGY-0B
SAWYT-15	CMSS10Y01196T-099TOPM-099Y-099M-099NJ-099NJ-5WGY-0B
SAWYT-16	CMSS10Y01241T-099TOPM-099Y-099M-099NJ-099NJ-5WGY-0B
SAWYT-17	CMSS10Y01311T-099TOPM-099Y-099M-099NJ-099NJ-7WGY-0B
SAWYT-18	CMSS10B00233S-099M-099NJ-099NJ-24WGY-0B
SAWYT-19	CMSS10B00473S-099M-0SY-9M-0WGY
SAWYT-20	CMSS10B00488S-099M-0SY-11M-0WGY
SAWYT-21	CMSS10B00497S-099M-099NJ-099NJ-14WGY-0B
SAWYT-22	CMSS10B00757T-099TOPY-099M-099NJ-099NJ-36WGY-0B
SAWYT-23	CMSS10B00779T-099TOPY-099M-0SY-26M-0WGY
SAWYT-24	CMSS10B00880T-099TOPY-099M-099NJ-099NJ-1WGY-0B
SAWYT-25	CMSS10B00995T-099TOPY-099M-099NJ-099NJ-1WGY-0B
SAWYT-31	CMSS10B01058T-099TOPY-099M-099NJ-099NJ-10WGY-0B
SAWYT-35	CMSS10B01157T-099TOPY-099M-099NJ-099NJ-23WGY-0B

Table 1: Continue...

genotypes. It shows that the material selected for this study brings significant diversity which is required by any breeding program. Similar outcomes were also found by Kaya and Turkoz (2016), Mehari *et al.* (2015).

Genotypic and phenotypic coefficient of variations

To compare the level of degree of difference between numerous characters of plant, phenotypic and genotypic components of variance, GCV, PCV and h^2b and genetic advance were analyzed and illustrated in Table 3. At location Rara the GCV and PCV ranged from 4.24% (number of grains) to 16.44% (grain yield) and 4.46% (number of grains) to 17.07% (grain yield). Plant height (9.58 and 9.63%), number of spikelet per spike (8.72 and 9.63%) and biological yield (4.61 and 5.04%) show low values of GCV and PCV while spike length (12.01 and 12.34%), number of tillers (13.75 and 13.17%), thousand grain yield (10.56 and 10.81%) and harvest index (13.76 and 14.01%) show moderate value GCV and PCV.

At location Danna the GCV and PCV ranged from 4.50% (number of grains) to 14.75% (grain yield) and 4.71% (number of grains) to 15.94% (grain yield) respectively. Spike length (9.55 and 10.27%), number of tillers (11.03 and 13.17%), thousand grain yield (10.24 and 10.45%) and harvest index (12.54 and 12.99%) show moderate value of genotypic coefficient of variance and phenotypic coefficient of variance. Height of plant (9.95 and 10.04%), number of spikelet per spike (9.52 and 10.27%) and biological yield (7.007 and 7.49%) show low values of GCV and PCV.

The present study tells that the phenotypic variation was contributed maximum to the genotypic variations. The phenotypic variation was high as compared to genotypic variation for all characters under study. Overall, the phenotypic coefficients of variance values were higher than genotypic coefficient of variance values while the differences were small. Analogous results were observed by Singh *et al*. (2018) representing a smaller influence of environment on the expression of characters considered. Similarly, research was supported out by Kyosev and Desheva (2015) the phenotypic coefficient of variation were higher than genotypic coefficient of variation for all the characters.

Estimates of heritability

Heritability was assessed for the 09 traits ranged from 82.82 to 98.80% were noted in number of spikelet per spike and height of plant at location Rara and 68.42 to 98.09% were observed in number of tillers and plant height at location Danna (Table 3). Other characters showed high heritability at both location spike length (94.91 and 87.19%), number of grains (89.75 and 91.28%), thousand grain weights (95.47 and 95.66%), grain yield (92.80 and 85.63%), biological yield (83.77 and 87.50%) and harvest index (96.84 and 93.32%) respectively.

In the present study highest heritability (H) was obtained for all traits. High heritability was also described by Tripathi *et al*. (2015) for thousand grain weight and Yahaya *et al*. (2014) for height of plant. Arya *et al*. (2013) was also noted high heritability in plant height. Monpara (2011) reported high heritability for height of plant followed by number of tillers number, biological yield, spike length, grains number per spike, harvest index and 1000 grain weight. High heritability evaluate for grain yield, number of spikelet per spike, number of seeds per spike, height of plant, 100-seed weight and tillers number per plant were also stated by Adewale *et al*. (2010) which support our findings. This showed that these characters were highly heritable and high performing genotypes selection is possible to the development of the characters. High heritability shows less environmental effect in the perceived variation (Eid, 2009).

Table 2: Analysis of variance for 09 morphological traits in 100 wheat genotypes.

	Replication	Location	Genotype	Loc*Gen	Error
	Df=3	Df=1	Df=99	Df=99	Df=1197
PH	85.57***	853.37***	402.59***	4.81***	2.59
NT	0.29	1.69**	1.55***	0.21$^{.N.S}$	0.17
SL	79.82***	60.30***	14.49***	1.02***	0.58
NSS	39.42***	112.89***	24.02***	2.11$^{N.S}$	2.13
NG	89.06***	533.61***	46.37***	2.44$^{N.S}$	2.21
TGW	80.62***	781.09***	97.27***	1.33$^{N.S}$	2.25
GY	64083.0***	414961.0***	859524.0***	22060.0***	9502.0
BY	260253.0***	2742998.00***	1994619.0***	53894.0***	24090.0
HT	15.52***	8.48$^{.N.S}$	114.60***	5.29***	2.26

Key: Loc= Location, Gen= Genotypes, PH= Plant height, NT= Number of tillers, SL= Spike length, NSS= Number of spikelet per spike, NG= Number of grains, TGW= Thousand grain weight, GY= Grain yield, BY= Biological yield, HI= Harvest index.

Significant Codes: P=0 '***' 0.001 '**' 0.01 '*' 0.05.

N.S= Non-significant.

Table 3: Genetic parameters of 09 traits in 100 wheat genotypes grown in two locations (Rara and Danna of district Muzaffarabad).

Traits	GCV (%)		PCV (%)		H^2		GA		GA (%)	
	R	D	R	D	R	D	R	D	R	D
PH	9.58	9.95	9.63	10.04	98.80	98.09	2.03	2.02	2.83	2.76
NT	13.75	11.03	15.0	13.17	83.12	68.42	1.71	1.4	53.45	42.89
SL	12.01	9.55	12.34	10.27	94.91	87.19	1.95	1.79	16.15	14.36
NSS	8.72	9.52	9.62	10.29	82.82	84.98	1.71	1.75	9.68	9.63
NG	4.24	4.5	4.46	4.71	89.75	91.28	1.84	1.88	3.46	3.47
TGW	10.56	10.24	10.81	10.45	95.47	95.66	1.96	1.97	6.07	5.84
GY	16.44	14.75	17.07	15.94	92.80	85.63	1.91	1.76	0.09	0.08
BY	4.61	7.007	5.04	7.49	83.77	87.50	1.72	1.8	0.02	0.02
HI	13.76	12.54	14.01	12.99	96.84	93.32	1.99	1.92	6.96	6.68

Keys: R= Rara site, D= Danna, GV= Genotypic variance, PV= Phenotypic variance, GCV= Coefficient of genotypic variance, PCV= Coefficient of phenotypic variance, H= Heritability, GA= Genetic advance, PH= Plant height, NT= Number of tillers, SL= Spike length, NSS= Number of spikelet per spike, NG= Number of grains, TGW= Thousand grain weight, GY= Grain yield, BY= Biological yield, HI= Harvest index.

The heritability of these characters is due to additive gene effects and choice may be effective in early generations for these traits (Ali *et al*., 2007).

Estimates of genetic advance (%)

Genetic advance is the progress in the mean genotypic value of selected individual above the parental population. At Rara the genetic advanced expressed as a percentage ranged from 0.02% (biological yields) to 53.45% (number of tiller) (Table 3). Spike length (16.15%) showed the moderate value of genetic advance while plant height (2.83%), spikelet number per spike (9.68%), grains number (3.46%), thousand grains weight (6.07%) and harvest index (6.96%) show low value of genetic advance.

At Danna the genetic advanced ranged from 0.02% (biological yields) to 53.45% (number of tiller). Spike length (14.36%) showed the moderate value of genetic advance while plant height (2.83%), spikelet number per spike (9.63%), grains number (3.47%), thousand grains weight (5.84%) and harvest index (6.68%). In this study the high genetic advance was found for number of tillers all other studied traits show low genetic advance. The results are in close conformity with Safi *et al*. (2017). Heritability and genetic development are significant considerations for selection. The assessment of genetic advance is more beneficial for tool choice after measured with heritability evaluations (Johnson *et al*., 1955). Low values of genetic advance are indicative of non-additive gene action whereas high values are indicative of additive gene action.

CONCLUSION

The current study revealed significant genetic variability among the genotypes of different locations and heritability for different characters that may be utilized to increase wheat productivity. Preference must be given to the characters which have moderate to high heritability and genetic advance in order to improve grain yield and produce new varieties.

Conflict of interest: None.

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