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Study of variability in bread wheat (*Triticum aestivum* L.)

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Abstract

A field experiment was conducted at Central Research Farm, Hajee Mohammad Danesh Science and Technology University, Dinajpur with 12 wheat genotypes collected WRC (Wheat Research Center), Dinajpur during 2013-2014 to study their variability and select genotypes for improvement of wheat. There was significant variation for all the 13 characters studied indicating the presence of considerable variations for selection. All the genotypes were earlier in heading than Agrani. Heading days (HD), plant/ m^2 (PPM), spikelet per spike (SPS) and 1000 grains weight (TGW) exhibited high heritability coupled with a moderate genetic advance. These characters had also medium to high genotypic coefficient of variation and phenotypic coefficient of variation coupled with high to moderate heritability and genetic advance. So, selection on the basis of these characters. Grain yield had positive and highly significant association with heading days, maturity days and 1000 grains weight at both genotypic and phenotypic levels. Grains per spike exhibited significantly negative association with grain yield per hectare. These results suggested that use of these traits in selecting high yielding genotypes would bring out good results and supplement empirical breeding approach.

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Introduction

Wheat is an ancient origin of agriculture and popular grain crop belongs to the family *Graminae*. It is essentially a temperate crop grown in a wide array of environments, from 67^{o}N in Norway, Finland and Russia to 45^{o}S in Argentina. It is also an important cereal crop and ranks first globally and second in Bangladesh both in terms of production and acreage (Anonymous 2008). The consumption of wheat is increasing with increasing food diversity in our country. The total area under wheat crop has been estimated 1061602 acre (429602hectares) as compared to 1029268 acres (416522 hectares) of the year 2013 which is 3.14% higher than previous year. Average yield of wheat has been estimated 3.03 metric tons per hectare which is 0.66% of the higher than the last year (BBS, 2014). The highest production of wheat in 2013 is estimated in EU 143.3 million metric ton followed by China (121.7 mmt), India (93.5 mmt), United States (60.00 mmt), Russia (52.1), Canada (37.5) Pakistan 24.2 (FAO, 2013) where as the production of wheat in Bangladesh is 1.302 million metric ton (BBS, 2014). All the naturally distributed species were adapted to their changing environments through the conservation of high genetic variability in their natural populations, and this resulting variability was the promoting force behind the evolution of the species and speciation.

The success of a breeding program depends on the presence of genetic variability in a material in hand. To make the heritable improvement in characters, estimation of genetic parameters and index of their transmissibility is required. Heritability estimates provide information about the extent to which a particular character can be transmitted to the successive generations. Knowledge of heritability of a trait thus guides a plant breeder to predict behavior of succeeding generations and helps in making desirable selections. Conventional analysis of variance and statistical parameters like phenotypic and genotypic coefficients of variability, heritability and genetic advance have been used to assess the nature and magnitude of variation in wheat breeding material. The result of a crop development program depends upon the amount of genetic variability existing in the germplasm. To bring the heritable improvements in economic characters through selection and breeding estimation of genetic parameters must be made before starting a program. There are different techniques available to compute the genetic parameters and the index of transmissibility of character. Heritability estimates provides information about the extent to which a particular character can be transmitted to the successive generations. Knowledge of heritability of a trait thus guides a plant breeder to predict behavior of succeeding generations and helps to predict the response to selection. High genetic advance coupled with high heritability estimates offer a most suitable condition for selection (Larik *et al.,* 2004). Therefore, availability of good knowledge of heritability and genetic advance existing in different yield parameters is a pre-requisite for effective plant improvement exercise. (Inamullah *et al.,* 2006) reported the presence of high heritability and genetic advance in different yield related attributes in wheat. A successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits with grain yield. (Mahfouzi *et al.* 2004)after examining breeding methods to increase wheat yield in cold and arid areas of Iran reported that genetic variation among genotypes may contribute to the grain yield increase in arid areas.

In this investigation, the study of different genotypes were made with an attempt to generate information on variability, heritability and genetic advance relationship of yield and its components and their implication in selection of better genotypes of wheat for the development or improvement of cultivars and germplasm. So the present study was undertaken to evaluate the genetic variability, heritability and genetic advance of yield and yield related traits to develop desirable wheat genotypes and to capture the potential genetic variability within wheat genotypes, cultivars and germplasm.

Materials and methods

The experiment was set up at the central research farm and laboratory of Genetics and Plant Breeding

Department, Hajee Mohammad Danesh Science and Technology University (HSTU), Dinajpur during October 2013 to June 2014. The experimental site is situated under the Dinajpur Sadar Upazila and located at 25°39′ N latitude and 88°41′ E longitude with an elevation of 37.58 meter above the sea level. For conducting the present study, the base materials were collected from the Wheat Research Center (WRC), Dinajpur. The experimental material materials of the study were consisted of twenty four wheat (*Triticum aestivum* L.) genotypes. The experiment was conducted in a Randomized Complete Block Design. The unit plot size was 2.0 m x 5.0 m where showing was done in ten rows with 20 cm interval between rows. The distance between plots was 0.75 m and block to block distance was 1.5 m. Fertilizer was applied at the rate of 300 kg, 170 Kg, 100 Kg, 110 Kg and 6 Kg Urea, TSP, MP, Gypsum and Boron respectively. After land preparation, full dose of P, K, S, Zn, B and one third of N were incorporated thoroughly into the soil as basal dose. The remaining amount of N was applied at 21 and 53 days after seedlings emergence split into two equal amounts. Data on thirteen characters were collected from some randomly and tagged 10 plants from the middle rows excluding borders and some from plant basis. These 10 plants were harvesting by uprooting. Data were recorded for Heading days, Anthesis, Days to maturity, Plant height (cm), Number of plants/ square meter, Number of spikelets per spike, Number of grains per spike, Grain weight of 10 spikes, Thousand grain weight (Kg), Grain yield (Kg/plot), Canopy temperature depression (CTD), Chlorophyll content of flag leaf at 14 days after anthesis(CHL_{21}) (SPAD unit) at either flowering time or physiological maturity. The CTD was recorded at 90 days after anthesis during noon period under bright sunlight and less wind with the help of hand held infra-red thermometer (Model: Crop TRAC item no. 2955L-Spectrum Technologies, Inc.). This trait Chlorophyll content was measured in 5 fully expanded sunlight flag leaves in *vivo* by a Minotola SPAD meter at 14 days after anthesis and expressed in SPAD unit.

Statistical analysis

The data collected on different yield contributing, morpho – physiological traits were subjected to different biometrical analysis to determine variances, genotypic and phenotypic coefficient of variations, heritability (broad sense) and genetic advances. Relationships between the characters were also computed through phenotypic and genotypic correlations and path coefficients were estimated. Analysis of variances was done for different characters according to the formula suggested by Steel and Torrie (1960). The data recorded from the present study were analyzed statistically in a computer based statistical package MSTAT – C program using the following methods:

i. General mean (X) = $\frac{\text{Sum of observation of all the plants for each genotype}}{\text{Number of plants}}$

ii. Range = The minimum and maximum values for each trait within population

iii. Coefficient of variation (CV%) = $\frac{\sigma_p}{\bar{x}}$ x 100

Where, σ_p = Phenotypic standrad deviation

X = General mean of the character

Analysis of variance (ANOVA)

The analysis of variance (ANOVA) for all characters was carried out separately. The structure of ANOVA

Source of variation	df	M.S.S	Expected values of M.S.S
Replication (r)	r-1	M_1	-
Genotypes (g)	g-1	M_2	$\sigma^2 e$ + $r\sigma^2 g$
Error	(r-1)(g-1)	M_3	$\sigma^2 e$
Total	(rg-1)	$M_1 + M_2 + M_3$	

Where, r = number of replication and g = number of genotypes

Estimation of genotypic and phenotypic variances

The genotypic and phenotypic variances were estimated according to the formula suggested by Johnson *et al.,* (2003). The error MS was considered as environmental variances (σ_e^2). Genotypic variances (σ_g^2) and phenotypic variances(σ_p^2) were calculated using the following formula:

$$\sigma_g^2 = \frac{GMS-EMS}{r} \text{with } (n - 1) \text{ df}$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Estimation of genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV)

Both genotypic and phenotypic coefficient of variability was computed as per the method suggested by Burton and Devane (1998).

1. Genotypic coefficient of variation, GCV (%) = $\frac{\sigma_g}{\bar{x}}$ x 100
2. Phenotypic coefficient of variation, PCV (%)= $\frac{\sigma_p}{\bar{x}}$ x 100

Where,
σ_g = Genotypic standard deviation
σ_p= Phenotypic standard deviation
$\bar{x}$ = General mean of the character

Estimation of heritability (Broad sense)

Heritability in broad sense (h^2b) was estimated for different characters by the formula suggested by Johnson *et al.,* (1955) and Hanson *et al.,* (1956). Heritability estimates from single environment was computed as the ratio of genotypic to the phenotypic variance and was expressed in percentage:

Heritability in broad sense, h^2b (%) = $\frac{\sigma_g^2}{\sigma_p^2}$ x 100

Where, σ_g^2= Genotypic variance
σ_p^2= Phenotypic variance

The heritability was categorized as low, moderate and high as given by Robinson *et al.,* (1949).
0 – 30 %: Low
30 – 60%: Moderate
60% and above: High

Estimation of genetic advance (GA)

The expected genetic advance (GA) for different characters under selection was estimated using the formula suggested by Johnson *et al.,* (1955).

Genetic advance (GA) = $h^2b.i.\sigma_p$
Where, h^2b = Heritability in broad sense (decimal)
i = Selection differential, the value of which is 1.76 at 10% level of selection intensity
σ_p= Phenotypic standard deviation

Estimation of genetic advance in percent of mean

Genetic advance over mean was estimated by using the following formula proposed by Comstock and Robinson (1952) as follows:

GA % mean= $\frac{GA}{\bar{x}}$ x 100
Where, GA = Genetic advance
$\bar{x}$ = Population mean

Estimation of genotypic and phenotypic correlation coefficients

Genotypic and phenotypic correlation coefficients different yield contributing morpho – physiological characters contributing to drought tolerance were estimated using the following formula as suggested by Miller *et al.,* (1958); Hanson *et al.,* (1956) and Johnson *et al.,* (1955).

Genotypic correlation, $r_{g1.2} = \frac{Cov.g1.2}{\sqrt{(\sigma_{g1}^2 \text{ x } \sigma_{g2}^2)}}$

Cov.g1.2 = Genotypic covariance between the variable (characters) X_1 and X_2

σ^2_{g1} = Genotypic variance of the variable X_1
σ^2_{g2} = Genotypic variance of the variable X_2

Similarly, phenotypic correlation,

$$r_{p1.2} = \frac{Cov.\ ph1.2}{\sqrt{(\sigma_{p1}^2 \text{ x } \sigma_{p2}^2)}}$$

Cov.ph1.2 = Phenotypic covariance between the variables (characters) X_1 and X_2
σ^2_{p1} = Phenotypic variance of the variable X_1
σ^2_{p2} = Phenotypic variance of the variable X_2

Estimation of simple correlation coefficients

Simple correlations between heat stress susceptibility indices and mean of different characters under late sowing were estimated using the following conventional formula used by Singh and Choudhary (2008).

Correlation, $r_{xy} = \frac{Cov_{.x.y}}{\sqrt{(V_x \cdot V_y)}}$

$Cov_{.x.y}$ = Covariance between the variable x and y
V_x = Variance of variable x
V_y = Variance of variable y

The correlation was tested by conventional t – test using following formula,

$$t = r\sqrt{n-2}/\sqrt{1-r^2}$$

Where, n = Number of observation
r = Correlation

Estimation of correlation coefficients were compared against r – values given in Fisher and Kertesz (2000) table t at (n-2) df at the probability level of 0.05 and 0.01 to test their significance.

Results and discussions

Analysis of variance and morphological characteristics for different quantitative characters

The analysis of variance revealed highly significant difference among lines for all traits studied except canopy temperature (Table 2). The significant difference among genotypes for the traits implies the presence of substantial variation among genotypes which is central to the study of traits and gives an opportunity to plant breeders for improvement of these characters through breeding. The mean squares for 13 characters are presented in Table 4.1.1.The minimum anthesis day was observed in the genotype E-12 (75 days) and the maximum (84 days) in the genotype E-9 with an average value of 78 days. The minimum number of plants m-2 was 328 as observed in E-8 and the maximum 413 in E-6 with an average of 361. The Spikes m-2 exhibited a wider variation, which ranged from 293 (E-9) to 361 (E-7) with overall mean 322. The minimum heading days was observed in the genotype E-1, E-4 and E-11 (67) and the maximum (76) in the genotype E-5 with an average value of 70. Minimum maturity days were recorded in the genotype E-4 (102 days) and the maximum (111 days) in E-5 with an average value of

Table 1. Name and sources of the genotypes used in this study.

Entry	Name	Source
1	Aghrani	WRC, BARI
2	Protiva	WRC, BARI
3	Sawrav	WRC, BARI
4	Gourav	WRC, BARI
5	Shatabdi	WRC, BARI
6	Sufi	WRC, BARI
7	Bijoy	WRC, BARI
8	Prodip	WRC, BARI
9	BARI-25	WRC, BARI
10	BARI-26	WRC, BARI
11	BARI-27	WRC, BARI
12	BARI-28	WRC, BARI

Table 2. Analysis of variance (MS) on fifteen characters in wheat.

Sl. No.	*Characters*	*Source of variation*			*Co-efficient of variation%*
		Replication	Genotype	Error	
1	Anthesis days	26.333	23.220**	15.393	4.99
2	Plants per meter square (no.)	1441.583	2317.159**	815.129	7.91
3	Spikes per meter square (no.)	445.528	1591.444**	795.77	8.76
4	Heading days	23.083	17.758**	1.932	1.98
5	Maturity days	351.361	19.785**	6.907	2.45
6	Plant height	135.577	109.760**	4.586	2.07
7	Grain weight per 10 spike (g)	15.742	2.257*	3.794	8.58
8	Grains per spike (no.)	90.910	35.910**	7.744	5.79
9	Thousand grain weight (g)	2.855	31.510**	3.502	3.95
10	Spikelet per spike (no.)	2.519	4.940**	0.900	4.90
11	Chlorophyll content	93.929	14.216**	8.474	6.96
12	Canopy temperature (^oC)	4.671	0.329	0.216	2.36
13	Yield per hectare (g)	606508.333	221206.061**	93059.848	6.15

** indicates significant at 1% level of probability

* indicates significant at 5% level of probability

107 days. The minimum plant height was observed in the genotype E-11 (96cm) and the maximum (l16cm) in the genotype E-2 with an average value of 103.62cm. The low grain weight /10 spikes was recorded in the genotype E-2 (18.92g) and the highest (25.95g) in genotype E-9. The low grain weight /10 spikes was recorded in the genotype E-2 (18.92g) and the highest (25.95g) in genotype E-9. Genotype E-7 produced minimum grains spike-1(43) while E-10 produced the maximum (55) grains. The low estimation of 1000-grain weight was recorded in the genotype E-6 (41.56g) and the highest (52.47) in Genotype E-8. Calderini *et al.* (1999) argued that most recently, the increase in grain yield has been mainly due to increased grain number per spike and this component of yield has proved more efficient than grain weight. Although both source and sink have limiting effect on the yield, it is well established that sink has been comparatively more limiting, even in new lines of wheat.

Genotypic and phenotypic co-efficient of variation, and heritability and genetic advance

Study of phenotypic and genotypic co–efficient of variation, heritability and genetic advance for yield and its different contributing characters are shown in Table 2 and 3. It was observed earlier that there was significant variation among the varieties / lines for all the characters. The variation among the varieties / lines was judged at phenotypic and genotypic levels. Genotypic coefficient of variation was more than 7% in grains weight 10 spikes. Phenotypic coefficient of variation was more than 8% in plants/m^2, grains/spike, 1000-grain weight, spikelet/ spike, chlorophyll content and yield/ ha. High to moderate heritability was recorded in heading days (HD), plant/ m^2 (PPM), spikelet per spike (SPS) and 1000 grains weight (TGW). Kabir *et al.* 2015 founded there was significant variation among the varieties / lines for all the characters. The variation among the varieties / lines was judged at phenotypic and genotypic levels. Among the different characters heading days, anthesis, plant height, maturity days, plants/m^2, spikes/m^2, grains/spike and 1000-grain weight displayed more than 10% variation at phenotypic level, which could be considered as high enough. At genotypic level, plant height, plants/m^2, spikes/m^2, and 1000-grain weight had more than 10% variation and others had less 8% variation. Genetic advance in percent of mean was also high in plant height and 1000 grain weight. The results revealed that moderate to high heritability coupled with moderate to high genetic advance was recorded in plant height, 1000 grain weight. Among these characters 1000 grain weight, grains weight 10 spikes, grains/spike had high genotypic coefficient of variations. So, selection for these characters will be efficient for improvement. On the other hand, plants/ m ^{2} and spikelet/ spike had also good genotypic coefficient of variation. Therefore, selection can be also done on the basis of these characters.

Character Association

This trait had positive association with TGW and yields both at genotypic and phenotypic level (Table 3). Insignificant but positive correlation both at genotypic and phenotypic level was also observed between plant height and thousand grain weight. Several investigators found plant height to be correlated significantly and positively with grain yield (Khan *et al.,* 1999). Canopy temperature at grain filling stage had negative correlation with grain yield at genotypic (r_g= -.26) and phenotypic level (r_p= -0.26). It has shown significant negative correlation with TGW at genotypic and insignificant at phenotypic level, grain spike-l and anthesis day (Table 3). This trait had positive association with plant/ m^{2,} heading days both at genotypic and phenotypic levels. It also had insignificant positive association with plant height activity to be positively correlated with grain yield. Rahman and Razzaque (2009) reported strong and negative correlation of CT with grain yield. Rouf *et al.* (2012) observed that high yielding genotypes possess significantly low canopy temperature indicated that higher leaf area index at grain filling stage will led to offers higher production of more photosynthates and it finally reflected in TGW, grain yield and total dry matter production. These results are similar to works of Bayoumi *et al.,* (2008). Maturity days showed negative correlation with spikes per m² and grain per spike both at genotypic and phenotypic levels. It showed positive correlation with 1000 grain weight and grain yield both at genotypic and phenotypic levels. This association indicates that late maturing genotypes had longer duration of grain filling. Rahman and Razzaque (2009) reported significant positive correlation of grain filling period with maturity period. Jagshoran (1995) and Sangam (1994) reported that this trait exhibited negative association with grain yield but Jadhav (1994) reported positive and significant association.

Table 3. Mean performance of 12 wheat varieties for yield and yield contributing characters.

Variety	AD	PPMS	SPMS	HD	MD	PH
Agrani	75.67b	331.7 b	300.0 c	67.67 de	103.3 cd	97.58 gh
Protiva	78.00 ab	407.7 a	357.3 ab	71.00 bc	108.7 ab	116.1 a
Sourav	77.00 ab	353.7 b	308.0 abc	72.67 b	108.0 abc	100.7 fg
Gourav	77.33 ab	354.0 b	304.0 bc	67.33 e	102.7 d	97.17 gh
Shatabdi	81.67 ab	349.0 b	313.7 abc	76.00 a	111.0 a	107.6 bcd
Sufi	76.00 b	413.0 a	342.0 bc	70.00 cd	106. 0 a-d	109.5 b
Bijoy	80.67 ab	382.0 ab	361.0 a	70.67 bc	108.7 ab	108.11 bc
Prodip	81.33 ab	328.3 b	303.3 bc	71.00 bc	109.7 ab	105.0 cde
BARI-25	84.00 a	346.3 b	293.7 c	69.00 cde	107.0 a-d	104.1def
BARI-26	79.33 ab	339.0 b	312.3 abc	69.67 cde	109.3 ab	98.32gh
BARI-27	76.67 ab	352.3 b	338.3 abc	67.67 de	106.3 a-d	96.05 h
BARI-28	75.33 b	376.0 ab	331.0 abc	71.33 bc	105.0 bcd	103.0 ef
LSD	6.644	48.34	47.77	2.35	4.45	3.63
Mean	7.583	361.08	322.06	70.33	107.14	103.63
Range	75.33-84.0	328.3-413.0	293.7-361.0	67.33-76.00	102.7-111.0	96.05-116.1

Table 3. continued..........

Variety	*GWTS*	*GPS*	*TGW*	*SPS*	*CC*	*CT*	*YPH*
Agrani	22.69 ab	51.40 abc	43.38 ef	18.50 c-e	42.57 ab	20.27 a	4633.0 b
Provati	18.92 c	43.67 ef	48.96 bcd	21.37 a	40.23 b	19.87 ab	5073.0 ab
Sourav	22.35 abc	52.07 ab	45.76 de	20.20 abc	42.50 ab	19.80 ab	4583.0 b
Gourav	22.50 abc	48.20 b-e	46.54 de	16.80 e	40.63 b	20.23 a	4863.0 ab
Shatabdi	23.69 ab	47.27 b-f	47.39 cd	19.67 a-d	43.07 ab	19.72 ab	5283.0 a
Sufi	21.19 bc	48.60 b-e	41.54 f	19.60 a-d	41.33 ab	19.85 ab	5227.0 a
Bijoy	21.17 bc	42.77 f	50.12 abc	19.13 bcd	41.87 ab	19.63 ab	4853.0 ab
Prodip	23.44 ab	49.57 a-d	52.47 a	20.57 ab	43.57 ab	19.12 b	4603.0 b
BARI-25	25.95 a	44.87 d-f	46.59 de	20.63 ab	41.07 b	19.45 ab	4920.0 ab
BARI-26	25.79 a	54.43 a	47.36 cd	17.97 de	39.07 d	19.76 ab	5393.0 a
BARI-27	23.76 ab	46.60 c-f	52.25 ab	18.43 cde	46.87 a	19.44 ab	4903.0 ab
BARI-28	20.92 bc	47.07 b-f	46.04 de	19.27 bcd	38.87 b	19.43 ab	5143.0 ab
LSD	3.30	4.71	3.17	1.61	4.93	0.79	516.6
Mean	22.70	48.04	47.37	19.34	41.80	19.71	4956.67
Range	18.92-25.95	42.77-54.43	41.54-52.47	16.80-21.37	38.87-46.87	19.12-20.27	4583.0-5393.0

AD= Anthesis Day, PPMS= Plant Per Meter Square, SPMS= Spikes Per Meter Square, HD= Heading Day, MD= Maturity Day, PH= Plant Height, GTWS= Grain Weight of Ten Spikes, GPS= Grain Per Spike, TGW= Thousand Grain Weight, SPS=Spikelet Per Spike, CC= Chlorophyll Content, CT= Canopy Temperature, YPH= Yield Per Hactare.

The significant negative correlation was noticed between grains/spike and 1000- grain weight at both genotypic and phenotypic level. The negative correlation between grains/spike and 1000-grain weight indicates a competitive demand of both sinks (grain number and size) for photosynthates from a common source, which expressed through a compensating balance between two traits under stress condition. However, positive significant correlation between grains/spike and grain yield was obtained in the tested experiment. Singh &

Sharma (1999) observed negative correlation of grains per spike and grain but several authors (Gautam *et al.,* 2002; Bergale *et al.,* 2001; Sufian 2005) had significant and positive correlation of grains per spike and grain yield.

Thus and grain weight (g) showed significant negative correlation with grain yield both at genotypic and phenotypic level (Table 3). Several authors (Singh *et al.,* 1997; Navin *et al.,* 2014; Jat *et al.,* 2003; Zecevic *et al.,* 2004) had reported significant and positive correlation of 1000-grain weight with grain yield.

Table 4. Estimation of variability of 13 characters in wheat.

Sl. No.	Character	Genotypic Variance (σ^2g)	Phenotypic Variance(σ^2p)	Environmental variance (σ^2e)	GCV (%)	PCV (%)
1	Anthesis days	2.61	18.00.30	15.39	2.06	5.40
2	Plants per meter square (no.)	500.68	1315.81	815.13	6.20	10.05
3	Spikes per meter square (no.)	265.23	1060.99	795.78	5.06	10.11
4	Heading days	5.28	7.21	1.94	3.27	3.82
5	Maturity days	4.30	11.91	6.91	1.94	3.22
6	Plant height	35.06	39.64	4.59	5.72	6.08
7	Grain weight per 10 spike (g)	2.82	6.62	3.80	7.40	11.33
8	Grains per spike (no.)	9.39	17.13	7.75	6.38	8.62
9	Thousand grain weight (g)	9.34	12.84	3.50	6.45	7.57
10	Spikelet per spike (no.)	1.35	2.25	0.90	6.00	7.75
11	Chlorophyll content	1.91	10.39	8.47	3.31	7.71
12	Canopy temperature (°C)	0.04	0.254	0.216	0.99	2.57
13	Yield per hectare (g)	42715.40	135775.25	93059.85	4.17	7.43

Table 5. Estimation of Heritability and genetic advance of different characters in wheat.

Sl. No.	Character	Heritability (%)	Genetic Advance (at 5% selection intensity)	Genetic Advance (as % of mean)
1	Anthesis days	14.50	1.27	1.62
2	Plants per meter square (no.)	38.05	28.43	7.87
3	Spikes per meter square (no.)	24.99	16.77	5.20
4	Heading days	73.18	4.06	5.77
5	Maturity days	36.05	2.56	2.39
6	Plant height	88.43	11.47	11.07
7	Grain weight per 10 spike (g)	42.65	2.26	9.96
8	Grains per spike (no.)	54.80	4.67	9.72
9	Thousand grain weight (g)	72.72	5.37	11.34
10	Spikelet per spike (no.)	59.95	1.85	9.56
11	Chlorophyll content	18.43	1.22	2.92
12	Canopy temperature (°C)	14.97	0.16	0.81
13	Yield per hectare (g)	31.46	238.84	4.82

Table 6. Genotypic correlation (r_g) coefficients among 13 characters of wheat.

Characters	AD	PPMS	SPMS	HD	MD	PH	GTWS	GPS	TGW	SPS	CC	CT	YPH
AD	0	-1.16*	-0.98*	0.48*	1.0**	0.41	1.0*	-0.6*	0.66*	0.51*	0.34	-1.08*	0.03
PPMS		0	0.87**	0.002	-0.34	0.002	-1.05**	0.002	-0.29	0.002	-0.54*	0.002	0.56*
SPMS			0	0.12	-0.06	0.77**	-0.94**	-0.92**	0.41*	0.17	-0.08	-0.32	0.71*
HD				0	0.82**	0.002	-0.09	0.002	0.08	0.002	-0.1	0.003	0.32
MD					0	0.56**	0.31	-0.1	0.71**	0.68**	0.38	-1.04**	0.19
PH						0	-0.73**	-1.82	0.01	0.79**	0.46*	0.002	0.3
GTWS							0	0.54*	-0.04	-0.26	0.18	-0.83*	0.02
GPS								0	-0.4*	-1.38	-0.25	0.002	0.02
TGW									0	0.21	0.73*	-1.23**	-0.39*
SPS										0	0.19	0.002	-0.08
CC											0	-0.32	-1.04*
CT												0	-0.26
YPH													0

AD= Anthesis Day, PPMS= Plant Per Meter Square, SPMS= Spikes Per Meter Square, HD= Heading Day, MD= Maturity Day, PH= Plant Height, GTWS= Grain Weight of Ten Spikes, GPS= Grain Per Spike, TGW= Thousand Grain Weight, SPS=Spikelet Per Spike, CC= Chlorophyll Content, CT= Canopy Temperature, YPH= Yield Per Hactare.

Table 7. Phenotypic correlation (r_p) coefficients among 13 characters of wheat.

Characters	AD	PPMS	SPMS	HD	MD	PH	GWTS	GPS	TGW	SPS	CC	CT	YPH
AD	0												
PPMS	-1.16*	0											
SPMS	-0.98*	0.87**	0										
HD	0.48*	0.002	0.12	0									
MD	1.0**	-0.34	-0.06	0.82**	0								
PH	0.41	0.002	0.77**	0.002	0.56**	0							
GWTS	1.0**	-1.05**	-0.94**	-0.09	0.31	-0.73**	0						
GPS	-0.6*	0.002	-0.92**	0.002	-0.1	-1.82	0.54*	0					
TGW	0.66*	-0.29	0.41*	0.08	0.71**	0.01	-0.04	-0.4*	0				
SPS	0.51*	0.002	0.17	0.002	0.68**	0.79**	-0.26	-1.38	0.21	0			
CC	0.34	-0.54*	-0.08	-0.1	0.38	-0.46*	0.18	-0.25	0.73*	0.19	0		
CT	-1.08*	0.002	-0.32	0.003	-1.04**	0.002	-0.83*	0.002	-1.23**	0.002	-0.32	0	
YPH	0.03	0.56*	0.71*	0.32	0.19	0.3	0.02	0.02	-0.39*	-0.08	-0.04*	-0.26	0

AD= Anthesis Day, PPMS= Plant Per Meter Square, SPMS= Spikes Per Meter Square, HD= Heading Day, MD= Maturity Day, PH= Plant Height, GTWS= Grain Weight of Ten Spikes, GPS= Grain Per Spike, TGW= Thousand Grain Weight, SPS=Spikelet Per Spike, CC= Chlorophyll Content, CT= Canopy Temperature, YPH= Yield Per Hectare.

Conclusion

Heading days (HD), plant/m^2 (PPM), spikelet per spike (SPS) and 1000 grains weight (TGW) exhibited high heritability coupled with a moderate genetic advance indicating that simple selection scheme would be sufficient for these traits to bring genetic improvement in desired direction. The correlation coefficients were determined to find out the inter relationship among the 12 most responsive traits in relation to grain yield. Grain yield had positive and highly significant association with heading days, maturity days and 1000 grains weight at both genotypic and phenotypic levels. Grains per spike exhibited significantly negative association with grain yield per hectare. These results suggested that use of these traits in selecting high yielding genotypes would bring out good results and supplement empirical breeding approach. Good number of genotypes had higher yields, 1000-grain weight, spikes/ m^2. So, these could be used in crossing program for the development of high yield.

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