



Genotypic and Phenotypic correlation amongst flowering and yield relating traits in bread wheat (*triticum aestivum* .l)

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ABSTRACT

The main objective of plant breeding programs is to identify and evaluate superior genotype. In order to investigate the genotypic and phenotypic correlation amongst flowering and yield relating traits a field experiment was conducted at the research farm of Agriculture department, Hazara University, Mansehra (Dhodial), Khyber Pakhtunkhwa Pakistan, during the growing season of 2018-19. Two replication of seventy different wheat genotypes including local checks were planted in design of Alpha Lattice design. Data was documented on days to heading, height of plant in cm, length of spike in cm, spikelet's per spike, yield of grain in kg per plot, yield of grain in kg per hectare and thousand grain weight. Our study observed significant differences amongst genotypes for maximum number of traits. In majority of the trait genotypic correlation was observed to be higher as compared phenotypic correlation by statistical analysis. Minimum days to heading were recorded for genotype No-5 which is 89 days and could be utilized for making selection for early maturity. Selecting desirable genotypes with medium plant height to resolve the problem of lodging, the medium plant height was observed for the genotype No10 which is 85cm. Maximum spike length was observed for genotype No8 which was 9.7cm while maximum number of spikelet's per spike (19) and maximum grain yield per plot was recorded for genotype No19. Correlation analysis revealed positive association in between days to heading, height of plant, spike length, number of spikelet's per spike and thousand grain weight with grain yield per hectare with both level of genotype and phenotype. Maximum positive direct effect on grain yield per hectare was detected by statistical analysis and this was mostly contributed by traits like length of spike, number of spikelet per spike, followed by yield of grain and weights of 1000-grain. Meanwhile there should be correlation between these two characters and could be a main concern for breeder of plant. We therefore suggested that for future wheat yield improvement programs importance should be given to higher performance for length of spike, number of spikelet per spike and thousand grain weight.

Key words: Genotype; phenotype; flowering; grain yield; spike; spike length

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INTRODUCTION

Wheat that belong to order of cyperales, Family of Poaceae and genus of *Triticum* (wheat) Species is a grass usually cultivated for its seed. Botanically, the wheat kernel is a type of fruit called a caryopsis. Hexaploid wheat possesses 42 chromosomes derived from its three ancestral genomes (ABD). The 21 pairs of chromosomes can be further divided into seven groups of six chromosomes (one chromosome pair being derived from each of the three ancestral genomes). On the basis of purpose, wheat types include common wheat (*Triticum aestivum*) and durum wheat (*Triticum turgidum ssp. durum*) is used in most dried pasta and couscous. In comparison to other crop for food, wheat is cultivated more on land. Wheat crop trade is greater in comparison to combine other crops trade. After maize, the second most produced cereal was wheat in 2016 as in the world the wheat production was 749 million tons. From 1960 onward triple production of other grain crops and wheat crop has been observed and there is expectation of further increase in 21 century. Due to exceptional viscoelastic and adhesive properties of

gluten protein of wheat the world demand for the wheat is increasing continuously. The presence of this protein help in processed food production. Basically wheat is a temperate zone crop but it has adopted all the climates of the world due to its genetic diversity. Wheat has the ability to adopt different environment ranging from -35°C in stage of vegetation to over 40°C in grain filling period [1]. For the mainstream population of world wheat is most vital and strategic crop. 36% population of the world use wheat as staple food. In the global consumption wheat delivers about 55% of the carbohydrates and 20% of the food calories. Wheat has its importance as a source of carbohydrate. It has led the world as a source of vegetal protein in human food. The content of protein in wheat is 13%. In the world as wheat is the most important crop, out of total crop land of globe it occupies 17%, 40% population of the world is feeding by wheat, in total food calories it cover about 20% and it is also a rich source of protein [2]. The aim of the world-wide breeding program is mainly for recognition of genotype in order to achieve good food quality, high yield and adaptation to various agro-ecosystems (3). As for as agricultural policies are concerned wheat in Pakistan is important grain crop. In Pakistan wheat cover about 70 percent of the season of winter and around 37% of the cropped area. It has contribution of about 10% in agriculture and around 2.1% contribution in national GDP [4]. At the end of last century self-sufficiency has been attained by Pakistan in wheat and entered into export market. To develop new varieties of wheat, Pakistan has done a considerable job and progress has been made to increase production. Considerable effort has been done to develop new varieties of wheat and production has been increased in the country. Pakistan has been produced 25.4 million tons of wheat from area of 9.23 million hectares during 2016. In Pakistan area total area under cultivation is 9.23 million hectares. Total area under cultivation in Khyber Pakhtunkhwa 730.5 thousand hectares. Wheat requirements of KP is 2.5 million tons, while it produced 1.5 million tons only. To make it self-sufficient in wheat, wheat regions must be improved [4]. The main focus on wheat breeding efforts in Pakistan is to develop high grain production varieties and rust tolerance and resistance varieties. Selection of progeny and its breeding depend upon the genetic variability in population. [5]. There are two ways to increase yield of wheat. It can be increased by cultivating large area or by increasing per unit area yield. Presently, there is no possibility to upturn cultivating area due to other crop of winter and scarcity of water. To get more yield per unit area is only possible by proper management and growing varieties that give high yield. It is important to get information about inter-relationship amongst several yield before the initiation of any breeding program. To determine the level of association of numerous yield attributing characters the correlation of genotype and phenotype is important. By proper utilization of the existing resources of information and genetics, the yield can be increased. Among different traits information of correlation is crucial in plant breeding. If there is positive correlation between two traits then by improving the other trait one trait can be improved. Understanding of the association of different characters with grain yield is provided by correlation studies beside with path analysis (6). Keeping in mind the previous evidence so our study was directed to get evidence on correlation of genotype and phenotype amongst flowering and yield relating traits in bread wheat. The main aim of our study was evaluation of wheat germplasm for maturity and yield qualities and to determine the genotypic and phenotypic correlation amongst several characters and their impact on grain production.

MATERIAL AND METHODS

In order to investigate the genotypic and phenotypic correlation amongst flowering and yield relating traits a field experiment was conducted at the research farm of Agriculture department, Hazara University, Mansehra (Dhodial), Khyber Pakhtunkhwa Pakistan, during the growing season of 2018-19. Two replication of seventy different wheat genotypes including local checks were planted in design of Alpha Lattice design (Table 1). Each genotype was planted in 4 rows. The distance between two rows was kept 30 cm while distance between plants was kept 15 cm. Data was documented on days to 50% heading, plant height (cm), spike length (cm), spikelets/spike, 1000 grain weight (g), grain yield (kg/ha). Data regarding yield related characters viz. days to heading, plant height (cm), spike length (cm), number of spikelets/spike, grain number/spike and one thousand grain weight (g) were documented from 4 protected plants nominated casually from central two rows. Data for days to heading were noted when 50 percent of the spikes appeared from the flag leaf region. Correspondingly, days to maturity were calculated from date of sowing to date when 50 percent spikes color changed from golden brown. Filling of grain time was calculated by decreasing heading days from the days of maturity. Days to heading data was measured by totaling the number of days from sowing to the days to till 50% of the head rise from leaf sheath. Plant height (cm) was calculated in cm by using meter rod from ground level to the top of the spike. Spike length (cm) was calculated in cm from the base to the tip of the spike and awns were excluded. Number of spikelet's/spike was measured by enumerating the number of spikelets per spike in

the middle two rows of plot. One thousand grain weight (gm) was calculated by counting 1000 grains of each genotype and weighed using digital weight balance.

Grain yield was determined by flailing all the plants of each genotype, weighed and converted in kg/ha. Grain Yield (kg ha⁻¹) of each plot was determined in tones after reaping and regulating fresh ear weight to 150 g kg⁻¹ grain moisture (7) using the formula given below:

$$\text{Grain Yield Kg ha}^{-1} = \frac{(100 - \text{MC}) \times \text{FEW} \times \text{Shelling Co-efficient} \times 10,000}{(100 - 15) \times \text{Plot Area}}$$

Here,

MC = moisture content (%) in grains at harvest

FEW=Fresh ear weight (kg) at harvest

Shelling Co-efficient = Shelling % age/100

Table 1. List of wheat genotypes/breeding lines

Entry 2018-19	Pedigree	Entry 2018-19	Pedigree
1	NELOKI//SOKOLL/EXCALIBUR	36	PRL/2*PASTOR//KACHU
2	KRL 19/QUAIU #1//BECARD/QUAIU #1	37	BORL14*2//KFA/2*KACHU
3	SUP152*2//TECUE #1//FRNCLN*2//TECUE #1	38	BORL14*2//KFA/2*KACHU
4	MUU/KBIRD//KACHU/KIRITATI	39	BORL14*2//MUNAL #1//FRANCOLIN #1
5	BECARD/QUAIU #1//BORL14	40	KUTZ*2/5/UP2338*2//VIVITSI/3//FRET2/TUKURU//FRET2/4//MISR 1
6	MUCUY	41	KUTZ*2//KFA/2*KACHU
7	KACHU #1//YUNMAI 47//KACHU/4//MUU #1//PBW343*2//KUKUNA/3//MUU/5//KUTZ	42	WBL1*2//SHAMA//BAJ #1*2/3//BORL14
8	TRCH/SRTU//KACHU/3//BORL14	43	KACHU//WBL1*2//BRAMBLING/3//BAJ #1//AKURI/4//KACHU//WBL1*2//BRAMBLING
9	PRL/2*PASTOR//PBW343*2//KUKUNA/3//ROLF07/4//KFA/2*KACHU	44	Gandum-I
10	NELOKI//KFA/2*KACHU	45	SUP152/BAJ #1//TRCH/HUIRIVIS #1/3//SUP152/BAJ #1
11	NELOKI//KFA/2*KACHU	46	SUP152/BAJ #1//TRCH/HUIRIVIS #1/3//SUP152/BAJ #1
12	BORL14/MUNAL #1	47	SUP152/BAJ #1/4//BAJ #1/3//KIRITATI//ATTILA*2//PASTOR/5//SUP152/BAJ #1
13	BORL14/MUNAL #1	48	SUP152/BAJ #1/4//BAJ #1/3//KIRITATI//ATTILA*2//PASTOR/5//SUP152/BAJ #1
14	BORL14/MUNAL #1	49	BAJ #1/3//KIRITATI//ATTILA*2//PASTOR*2/4//MUTUS*2//TECUE #1
15	BORL14/FITIS	50	WBL1*2//BRAMBLING//WBL1*2//BRAMBLING/3//2*BORL14
16	BORL14//BECARD/QUAIU #1	51	PRL/2*PASTOR//KACHU
17	FITIS/3//KACHU #1//KIRITATI//KACHU	52	WBL1*2//BRAMBLING//WBL1*2//BRAMBLING/3//2*BORL14
18	FITIS/3//KACHU #1//KIRITATI//KACHU	53	WBL1*2//BRAMBLING/3//KIRITATI//PBW65/2*SERI.1B*2/4//PRL/2*PASTOR*2//FH6-1-7
19	KACHU//WBL1*2//BRAMBLING/3//KACHU/KIRITATI	54	KIRITATI/WBL1//2*BLOUK #1*2/3//KACHU #1//KIRITATI//KACHU
20	SUP152/BAJ #1//KFA/2*KACHU	55	FRANCOLIN #1*2//HAWFINCH #1//2*MUCUY
21	SUP152/BAJ #1//KFA/2*KACHU	56	KACHU/KIRITATI//2*BORL14
22	FSD-08	57	UP2338*2//SHAMA//2*BAJ #1/3//BECARD//ND643/2*WBL1
23	BECARD//FRNCLN/3//ATTILA*2//PBW65*2//MURGA	58	WBL1*2//BRAMBLING//VORB/FISCAL/3//BECARD/5//ATTILA/3*BCN*2//BAV92/3//KIRITATI/WBL1/4//DANPHE
24	WBL1*2//KUKUNA//KIRITATI/2*TRCH/3//BAJ #1//AKURI	59	BORL14*2//MUNAL #1//FRANCOLIN #1
25	BABAX/LR42//BABAX*2/3//KUKUNA/4//CROSBILL #1/5//BECARD/6//KFA/2*KACHU	60	BORL14*2/3//WBL1*2//TUKURU//CROSBILL #1
26	BAJ #1*2//BORL14	61	BORL14*2//KFA/2*KACHU
27	PRL/2*PASTOR*2//MISR2, EGY/3//2*BECARD//ND643/2*WBL1	62	BORL14*2//KFA/2*KACHU
28	TRCH/SRTU//KACHU*2/5//UP2338*2//VIVITSI/3//FRET2/TUKURU//FRET2/4//MISR 1	63	BORL14*2//BECARD/QUAIU #1
29	PRL/2*PASTOR//KACHU	64	NADI
30	ROLF07*2/5//FCT/3//GOV/AZ//MUS/4	65	BORL14*2/6//BABAX/LR42//BABAX*2/3//KUKUNA/4//CROSBILL

	/DOVE/BUC*2/6/ATTILA*2/PBW65// MUU #1/3/FRANCOLIN #1		LL #1/5/BECARD
31	KSW/SAUAL//SAUAL/3/2*BORL14	66	Anaj-17
32	KFA/2*KACHU*2//SUP152	67	CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/HAR311/6 /BECARD/QUAIU #1/7/BECARD/QUAIU #1
33	KFA/2*KACHU*2//MISR 1	68	KACHU #1/KIRITATI//KACHU*2/3/GRACK/CHYAK
34	KFA/2*KACHU*2/3/ATTILA*2/PBW65 //MURGA	69	WBLL1*2/SHAMA//BAJ #1*2/6/ATTILA/3*BCN//BAV92/3/TILHI/4/SUP152/5/SUP1 52
35	KFA/2*KACHU*2/3/ATTILA*2/PBW65 //MURGA	70	CHIPAK*2/3/KSW/SAUAL//SAUAL

Statistical analysis

According to Kwon and Torrie [8], genetic (r_g) and phenotypic correlations (r_p) between two characters, x_1 and x_2 , were assessed. For Alpha lattice design, analysis of variance with combined data from the two seasons was done for each variant by using the procedure of Steel et al. [9]. According to Kwon and Torrie [8] both phenotypic and genotypic correlation coefficients were determined as given below:

$$r_g = \frac{Covg(X1, X2)}{\sqrt{Vg(X1) \cdot Vg(X2)}}$$

Where, COVG (X_1, X_2) = Genetic covariance among x_1 and x_2 ; VG (x_1) and VG (x_2) = Genetic variance for trait X_1 and X_2 , respectively. By using the method of Reeve (1955) (10) and Robertson (1959) (11), for statistical significance genotypic correlation was tested. If the absolute value of genotypic correlation is more than twice of its standard value then it is considered as significant.

$$r_p = \frac{Covp(X1, X2)}{\sqrt{Vp(X1) \cdot Vp(X2)}}$$

Where, COVp (X_1, X_2) = Phenotypic covariance among trait X_1 and X_2 ; VP (X_1) and VP (X_2) = Phenotypic variance for trait X_1 and X_2 , respectively. Computer software SAS (version 9.1) was used for this purpose. To estimate components of variance, combined analysis of variance procedure for Alpha lattice design for two locations was used to determine the presence of significant variation among standard parameter of plant. This was done by using computer program SAS (version 9.1) [12].

RESULTS AND DISCUSSION

Analysis of variance for days to heading revealed highly significant differences (Figure 1). Co-efficient of variance (1.48%) for days to heading was in acceptable range (Figure 1). Significance differences for days to heading represent the genetic variance among the wheat genotypes which can be effectively utilized for making selection for early maturity. Mean value for days to heading was 95.26. Maximum 100 days to heading were observed for genotypes No-17 followed by genotype No-48 and 7 with days to heading 100, 99 and 98 respectively. Similarly, the minimum 89, 90 and 91 days to heading were observed for genotype No-5, 4, and 2. The genotypes with minimum days to heading could be utilized in making selection for early maturity (Figure 2). Correlation analysis showed that days to heading has positive and highly significant correlation with plant height, spikelets/spike and grain yield (Table 7). The presence of positive and significant correlation can be used in making indirect selection. A previous study done by Bhanu et al. [13] also shows positive and significant association of the yield components with days to heading. Among genotypes non-significant differences were observed by analysis of variance for plant height (Figure 1). Co-efficient of variance for plant height was in acceptable range of 6.31% (Figure 1). Significance differences among wheat genotypes for plant height represent the presence of genetic variance which provide a chance for selecting desirable genotypes with medium plant for resolve the problem of lodging. Mean value for plant height was 85.43 cm. Maximum 94.2 cm were observed for genotype No. 21 followed by genotype No. 43 and 37 with plant height 94.2 cm, 93.85 cm and 90 cm, respectively. Similarly, the minimum 78 cm, 81 cm and 81.5 cm plant height were observed for genotype No. 25, 14 and 29, respectively (figure 2). Correlation analysis revealed that plant height has no significant positive correlation ($r = 0.01$) with grain yield only. However, rest of the traits also showed positive correlation with plant height (Table 7). The results of the our study are in contrast with the earlier study done by Kashif et al. (2004) they reported that plant height has non-significant positive correlation with grain yield [14]. For spike length statistical analysis presented highly significant differences amongst

genotypes (Figure 1). Co-efficient of variance for spike length was observed in acceptable range of 3.42% (Figure 1). Significance differences of spike length among wheat genotypes shows the genetic variances among genotypes which directly associated with grain yield. Mean value for spike length was recorded 7.99cm, maximum value 9.7cm, 9.85cm and 9.3cm were observed for genotype No-8 followed by genotype No-14 and 2 respectively. Similarly, the minimum value 5.6cm, 5.95cm and 6.27cm spike length was observed for the genotype No69, 56 and 57 respectively (figure 2). Correlation analysis showed that days to heading and plant height had positive and non-significant correlation with spike length, while highly significant correlation with other of the traits (Table 7). The results of current study are in close conformity with the earlier study of Akram *et al.* [15], they also stated significant association of spike length with yield and yield components traits [15]. Highly significant differences amongst the genotypes for spikelet per spike are revealed by analysis of variance (Figure 1). Co-efficient of variance for spikelets spike⁻¹ was observed in acceptable range of 5.07% (Figure 1). Mean value for spikelets spike⁻¹ was observed 14.48, maximum number of spikelets spike⁻¹ 19, 18, and 17 was observed for genotype NO-19, 18 and 14 respectively. Similarly, the minimum number of spikelets spike⁻¹ 11.1, 11.6, and 12 was observed for the genotype No-45, 6 and 27 respectively (figure 2). More the number of spikelets spike⁻¹ more will be number of grains formation and hence ultimately increase in the grain yield will occur. Spikelet's per spike has positive and highly significant correlation with days to heading and spike length by correlation analysis whereas with plant height and grain yield non-significant and positive correlation was observed (Table 7). Highly significant differences amongst genotypes are shown by analysis of variance for grain yield (Figure 1). Co-efficient of variance for grain yield was observed in acceptable range of 14.06% (Figure 1). Mean value for grain yield was observed 2962kg/ha, maximum grain yield 4037kg, 3862kg, and 3725kg was observed for genotype NO-19, 54 and 1 respectively. Similarly, the minimum grain yield 2162kg, 2225kg, and 2350kg was recorded for the genotype No-11, 25 and 24 respectively (figure 2). The prime objective of any breeding program is to increase grain yield. Therefore, we need to develop such genotypes which having more grain yield. Correlation analysis showed that grain yield has positive and highly significant correlation with days to heading, plant height and spike length, while has non-significant positive correlation with spikelets/spike (Table 7). Kudzelk *et al.* [16] also observed positive correlation of grain yield with other yield relating traits (16). Mean and Standard deviation for days to heading (DH), plant height (PH), spike length (SPKL), spikelets per spike (SPKT/SPK) and grain yield (GY) are given in table 2, 3, 4, 5 and 6 respectively.

Table 2. Mean and Standard deviation table for days to heading (DH)

Entry	DH		Entry	DH		Entry	DH		Entry	DH		Entry	DH	
	Mean	Std Dev		Mean	Std Dev		Mean	Std Dev		Mean	Std Dev		Mean	Std Dev
1	97	1.41	15	96.5	2.12	29	94.5	0.70	43	98.5	0.70	57	95.5	2.12
2	91.5	0.71	16	95.5	0.70	30	93	0	44	96.5	0.70	58	94.5	2.12
3	96	0	17	100	1.41	31	94.5	0.70	45	95	1.41	59	94	0
4	91	1.41	18	97	0	32	94	0	46	94.5	0.70	60	98.5	0.70
5	90	1.41	19	97	1.41	33	95	1.41	47	98.5	2.12	61	96.5	0.70
6	96	1.41	20	92.5	0.70	34	94	1.41	48	99.5	2.12	62	97	1.41
7	98	1.41	21	94	2.82	35	97	1.41	49	97.5	2.12	63	96	1.41
8	96	1.41	22	95.5	0.70	36	92	0	50	94.5	2.12	64	96	4.24
9	97	1.41	23	95	1.41	37	97	2.82	51	95.5	2.12	65	93.5	2.12
10	96	0	24	92.5	2.12	38	94.5	2.12	52	96	1.41	66	95.5	0.70
11	95.5	0.70	25	94.5	2.12	39	91.5	0.70	53	95.5	0.70	67	95	1.41
12	95	1.41	26	96.5	0.70	40	96	1.41	54	95.5	0.70	68	97	0
13	94	0	27	91.5	2.12	41	98.5	0.70	55	94	0	69	96	0
14	96	1.41	28	95	0	42	92.5	0.70	56	91.5	0.70	70	95	1.41

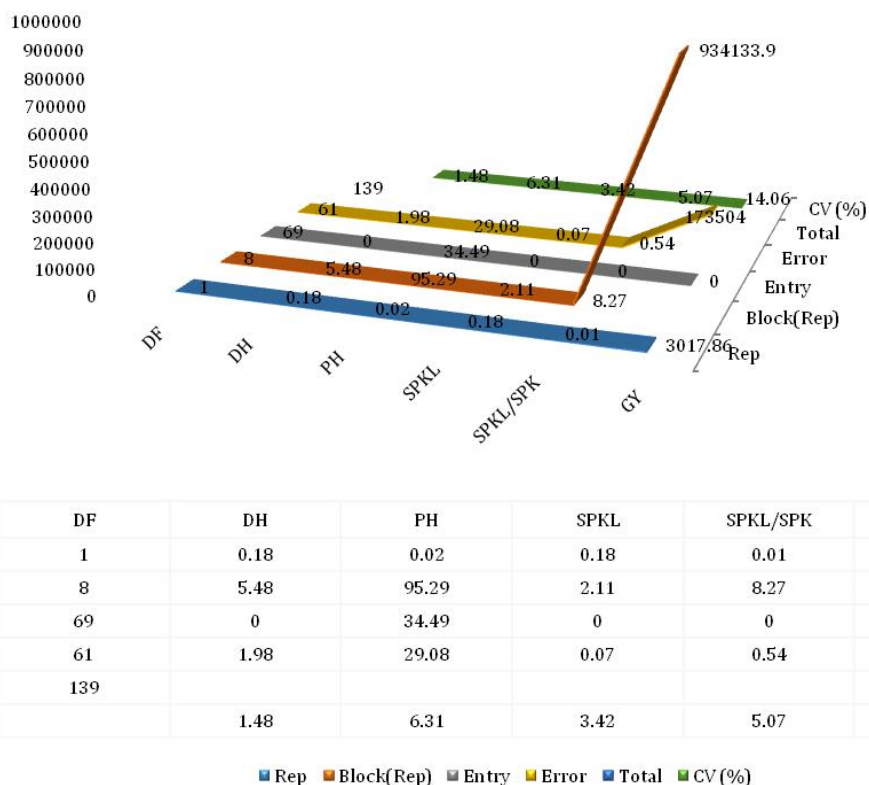
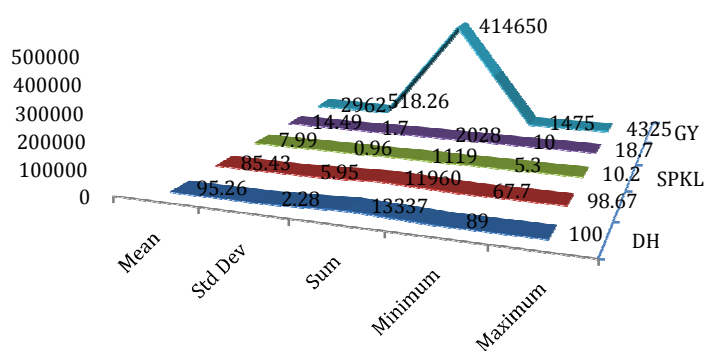


Figure 1. Mean square analysis for days to heading (DH), plant height (PH), spike length (SPKL), spiklets per spike (SPKT/SPK) and grain yield (GY).

Table 3. Mean and Standard deviation table for plant height (PH)

Entry	PH	Mean	Std Dev	Entry	PH	Mean	Std Dev	Entry	PH	Mean	Std Dev	Entry	PH	Mean	Std Dev
1	80.83	2.59	15	89.17	9.66	29	81.52	3.98	43	93.85	5.4	57	85.52	8.74	
2	80.33	3.30	16	82.83	11.54	30	84.25	6.71	44	93.5	3.5	58	87.52	9.64	
3	86	11.31	17	82.5	10.61	31	88.02	3.27	45	81.52	5.3	59	86.02	0.96	
4	86.99	13.67	18	88.15	9.68	32	84.98	6.62	46	86.85	2.61	60	85.82	0.68	
5	80.16	1.178	19	88.83	0.23	33	83.67	6.59	47	86.5	6.36	61	88.16	1.64	
6	80.33	0.471	20	97.58	1.53	34	85.16	8.25	48	90.15	3.04	62	83	2.82	
7	84.98	14.59	21	94.17	0.23	35	89.15	3.04	49	87.85	2.62	63	83.15	3.04	
8	83.67	10.84	22	90	5.65	36	83.67	3.77	50	83.85	5.87	64	92	2.82	
9	88.98	0.97	23	85.16	5.42	37	90.18	2.14	51	83.18	3.56	65	89.5	7.77	
10	85.33	0.47	24	84.67	3.77	38	74.85	10.1	52	80.15	1.20	66	84.67	6.12	
11	80.5	6.36	25	78.33	2.35	39	83.98	3.27	53	91.83	0.23	67	86.5	3.53	
12	84.85	2.61	26	86.52	3.08	40	88.35	2.33	54	89.17	0.23	68	84.83	7.30	
13	86.52	3.98	27	89	1.41	41	83	9.89	55	82.35	2.33	69	76.98	11.76	
14	81.68	2.80	28	84.17	5.42	42	80.02	1.86	56	82.08	4.83	70	80.67	0.94	



	Mean	Std Dev	Sum	Minimum	Maximum
DH	95.26	2.28	13337	89	100
PH	85.43	5.95	11960	67.7	98.67
SPKL	7.99	0.96	1119	5.3	10.2
SPKT/SPK	14.49	1.7	2028	10	18.7
GY	2962	518.26	414650	1475	4325

■ DH ■ PH ■ SPKL ■ SPKT/SPK ■ GY

Figure 2. Descriptive statistics for days to heading (DH), plant height (PH), spike length (SPKL), spiklets per spike (SPKT/SPK) and grain yield (GY).

Table 4. Mean and Standard deviation table for spike length (SPKL)

Entry	SPKL		Entry	SPKL		Entry	SPKL		Entry	SPKL		Entry	SPKL	
	Mean	Std Dev		Mean	Std Dev		Mean	Std Dev		Mean	Std Dev		Mean	Std Dev
1	8.60	0.14	15	7.75	0.35	29	8.1	0.14	43	8.3	0	57	6.25	0.35
2	9.3	0	16	9.7	0.14	30	9.25	0.07	44	8.5	0	58	6.95	0.35
3	7.8	0.14	17	8.25	0.35	31	9.3	0	45	7.3	0	59	7.1	0.14
4	9	0	18	10.1	0.14	32	7.85	0.21	46	7.2	0	60	7.2	0
5	8.75	0.35	19	9.45	0.35	33	8.25	0.35	47	9.4	0.14	61	8.75	0.35
6	6.95	0.35	20	8	0	34	7.8	0.28	48	9.3	0.14	62	7.5	0.28
7	6.85	0.49	21	7.25	0.35	35	7.2	0	49	8.4	0.14	63	7.4	0.14
8	9.85	0.21	22	7.25	0.07	36	7.25	0.07	50	7.25	0.07	64	8.25	0.35
9	8.115	0.12	23	8.15	0.21	37	8.4	0.14	51	7.5	0	65	6.85	0.49
10	9.1	0.14	24	6.85	0.21	38	8.2	0	52	7.65	0.21	66	8.15	0.21
11	8	0	25	8.5	0	39	7.15	0.21	53	7.5	0	67	8.1	0.14
12	8.6	0.14	26	8.4	0.84	40	7.5	0	54	9.25	1.06	68	6.6	0.14
13	8.7	0	27	7.4	0.14	41	7.75	0.07	55	7.4	0.14	69	5.65	0.49
14	9.7	0	28	8	0	42	8.15	0.21	56	5.95	0.35	70	7.4	0.14

Table 5. Mean and Standard deviation table for spikelet per spike (SPKT/SPK)

Entry	SPKT/SPK		Entry	SPKT/SPK		Entry	SPKT/SPK		Entry	SPKT/SPK		Entry	SPKT/SPK	
	Mean	Std Dev		Mean	Std Dev		Mean	Std Dev		Mean	Std Dev		Mean	Std Dev
1	14.85	0.21	15	14.65	0.49	29	16.35	0.49	43	14.65	0.49	57	14.35	0.92
2	14.6	0.14	16	16	1.41	30	15.65	0.49	44	14.85	0.21	58	13	0
3	13.3	0	17	15.3	0	31	16.15	0.21	45	11.15	0.21	59	13	0
4	14.5	0.28	18	17.65	0.92	32	18	0	46	11.5	0.71	60	13.85	0.21
5	12.45	0.35	19	18.5	0.28	33	15.15	0.21	47	16.15	0.21	61	15.5	0.28
6	11.65	0.49	20	15	0	34	14.7	0	48	15.7	0	62	14.85	0.21
7	14	0.42	21	13.65	0.49	35	14.7	0	49	15	0	63	13.5	0.28
8	16.3	0	22	13	0.99	36	13.15	0.21	50	13	0	64	15	0.99
9	14	0.42	23	14.15	0.21	37	13.85	4.45	51	14	0	65	12.5	0.28
10	15.85	0.21	24	12.85	0.21	38	16.65	0.49	52	12.85	0.21	66	14.5	0.28
11	14.85	0.21	25	16.5	0.71	39	12.65	0.49	53	14	0.42	67	16.3	1.41
12	15	0.42	26	17	0.42	40	14	0	54	13.35	2.33	68	14.15	0.21
13	16.15	0.21	27	12	0	41	15	0	55	14.3	0	69	12	0
14	17.15	0.21	28	15	0	42	14.3	0	56	10.15	0.21	70	14.7	0

Table 6. Mean and Standard deviation table for grain yield (GY)

Entry	GY		Entry	GY		Entry	GY		Entry	GY		Entry	GY	
	Mean	Std Dev		Mean	Std Dev		Mean	Std Dev		Mean	Std Dev		Mean	Std Dev
1	3725	742.46	15	3112.5	17.68	29	2812.5	88.39	43	3712.5	53.03	57	2950	459.61
2	2937.5	88.38	16	3700	141.42	30	2650	176.77	44	3350	35.355	58	2800	70.71
3	3050	424.26	17	2850	247.48	31	3525	848.52	45	2950	636.39	59	2562.5	17.68
4	2737.5	866.20	18	2600	353.55	32	2987.5	88.38	46	3137.5	548.01	60	2937.5	88.38
5	2787.5	441.94	19	4037.5	406.58	33	2412.5	618.72	47	3237.5	159.09	61	2675	106.06
6	2950	919.23	20	2850	494.97	34	2775	388.91	48	3237.5	229.81	62	2612.5	300.52
7	3625	530.33	21	2862.5	371.23	35	2450	141.42	49	2887.5	123.74	63	2800	601.04
8	3325	282.84	22	2875	530.33	36	3450	318.19	50	2625	459.62	64	2950	530.33
9	3137.5	159.10	23	2837.5	477.29	37	3575	35.35	51	2762.5	441.94	65	2587.5	760.14
10	2637.5	441.94	24	2350	388.91	38	3137.5	17.68	52	2487.5	689.43	66	3000	1131.37
11	2162.5	229.81	25	2225	141.42	39	2787.5	53.03	53	2975	530.33	67	3137.5	512.65
12	3537.5	88.38	26	3075	70.71	40	2462.5	1396.53	54	3862.5	229.81	68	2837.5	88.38
13	3050	671.75	27	3037.5	1042.98	41	3150	388.91	55	2562.5	17.68	69	3100	813.17
14	3400	106.1	28	2937.5	53.03	42	3075	35.35	56	2600	459.61	70	2325	106.07

Table 7. Phenotypic (below diagonal) and genetic (above diagonal) correlation among days to heading (DH), plant height (PH), spike length (SPKL), spikelets per spike (SPKT/SPK) and grain yield (GY).

Traits	DH	PH	SPKL	SPKTSPK	GY
DH	1	0.66**	0.14	0.40**	0.47**
PH	0.15	1	0.64**	0.33**	0.01
SPKL	0.12	0.10	1	0.76**	0.46**
SPKTSPK	0.31**	0.02	0.70**	1	0.20
GY	0.23**	0.21**	0.31**	0.14	1

CONCLUSIONS AND RECOMMENDATION

Analysis of variance showed the significant differences for morphological and yield related traits which depicts the presence of genetic variability and hence could be exploited in future breeding program. Analysis of correlation shown positive significance of grain yield with days to heading, length of spike and thousand grain weight however positive and non-significant correlation was shown for grain yield with plant height and spikelet per spike. For yield improvement traits having positive correlation with grain yield should be utilized. On the basis of mean performance, the genotypes No. 2, 4, and 5 showed early maturity and could be used as indirect criteria that can be used in onward breeding programs. Among the genotypes the Line No. 1, 19, and 54 showed superior performance for grain yield and could be recommended for commercial cultivation after further evaluation at multi-locations.

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