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Quantitative analysis of yield contributing trait in F$_4$ segregating generation of wheat (*Triticum aestivum* L.)

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Abstract
The present investigation was conducted to examine the genetic variability among 30 genotypes of wheat, during *Rabi*-2016-17 under randomized block design with three replications. The data were recorded for fourteen quantitative characters to obtain estimates of variability, heritability, genetic advance and correlation coefficient. Significant differences were observed among the genotypes for all the characters studied. A perusal of coefficient of variation showed that difference between PCV and GCV was high for most of the characters studied indicating more effect of environment on the expression of these characters. The genotypic coefficient of variation (GCV) was observed high for plant height followed by, frist node to spike, Tillers per plant, seed yield per plant and spike length. The phenotypic coefficient of variation (PCV) was exhibited high by Plant height followed by tillers per plant, spike length and seed weight per plant. Heritability was observed high for plant height followed by 1000 seed weight and flage width. Genetic advance was recorded moderate for plant height. Seed yield exhibited positive and significant correlation with 1000 weight, spike length, frist node to spike, spiklets per plant, tillers per plant, plant height and biological yield at genotypic level. Therefore, selection can be exercised upon these characters for yield improvement of wheat.

Keywords: wheat, genetic variability, correlation coefficient

Introduction
Wheat (*Triticum aestivum* L.) is the 2nd most important cereal in India after rice and its improvement in the productivity has played a key role in making the country self-sufficient in food production (Mahpara *et al*., 2008) [14]. It provides food for 36% of the global population and contributes 20% of the food calories (Singh and Choudhary, 2006). Wheat (*Triticum aestivum* L.) is considered to be one of the first domesticated crops and has been a staple food in North Africa, West Asia and Europe for more than eight thousand years (Curtis, Rajaram, and Macpherson 2002) [6] and is the single most important crop planted for human food and animal feed (Colmer, Flowers, and Munns 2006; Akman 2009) [5, 3]. It has been reported that wheat is a staple food for one third of the world's population and an important source of carbohydrates, fibre, vitamins, proteins, and provides nutrition for both human beings and animals (Basra, Pannu, and Afzal 2003) [4]. The tetraploid, *Triticum durum* (Desf) and diploid, *Triticum* dicoccum and *Triticum monococcum*. Globally *Triticum aestivum* is most important species which has been evolved from the cross between genera *Triticum* and Aegilops (goat grass) and possessing AABBDD genome (Levy and Feldman, 2002) [12]. The crop has been under cultivation in a wide range of ecosystem and perhaps considered as the oldest domesticated plant holding largest acreage globally and second largest produced commodity next to rice. Wheat is one of the most important cereals in India. Bread wheat contributes approximately 95% to total production while another 4% and 1% comes from durum wheat and dicoccum wheat respectively. In the past decade, there has been marginal increase in the productivity of wheat, particularly under those environments which are relatively favorable for growth and development of wheat (Joshi *et al*., 2007) [10]. In India, wheat is the second most important crop after rice occupying 29.90 million ha, with production of 94.88 million tones with an average productivity of 3177 kg per hectare (DWR, 2012) [8]. This reduction in yield is due to the sub-optimal temperature during the germination, stand establishment and supra-optimal during the reproductive growth. (Sattar *et al.,* 2010). Germination is a critical process, as temperature below 12°C result in poor and uneven emergence (Timmermans *et al.,* 2007). The production rate has remained better in China (2.6%) while India (1.28%) and U.S (1.25%) are at par in the growth of wheat production. Average yield of wheat in the world is around 2.6 tons/ha and the yield in India is almost at par with it at 2.52 tons/ha (FAO, 2011) [9].

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The major States where, wheat is cultivated are Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Rajasthan and Bihar. Uttar Pradesh is the highest producer of wheat with 24.3 million tons (mt), followed by Punjab (14.7 mt) and Haryana (9.1 mt) (Singh, 2010).

Keeping the above facts in mind especially the growing habit of the farmers of Eastern Utter Pradesh, the present investigation was carried out in late sown conditions to obtain information on the following objectives:-

- To identify the best genotype based on mean performance for yield
- To assess genetic variability parameters for different quantitative traits in wheat
- To find out correlation between yield and its components traits.

Materials and Methods
The experiment was carried out at Field Experimentation Centre of the Department of Genetics and Plant Breeding, (Naini Agricultural Institute,) Sam Higginbottom University of Agriculture, Technology & Sciences, Allahabad (UP) during Rabi-2016-17. The details of experimental materials are as follows.

Experimental Materials
Experimental materials for the present study consists of 30 genotypes of Wheat were obtained from Department of Genetics and Plant Breeding SHUATS, during *Rabi* 2016-2017. These genotypes exhibited wide spectrum of variation for various agronomic and morphological characters.

Design of Experiment
These genotypes were evaluated in completely Randomized Block Design with three replications during *Rabi* 2016 at Agriculture Research farm Allahabad, SHUATS, Allahabad (U.P).

Fertilizer Applications
The recommended doses of fertilizer @ 120:60:60 kg (N: P: K) per ha. was applied. Total quantity of phosphorous and potash and 25% of total nitrogen was applied in the soil at the time land preparation. 50% of total nitrogen was top dressed at tillering stage and the remaining 25% nitrogen was top dressed at panicle initiation stage.

Characters Studied
The observations were recorded on five randomly selected competitive plants in each entry of each replication. which were recorded on plot basis. The data were recorded for following characters. Plant height (cm). Number of tillers per plant. Spike length (cm)**.** Frist node to spike. Flag leaf length (cm). Flag leaf width**,** Length of peduncle, Spikelets per plant, Biological yield per plant (g)**,** 1000 seed weight (g), Seed yield per plant (g).

Analysis of Variance (ANOVA)
The analysis of variance was worked out to test the significance of F and t-tests. It was carried out according to procedure of RBD analysis for each character as per methodology suggested by Panse and Sukhatme (1967).

Genotypic Variance
The genotypic variance (VG or σ^2_g) is the variance due to the genotypes present in the population. The formula used for calculation of genotypic variance was

$$VG = \frac{V_t - EMS}{r}$$

Phenotypic Variance
Phenotypic variance (VP or σ^2_p) denotes the total variance present in a population for particular character and is calculated by following formula
VP = Genotypic variance (VG) + Error variance (VE)

Coefficient of Variation
It is the measure of variability evolved. Coefficient of variation is the ratio of standard deviation of a sample to its mean and expressed in percentage.
CV (%) = Standard deviation/Mean X 100

Genetic Advance
Genetic advance is the improvement in mean genotypic value of selected plants over the parental population. The estimates of genetic advance were obtained by the formula given by Lush (1949) [13] and Johnson *et al.* (1955) [11].

$$G.A. = K.\sigma p.h^2$$

Correlation Coefficient Analysis
Single correlation coefficients were computed at genotypic and phenotypic levels between pair of characters adopting following formula given by Al-Jibouri *et al.* (1958) [2].
Genotypic correlation between traits X and Y:

$$r_{xy}(g) = \frac{\sigma^2_g(xy)}{\sqrt{\sigma^2_{xg} \times \sigma^2_{yp}}}$$

Phenotypic correlation between traits X and Y:

$$r_{xy}(p) = \frac{\sigma^2_p(xy)}{\sqrt{\sigma^2_{xp} \times \sigma^2_{yp}}}$$

Result and Discussion
Analysis of Variance
The mean sum of square values for fourteen characters *viz.*, plant height (cm), grain per spike, tillers per plant, spike length (cm), 1000 seed weight (g), biological yield (g), and grain yield per plant (g) were subjected to analysis of variance for experimental design.

The mean sum of squares for the character studied are presented in Table-1. The mean sum of squares due to genotypes were significant for all the fourteen characters studied, suggesting that the genotypes selected were genetically variable and considerable amount of variability existed among them. Similar findings in wheat has also reported by Dwivedi *et al.* (2002) and Asif *et al.* (2004).

Table 1: Analysis of variance for different quantitative and physiological 11characters in 30 genotypes of wheat.

S. No	Characters	Mean Sum of Squares		
		Replications	Genotypes	Error
		(df = 2)	(df = 29)	(df = 58)
1.	Plant height	6.14	406.48**	11.65
2.	Frist node Per spike	0.43	36.63**	0.48
3.	Tillers per plant	2.05	3.29**	0.87
4.	Spike length	0.45	3.67**	0.45
5.	Spikelet per plant	0.69	43.77**	0.96
6.	Flage leaf leaf length	2.05	19.7**	2.60
7.	Peduncle length	4.79	46.55**	1.84
8.	Flage width	0.51	0.20**	0.00
9.	1000 seed weight	0.88	3.50**	1.25
10.	Biological yield	0.26	12.57**	4.25
11.	Seed yield per plant	3.43	12.77**	2.85

** Significant at 1% level of significance

The variability exploited in breeding programme is desired from the naturally occurring variants and wild relative of main crop species as well as from strains and genetic stock artificially developed by human efforts. Through this study, an attempt was made to assess the mean performance and extent of variability in 30 wheat genotypes. Table 2 depicts the mean performance of 30 wheat genotypes of fourteen characters along with standard error of difference and critical difference, which is elaborated as under.

Plant height exhibited a range from 45.33 (SBW-13) to 95.33cm (SBW-2) with grand mean of 77.97 cm. Dwarf plant observed in SBW-13 (45.33cm) while tallest plant was observed in genotype SBW-2 (95.33) followed by genotypes SBW-19 (94.33cm), SBW-12 (93.66cm), SBW-8 (92.00cm) and SBW-29 (92.00cm). Spike per plant revealed that it ranged from 27.33 (SBW-15) to 40.80 (SBW-2) with grand mean of 34.26. Highest spike per plant were recorded for genotype SBW-2 (40.80) followed by genotypes SBW-6 (40.13), SBW-23 (61.57), SBW-8 (39.56). Frist Node to Spike revealed that it ranged from 8.93 (SBW-17) to 24.16 (SBW-2) with grand mean of 18.1. frist Node to Spike were recorded for genotype SBW-2 (24.16) followed by genotypes SBW-7 (22.46), SBW-6 (21.92), tillers per plant revealed that it ranged from 6.00 (SBW-7) to 9.81 (SBW-2) with grand mean of 7.63 The experimental data on spike length revealed that it ranged from 8.16 (SBW-10) to 11.76cm (SBW-2) with grand mean 10.03 cm. The longest Spike was recorded for genotype SBW-2 (11.76cm) followed by genotype SBW-12 (11.50cm), Flage Leaf Length ranged from 19.66 (SBW-16) to 30.66 (SBW-2) with grand mean of 24.00. Highest Flage Leaf Length were recorded for genotype SBW-2 (33.66) followed by genotypes SBW-12 (28.68), Data for flage width revealed that it ranged from 1.12 (SBW-7) to 2.26 g/spike (SBW-2) with grand mean of 1.67g/spike. Highest grain weight per spike was recorded for genotype SBW-2 (2.26g/spike) followed by genotypes SBW-18 (1.92g/spike), Data for flage width revealed that it ranged from 1.12 (SBW-7) to 2.26 g/spike (SBW-2) with grand mean of 1.67g/spike. Highest grain weight per spike was recorded for genotype SBW-2 (2.26g/spike) followed by genotypes SBW-18 (1.92g/spike), Biological yield per plant ranged from 15.66 (SBW-15) to 24.16g (SBW-2) with grand mean of 19.91g. Highest biological yield recorded for genotype SBW-2 (24.16g) followed by genotypes SBW-4 (23.70g), SBW-7 (22.46g) and SBW-19 (21.93g), seed yield per plant ranged from 14.30 (SBW-17) to 22.33 g /plant (SBW-2), with grand mean of 18.20g/plant. Highest grain yield was recorded for genotype SBW-2 (22.33g/plant) followed by genotypes SBW-6 (21.43g/plant),

Table 2: Mean performance of 11 characters of 30 wheat genotypes during Rabi, 2016-17

S. No	Genotypes	Plant height (cm)	No of Spikets / plant	No. of tillers /plant	Spike length (cm)	Peduncle length (cm)	Flage width (cm)	Flage Leaf length	Biological Yield/ Plant (g)	First Node to spicke	Seed Yield/ plant (g)	1000 Grain yield (g)
1	SBW1	68	40.73	7.00	11.06	36.70	1.68	28.13	22.00	21.61	19.10	52.66
2	SBW2	95.33	40.00	9.00	11.76	41.36	2.26	30.66	20.13	24.16	22.33	55.00
3	SBW3	78.00	33.43	7.66	8.96	34.60	1.79	22.66	24.16	16.46	16.46	52.33
4	SBW4	79.66	36.30	8.00	10.00	37.83	1.42	23.33	23.70	21.92	15.66	52.86
5	SBW5	75.33	37.00	7.66	10.50	40.36	1.98	26.00	17.76	19.33	19.33	51.96
6	SBW6	94.00	40.13	9.66	11.23	40.38	1.98	27.33	18.33	21.2	21.43	54.36
7	SBW7	68.66.	35.50	6.00	10.40	33.30	1.12	24.10	22.46	22.46	19.73	52.00
8	SBW8	92.00	39.56	9.66	11.16	40.36	1.99	27.33	21.46	21.46	20.60	53.04
9	SBW9	66.33	33.30	7.00	8.40	36.03	1.38	21.33	19.30	17.73	16.10	53.66
10	SBW10	66.66	34.40	7.33	8.16	33.56	1.90	22.00	20.23	20.23	19.70	50.36
11	SBW11	74.00	37.66	7.00	10.23	35.30	1.85	22.66	19.56	17.73	17.73	53.33
12	SBW12	93.66	39.00	9.33	11.50	39.56	2.15	28.66	18.83	16.10	20.50	53.36
13	SBW13	45.33	31.76	6.66	9.43	24.93	1.54	21.33	17.73	9.26	17.36	51.66
14	SBW14	70.00	28.36	7.00	8.33	34.28	1.97	25.33	17.00	17.00	17.00	52.67
15	SBW15	68.66	27.33	6.00	8.59	38.20	1.59	23.33	15.66	19.83	19.83	53.33
16	SBW16	75.00	34.36	6.33	11.26	35.66	1.67	19.66	16.81	16.81	16.81	51.33
17	SBW17	57.33	28.06	9.00	10.70	24.53	1.56	19.80	20.46	8.93	14.30	52.66
18	SBW18	81.00	33.30	7.6	10.60	36.20	1.92	23.23	17.20	16.13	16.13	51.96
19	SBW19	94.33	38.33	8.33	11.66	34.40	1.40	26.33	21.93	20.50	20.06	52.26
20	SBW20	75.00	31.46	8.00	8.26	34.00	1.84	23.00	20.16	19.66	19.66	52.30

21	SBW21	88.00	28.63	7.00	8.36	36.30	1.39	23.00	19.90	18.96	18.96	50.96
22	SBW22	83.00	31.56	6.00	9.60	37.30	1.30	23.33	19.63	18.06	18.33	53.00
23	SBW23	73.00	31.56	7.6	9.34	35.53	1.94	23.33	19.93	20.50	17.73	52.43
24	SBW24	73.33	32.73	7.00	10.26	33.36	1.58	23.80	18.43	15.53	15.53	53.50
25	SBW25	83.66	35.00	8.00	10.26	35.53	1.55	23.00	18.36	16.20	16.20	52.00
26	SBW26	76.00	30.90	8.33	8.83	30.33	1.39	22.66	20.80	15.13	17.10	53.33
27	SBW27	82.66	40.80	7.00	10.76	32.13	1.82	22.00	20.76	14.40	14.40	52.33
28	SBW28	84.00	32.93	7.33	11.00	38.80	1.48	24.00	20.36	19.43	18.50	51.03
29	SBW29	92.00	37.20	9.00	10.00	40.46	1.70	25.66	21.43	18.50	19.83	52.06
30	SBW30	84.33	33.20	7.33	10.46	37.93	1.60	23.00	21.10	21.23	19.96	52.96
	Mean	77.97	34.42	7.63	10.03	35.63	1.67	24.00	19.91	18.10	18.20	52.75
	S.E.	1.97	0.56	0.53	0.38	0.78	0.16	0.93	1.19	0.40	0.97	0.64
	C.D.5%	5.57	1.60	1.52	1.09	2.22	3.58	2.63	3.37	1.60	2.7	1.83
	Range	45.33-95.33	27.33-40.80	6.00-9.66	8.16-11.76	24.53 -41.33	1.12-2.26	19.66-30.66	15.66-24.16	8.93-24.16	14.30-22.33	50.36-55.00

Table 3: Five best genotypes identified on the basis of per se performance for grain yield per plant.

S. No	Characters / Genotypes	1000 Grain yield (g)	Seed yield per plant(g)	Days to maturity	Number of tillers/plant	Spikelet/plant
1	SBW-2	55.00	22.33	109.33	9.81	40.00
2	SBW-6	54.36	21.43	111.00	11.23	40.13
3	SBW-8	53.66	20.60	110.00	9.66	39.56
4	SBW-12	53.36	20.50	110.66	9.33	39.00
5	SBW-19	52.67	20.06	107.00	8.33	38.33

Estimates of phenotypic variance and genotypic variance

A wide range of variance was observed for all the characters. The highest variability (VG) was recorded for plant height (131), while moderate values were observed for biological yield (2.77), spikelet per plant (14.26), highest variability (VP) was recorded for plant height (143.26), while moderate values were observed for biological yield (7.02), followed by spikelet pre plant (15.32). Whereas 1000 grain weight (2.00),

Phenotypic and genotypic coefficient of variation

Phenotypic coefficient of variation (PCV) was observed for all the traits ranged from 2.68 (1000 seed weight) to 16.98 (Tillers per plant). Higher magnitude of PCV was recorded for tillers per plant (16.98), plant height (15.34), seed yield per plant (13.63), biological yield (13.31) spike length (12.31), while moderate estimates were observed for and flage leaf length(12.01%), peduncle(11.48), and low estimates of phenotypic coefficient of variation was observed for flage width (8.95), frist node per spike (6.49), 1000 seed weight

(2.68), genotypic coefficient of variation (GCV) was observed for all the traits ranged from to 14.71 (plant height). Higher magnitude of PCV was recorded for plant hight (14.71), tillers per plant (11.76), and moderate magnitude of genotypic coefficient of variation was plant height (14.71), seed yield per plant (9.99) and spike length (10.33), while low estimates of genotypic coefficient of variation values was observed in biological yield (8.36), spike per plant (11.2), 1000 seed weight (1.64),

Correlation Coefficient: The results showed that, in general, the genotypic correlation coefficients (rg) were higher than the phenotypic correlation coefficients (rp) which indicated that association among these characters was under genetic control and indicating the preponderance of genetic variance in expression of characters.

Phenotypic Coefficient of Correlation for different quantitative characters in wheat genotypes.

Table 4

Characters	Flag width	Spike length	Penducle length	Flage leaf length	Spicklets per plant	Frist Node to spick	Plant height (cm)	Tillers/ plant	Biological yield	Seed yield per plant	1000 seed weight
Flag width	1.00	-0.12*	-0.09*	-0.24*	-0.10**	- 0.046	0.21	-0.13	-0.13	- 0.071	0.129
Spike length		1.00	0.20	0.19	0.54**	-0.03	0.29**	- 0.2	-0.1	0.10	0.2
Penducle length			1.00	0.49**	0.42**	0.85**	0.69**	-0.07	0.31**	0.56**	0.10
Flage leaf length				1.00	0.32**	0.37**	0.47**	0.01	0.14	0.11	0.24**
Spicklets per plant					1.00	0.31**	0.34**	-0.11	0.14	0.07	0.02
Fris tNode to spick						1.00	0.57**	-0.06	0.45**	0.71**	0.13
Plant height (cm)							1.00	0.16	0.23*	0.22*	0.56**
Tillers/ plant								1.00	-0.06	-0.02	0.38**
Biological yield									1.00	0.35**	0.67
Seed yield per plant										1.00	0.67
1000 seed weight											1.00

Genotypic Coefficient of Correlation for different quantitative characters in wheat genotypes.

Grain yield per plant showed the positive significant genotypic association with flage leaf length (0.37**), Tillers per plant (0.30**), biological yield (0.30**), Pendulam length (0.20**) Frist Node to spike (0.17**)Flage leaf length showed the positive significant phenotypic (0.24*), spike length (0.12), peduncle length (0.09), spiklets per plant (0.10), 1000 seed weight (0.12), and plant height (0.02).

Characters	Flag width	Spike length	Penducle length	Flage leaf length	Spicklets per plant	Frist Node to spick	Plant height (cm)	Tillers/ plant	Biological yield	Seed yield per plant	1000 seed weight
Flag width	1.00	0.16	0.14	0.41	0.20	- 0.06	0.12	0.32*	-0.11	- 0.10	0.15
Spike length		1.00	0.31	0.31*	0.67**	0.04	0.39	0.02	-0.01	-0.06	0.13
Penducle length			1.00	0.65	0.44	0.92**	0.76*	-0.06	0.41*	0.70	0.20
Flage leaf length				1.00	0.38*	0.45*	0.47**	-0.04	0.32*	0.39	0.37*
Spicklets per plant					1.00	0.31*	0.38**	-0.15	0.22	0.10	0.03
Fris tNode to spick						1.00	0.6*	-0.13	0.62	0.95	0.17
Plant height (cm)							1.00	0.20	0.37	0.37*	0.15
Tillers/ plant								1.00	0.02	-0.28	0.30
Biological yield									1.00	0.76	0.30
Seed yield per plant										1.00	0.11
1000 seed weight											1.00

*,** significant at 5% and 1% level of significance

Conclusion
Genotypes SBW-2 and SBW-6 were found best for grain yield and genotypes SBW-8, SBW-12, SBW-19, were found not suited for late sown conditions. Number of grains per spike, tillers per plant and grain filling period can be selected as selection criteria for yield improvement in wheat, as they showed positive significant correlation with yield.

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