Study of genetic variability, Heritability, Correlation and path Coefficient Analysis for yield and it is related components and rust resistance in F_5 and F_6 population of bread wheat (*Triticum aestivum* L.)

ABSTRACT

Aims: To study the variability for morphological traits and yellow rust resistance.

Study design: Randomized block design (RBD) at a 5% level of significance.

Place and Duration of Study: The study was undertaken in the Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar during the 2018-2019 and 2019-2020 cropping seasons

Methodology: A total of 210 F_5 and F_6 progenies from the cross WH711 (susceptible) x PBW698 (resistant) including parents were evaluated) in a single row of 1m length and 11 different morphological traits were included in the study. Infector rows were planted and artificial inoculation (using spray method) was carried out under field conditions using Pst (Puccinia striformis) isolate as a source of inoculums.

Results: The analysis of variance was highly significant ($P<0.01$) for yield and yield-related components. In F_5 and F_6 generations, the high to moderate PCV and GCV were recorded for harvest index, biological yield/plant, 1000-grain weight, grain yield/plant, number of spikelets/spike, and number of grains/spike. The high heritability coupled with high genetic advance as a percent of mean was observed for the number of grains/spike, number of spikelets/spike, 1000-grain weight, biological yield/plant, harvest index, and grain yield/plant in F_5 and F_6 generations. The correlation coefficient studies revealed that grain yield/ plant is significantly correlated with all yield-attributing characters except with days to heading in F_5 and plant height in F_6 generation. The path analysis recommended that all the traits had maximum positive direct contribution towards grain yield/plant except plant height and days to heading in F_5 and F_6 generation. The 135 and 148 progenies showed no infection in F_5 and F_6 generations.

Conclusion: The presence of substantial variability has existed among the tested wheat lines and the possibility of improving yield and other desirable traits through selection or hybridization. Phenotypic and genotypic correlation analysis showed a positive correlation of grain yield with important quantitative characters. Hence, improving one or more of these traits could result in a high grain yield/ plant.

Keywords: Bread Wheat, Genetic Variability, GCV, PCV, Heritability, Yield Component and Yellow Rust.

1. INTRODUCTION

Wheat (*Triticum* sp. L.) is the most significant food crop used by nearly 40% of the whole world's population [1, 2]. Wheat occupies a notable position among food grain crops of the world not only in terms of acreage and in terms of production but also its versatile adaptation to a wide range of agro-climatic conditions, wheat production of India is 107.20 MT from 29.55 Mha area with the productivity of 3.45 Tha and Haryana occupied about 2.510 Mha with a total production of 11.65 MT and productivity of 4.64 Tha [3].

As the world population is increasing day by day, it is essential to increase heat production up to 60% by 2050 to meet all the requirements [4, 5, 6]. The high-yielding wheat cultivars are a major objective of wheat breeding programs and their success largely depends on genetic variability and heritability of related traits under study which is used as a dependable tool to the breeder for improvement and quantitative traits to provide an estimation of genetic variability among wheat genotypes.

The estimate of heritability is mostly used to quantify the proportion of phenotypic variation that is controlled by genotype. In practice, heritability is greatly influenced by the genetic architecture of the trait of interest, which is governed by the number of genes, the magnitude of their effect and the type of gene action associated with phenotypes. Better knowledge of genetic architecture often has the greatest impact on improving genetic gain. The genotypic and phenotypic coefficients of variations help to understand the clear picture of existing variability in the populations, whereas, the estimates of heritability and genetic advance provide the indices of transmissibility of characters. Thus, estimates of variability parameters like coefficients of variation, heritability, and genetic advance are very useful for devising a suitable selection strategy for evolving high-yielding progenies in wheat crops. The estimate of GCV and PCV were classified as low, medium and high [7]. Genetic advance has considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection [8]. A high magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characteristics [9]. The present study was designed to evaluate genetic variability and heritability parameters of yield and its component traits in advanced breeding lines of bread wheat.

2. MATERIAL AND METHODS

The study was carried out in the Department of Genetics & Plant Breeding, CCS Haryana Agricultural University in Hisar, Haryana, during two crop seasons (2018-2019 and 2019-20). The research site is located between 29°09'01.3" N latitude, and 75°41'33.6" E longitudes, receiving high to low rainfall of 160 mM to 4 mM in the month of August and April.

2.1 PLANT MATERIALS AND EXPERIMENTAL DESIGN

Genetic material consisted of 210 F_5 and F_6 progenies derived from cross WH 711 x PBW 698. The PBW 698 is resistant to yellow rust, whereas, WH 711 is susceptible to yellow rust. The experiment was laid out in randomized complete block design (RCBD) with two replications. Each line is planted in a single row of 1 meter and 25 cm space between rows. The sowing was done on (date) by hand.

2.2 DATA COLLECTION

The data was collected randomly from five plants in each row for all the characters and tagged before heading *i.e.* days to heading (DH), number of tillers per plant (NTPP), plant height (PH), flag leaf length (FLL), spike length (SL), number of grains per spike (NGPS), number of spikelet per spike (NSPS) grain yield (GY), 1000 grain weight (1000GW), biological yield (BY) and harvest index (HI).

2.3 STATISTICAL ANALYSIS

2.3.1 ANALYSIS OF VARIANCE (ANOVA): All morphological data was subjected to analysis of variance [10] by using the statistical software for analysis as OPSTAT (software available at http: //www.hau.ernet.ac.in.) and INDOSTAT (version 8.0). The model used for analysis of variance of various characters is follow: $Y_{ij} = \mu + \alpha i + \beta j + eij$, Where: $Y_{ij} =$ observation of i^{th} treatment and j^{th} block, μ = General mean, $\alpha i = i^{th}$ treatment effect, $\beta j = j^{th}$ block effect, eij = random error associated with the i^{th} treatment and j^{th} block

2.3.2 PHENOTYPIC AND GENOTYPIC VARIABILITY: The difference present in tested lines were estimated by sample mean, range, phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV). The following formula is used for the calculation of phenotypic and genotypic variance and coefficient of variation as suggested by [11]: $\sigma^2 g = \frac{\mathrm{Mg-Me}}{r}$

Where; $\sigma^2 p$ = Phenotypic variance, $\sigma^2 g$ = Genotypic variance, $\sigma^2 e$ = Environmental (error) variance (Error mean square), Mg=mean square of genotypes, Me=mean square of error, r=Number of replication.

Phenotypic coefficient of variation, PCV= $\frac{\sqrt{\sigma^2 \mathrm{P}}}{\mathrm{x}} - 100$ and Genotypic coefficient of variation, GCV= $\frac{\sqrt{\sigma^2 \mathrm{G}}}{\mathrm{x}} - 100$, Where x= population mean,

2.3.3 ESTIMATE OF HERITABILITY: The existence of total genetic variability in offspring specifies by the estimation of the heritability which provides practical information for selection of individual character. The estimation of heritability is classified as low (<30%), moderate (30 -60%), and high (>60%) [12]. The board sense heritability is calculated based on the following formula: $\mathrm{H}^2 = \frac{\sigma^2}{x\sigma^2} x\ 100$ Where: σ^2g=genotypic variance, σ^2p= phenotypic variance, and σ^2e= error variance.

2.3.4 ESTIMATION OF EXPECTED GENETIC ADVANCE: Heritability estimation is more effective in the selection of superior genotypes based on phenotypic performance [12]. The estimation of heritability along with genetic advance will be more practical in the selection and prediction of individual characters. Expected genetic advance over the population mean is the percent of mean computed by using the formula given by [12, 13]. The calculation of genetic advance (GA) for any specific character was adapted to the following formula:

$$\mathrm{GA}= (\mathrm{k})\ (\sigma^2\ p)^*\ (\mathrm{H}^2), \text{ and GA (as\% of the mean)} = \left[\frac{(GA)}{X}\right] \mathrm{x}100,$$

Where, k= selection differential (k=2.06 at 5% selection intensity), $\sigma^2{}_p$= phenotypic standard deviation, H^2= heritability (Broad sense), and X =Grand mean.

2.3.5 ESTIMATION OF CORRELATION COEFFICIENT: The phenotypic correlation coefficients were computed between all possible pairs as described by [14].

$$\mathrm{r_p(xy)} = \frac{\mathrm{Cov_p(xy)}}{\sqrt{\sigma_p^2(\mathrm{x})\ .\ \sigma_p^2(\mathrm{y})}}$$

2.3.6 ESTIMATION OF PATH COEFFICIENT: The path coefficient analysis was carried out as per the formula given by [15]. Standard path coefficients also referred to as the standardized partial regression coefficients, were calculated using the correlation between variables. Thus, the correlation coefficient of different characters with grain yield was partitioned into direct and indirect effects adopting the following formula:

$$\mathrm{rij = Pij + \Sigma rik\ pkj}$$

The residual effect, which determines how best the causal factors account for the variability of the dependent factor yield, as computed using the formula:

$$1=\mathrm{p2R} + \Sigma\ \mathrm{p\ ij\ rij}$$

Where, p2R is the residual effect; p ij rij = the product of direct effect of any variable and its correlation coefficient with yield.

2.3.7 DISEASE SCREENING METHODS: The disease data were recorded following the modified Cobb's scale. The screening, for reaction to stripe rust, was done and based on that lines were classified as highly resistant (HR), moderately resistant (MR), moderately susceptible (MS) and highly susceptible (HS).

Table 1. Modified Cobb’s Scale for screening against stripe rust

Modified Cobb’s Scale	Reaction	Visible symptoms
0	HR	No visible infection on plant

5-10	R	Visible chlorosis or necrosis but no uredia are present
20	MR	Small uredia are present and surrounded by either chlorotic or necrotic areas
40	MS	Variable sized uredia are present (some with chlorosis, necrosis or both)
60	S	Large uredia are present, generally with little or no chlorosis and no necrosis
100	HS	Large uredia are present, generally with little chlorosis and necrosis

3. RESULTS AND DISCUSSION

3.1 Analysis of variance (ANOVA)

The result of the analysis of variance for F_5 and F_6 generation of wheat is presented in Table 2 and 3. It showed that the mean square due to genotypes was highly significant ($P<0.01$) among the parent and 210 tested wheat advanced lines for all the characters. It is further indicated that the mean of tested lines were different for all the characters and encouraged further genetic analysis. This indicates that the presence of significant variation among genotypes for tested characters and validates the performance of the further genetic analysis. A similar result was reported by [16, 17, 18, 19, 20] They reported significant mean difference obtained for difference wheat characters like days to maturity, days to 50% flowering, days to heading, plant height, spike length, spikes per plant, grains/ spike, 1000 grain weight, harvest index, grain yield per plant among tested lines.

Table 2. Analysis of variance (ANOVA) for various traits in F_5 generation during 2018-19

Characters	Genotypes (df=211)	Replication (df=1)	Error (df=211)
Days to Heading	66.974**	12.683	4.168
Number of tillers/plant	7.177**	0.01	0.041
Plant Height (cm)	49.647**	0.112	5.572
Flag leaf length (cm)	7.908**	0.076	0.221
Spike Length (cm)	1.256**	0.023	0.048
Number of grains/spike	235.636**	0.49	1.68
Number of spikelets/spike	14.852**	0.138	0.233
1000 grain weight (g)	0.875**	0.002	0.009
Biological yield/plant (g)	57.950**	0.573	0.7
Harvest index (%)	128.432**	0.088	1.116
Grain yield/plant (g)	11.882**	0.01	0.119

Table 3. Analysis of variance (ANOVA) for various traits in F_6 generation during 2019/20

Characters	Genotypes (df=211)	Replication (df=1)	Error (df=211)
Days to Heading	12.996**	20.444	4.631
Number of tillers/plant	0.579**	0.35	0.051
Plant Height (cm)	69.391**	1.287	6.111
Flag leaf length (cm)	6.622**	0.32	0.296
Spike Length (cm)	0.964**	0.19	0.059
Number of grains/spike	43.809**	2.061	1.299
Number of spikelets/spike	7.833**	0.708	0.222
1000 grain weight (g)	0.944**	0.008	0.021
Biological yield/plant (g)	112.631**	0.64	1.534
Harvest index (%)	49.365**	12.242	1.6
Grain yield/plant (g)	2.207**	1.29	0.09

* Significant at p= 0.05, ** Significant at p= 0.01

3.2 Mean performance variations among genotypes

3.2.1 Yield and yield components variation.

The study reported a high significant mean square for grain yield and biological yield. The mean and range of 11 wheat characters are given in Tables 4 and 5. The grain yield and biological yield mean was varied from 20 g to 45 g and 19 g to 38 g with an average mean of 14 g, 15 g and 41.04 g and 31.9 g respectively and coefficient of variation 8.49 % and 7.64% and 11.68% and 10.2% in both generation, which indicated a wide range of variation existed among tested lines. [16] also reported a high significant mean square for grain yield and biological yield from four promising lines of wheat. Harvest index indicated a highly significant mean square among lines and the mean was in the range of 7.17% to 20.30% with a mean of 12.43 g and coefficient of variation of 18.06%. Furthermore, the minimum and maximum values varied from 7 to 11 tillers per plant and from 9 to 13 tillers per plant with a mean of 9±0.09 and 10±0.03 and the coefficient of variation is 3.68% and 3.44% in both years. Analysis of variance showed highly significant differences among lines or 1000 seed weights. The range of mean for 1000 seed weight was 38.5 g to 40 g with a mean of 6.26 g. The highly significant difference was observed among the lines for the number of grains per spike and the Number spikelets per spike. The result indicated that a large variation existed between lines for the number of grains per spike and the number of spikelets per spike.

3.2.2 Phonological Characters

The variation with respect to the day of heading was in the range of 76 to 99 days and 75 to 93 days in both years respectively, indicating that great variability was found in tested lines as early and late heading.

3.2.3 Growth Characters

A highly significant variability was obtained among the lines for plant height and flag leaf length, which mean was ranged from 90 cm to 97.67 cm and from 17.5 cm to 18.71 cm, and coefficient of variation 2.54% and 2.88%.

Table 4. Mean performance of F_5 generation for yield and other contributed characters

Characters	Mean	Minimum	Maximum	S.E (m)	CV (%)
Days to Heading	87.5	76	99	0.29	2.62
Number of tillers/plant	9	7	11	0.09	3.68
Plant Height (cm)	90	78	102	0.25	4.48
Flag leaf length (cm)	17.5	13	22	0.1	2.54
Spike Length (cm)	9.5	8	11	0.04	2.66
Number of grains/spike	33.5	19	48	0.53	6.69
Number of spikelets/spike	17	15	19	0.13	3.54
1000 grain weight (g)	40	33	47	0.03	6.26
Biological yield/plant (g)	37.5	33	42	0.26	11.68
Harvest index (%)	40.5	36	45	0.39	9.57
Grain yield/plant (g)	14	8	20	0.77	8.49

Table 5. Mean performance of F_6 generation for yield and other contributed characters

Characters	Mean	Minimum	Maximum	S.E (m)	CV (%)
Days to Heading	84	75	93	0.14	2.76
Number of tillers/plant	10	9	13	0.03	3.44
Plant Height (cm)	97.67	90	106	0.3	2.6
Flag leaf length (cm)	18.71	15	22	0.09	2.88
Spike Length (cm)	11.5	10	13	0.03	3.03

Number of grains/spike	44.58	34	56	0.23	5.6
Number of spikelets/spike	16	11	21	0.1	7.88
1000 grain weight (g)	38.5	32	45	0.03	6.34
Biological yield/plant (g)	35.99	29	42	0.37	10.02
Harvest index (%)	34.5	31	38	0.51	8.36
Grain yield/plant (g)	15	11	19	0.32	7.64

3.2.4 Phenotypic and Genotypic Coefficient of Variation

The estimation of phenotypic (PCV), genotypic coefficients of variation (GCV), broad-sense heritability, and genetic advance are presented in Tables 6 & 7. The result showed high phenotypic variance over the genotypic variance for all characters understudy, the phenotypic expression is the result of genotype, environment contribution, and their interaction [21]. In this study, the phenotypic and genotypic variance was highly different for the characters; days to heading, plant height, flag leaf, number of grains per spike, biological yield, and harvest index. This result is compatible with the result of [16], which found high phenotypic and genotypic differences for the number of productive tillers per meter, biological yield per plot, harvest index, and 1000 seed weight. The result of this study is indicated that the selection will be not affected by the improvement of those characters that had large environmental variation as number of tillers per plant, plant height, flag leaf, spike length, number of grains per spike, number of spikelets per spike, 1000 grain weight, biological yield, grain yield, and harvest index.

The estimates of the phenotypic coefficient of variability ranged from 5.53% (plant height) to 25.11% (number of tillers per plant) in (2018-19) and 3.81 (days to heading) to 18.45 (2019-20) (Table 2). The PCV and GCV values are classified by [11], as high (> 20 %), medium (10-20%), and low (<10%). Accordingly, a high PCV was observed for the number of tillers per plant (25.11%), biological yield (22.58%), and harvest index (19.6%). These characters were noticeably affected by environmental factors. On the other hand, the lowest PCV was recorded for the plant height (6.31%) and (5.53%). [22] was reported high PCV and GCV for the grain yield and PCV for biomass Kgha^{-1}, while recorded moderate PCV and GCV for harvest index%, 1000 seed weight (g), days to heading, plant height (cm), and number spikes/m^2.

The genotypic coefficient of variability ranged from 3.21% (plant height) to 24.73% (number of tillers per plant). A high GCV (> 20 %) was observed for the number of tillers per plant (24.73%) and the number of grains per spike (22.40%). The grain yield (18.82%), biological yield (10.11%), 1000 grain weight (4.47%), number of spikelets per spike (14.31%), and harvest index (14.71%) showed medium GCV (10-20%). On the other hand, the low (<10%) GCV was observed for spike length (8.11%) followed by the flag leaf (7.13%), days to heading (5.14%), and plant height 3.22%) respectively. This result is in contrast to the finding by [23], which reported low and medium PCV and GCV values for yield and quality characters.

3.3 Estimates of Heritability

Broad sense heritability calculated for morphological characters in this study is shown in Tables 6 and 7. [12] Classified the heritability by three groups as low (<30%), moderate (30 - 60%), and high (>60%). Accordingly, high heritability recorded for the number of spikelets/spike (92.9%), spike length (91.6%), flag leaf length (84.6%), plant height (79.8%), number of tillers/plant (78.9%), 1000 grain weight (78.5%), grain yield/plant (77.0%), number of grains/spike (76.6), biological yield/plant (75.6%) and harvest index (75.3%) while days to heading (58.3%) recording moderate in both the generations. The result of this study clearly revealed that the expression of these characters was effect by the environment in the lowest level and the suggested direct selection for these characters. [24] Reported high level of heritability for PH (98.69%), DTH (97.98%), DTA (97.93%), DTM (93.77%), TNPP (93.75%), NSPS (98.06%), GNPS (98.63%), SL (99.72%), TGW (99.95%) and GYPP (97.02%).

3.4 Estimates of Genetic Advance

Genetic advance as a percentage of mean measurement of genetic gain under selection or the variation between the mean of the genotypic value of progenies under selection and base population and it is classified as low (<10%), moderate (10-20%) and high (>20%) [12]. In F_5, high to moderate estimates of GA for the number of tillers/plant (51.14%), grain yield/plant (48.76%), number of grains/spike (45.87%), harvest index (39.69%), biological yield/plant (34.83%), 1000 grain weight (31.56%), number of spikelets/spike (28.88%) and flag leaf length (21.24%), while moderate was observed in spike length (18.61) and days to heading (13.93%), the low (<10%) GA was showed by plant height (9.09%). In the F_6 generation, the high to moderate GA observed for harvest index (48.99 %), 1000 grain weight (31.72%), grain yield/plant (29.91%), biological yield/plant (26.98%), number of spikelets/spike (23.86%), number of grains/spike (21.02%), flag leaf length (18.57%), spike length (16.32%), number of tillers/plant (14.81%), plant height (11.15), days to heading (10.72%), where low GA estimated for days to heading (10.72%). [25, 16] had found moderate genetic advance as a percentage of mean for all the characters except spikelets per spike (9.69%), days to maturity (8.66%) and harvest index (6.80) that shows low genetic advance as percent of the mean.

Table 6. The estimation of phenotypic coefficient of variance (PCV), genotypic coefficients of variance (GCV), broad-sense heritability and the genetic advance in F_5 generations during 2018-19

Characters	PCV (%)	GCV (%)	Heritability (bs) (%)	Genetic advance	Genetic advance as 5 (%) mean
Days to heading	7.66	7.20	58.30	10.85	13.93
Number of tillers/plant	25.11	24.97	78.90	3.87	51.14
Plant height (cm)	5.53	4.94	79.80	8.64	9.09
Flag leaf length(cm)	10.90	10.6	84.60	3.93	21.24
Spike length (cm)	9.76	9.39	91.60	1.54	18.61
Number of grains/spike	22.58	22.42	76.60	22.12	45.87
Number of spikelets/spike	14.47	14.24	92.90	5.48	28.88
1000 grain weight (g)	15.65	15.49	78.50	1.34	31.56
Biological yield/plant(g)	17.32	17.11	75.60	10.89	34.83
Harvest index (%)	19.60	19.44	75.30	16.29	39.69
Grain yield/plant (g)	19.69	19.50	77.00	4.95	48.76

Table 7. The estimation of phenotypic Coefficient of variance (PCV), genotypic coefficients of variance (GCV), broad-sense heritability and the genetic advance in F_6 generation during 2019-20

Characters	PCV (%)	GCV (%)	Heritability (bs) (%)	Genetic advance	Genetic advance as 5(%) mean
Days to heading	3.81	2.62	57.50	2.90	10.72
Number of tillers/plant	8.57	7.85	73.90	0.97	14.81
Plant height (cm)	6.46	5.91	83.80	10.61	11.15
Flag leaf length (cm)	9.86	9.43	91.40	3.50	18.57
Spike length (cm)	8.95	8.42	88.50	1.30	16.32

Number of grains/spike	10.83	10.51	74.20	9.22	21.02
Number of spikelets/spike	12.26	11.92	94.50	3.91	23.86
1000 grain weight (g)	16.09	15.74	75.70	1.37	31.72
Biological yield/plant (g)	18.45	18.20	77.30	15.15	26.98
Harvest index (%)	14.37	24.56	73.70	9.75	48.99
Grain yield/plant (g)	13.65	13.11	75.10	2.03	29.91

3.5 Correlation Coefficients

Estimation of the correlation among yield and yield contributing characters was done to find out their correlation in progenies under study (Table 8 and 9). In F_5 generation, grain yield/plant had positive and significant correlation with 1000 grain weight (0.168**), harvest index (0.529**), biological yield/plant (0.316**), number of tillers/plant (0.111*) and number of grains/spike (0.051*), while positive but non-significant correlation with flag leaf length (0.094), spike length (0.088), plant height (0.036), number of spikelets/spike (0.001),but showed negative and non-significant association with days to heading (-0.043). However, the 1000 grain weight showed positive and high significant association with number of tillers/plant (0.142**) and number of spikelets/spike (0.238**) had positive and non-significant association with plant height (0.056), spike length (0.046) and lag leaf length (0.022), whereas it shows negative and non-significant association with days to heading (-0.066) and number of grains/spike (-0.0144). The grain yield/plant had positive and high significant association with number of tillers/plant (0.365**), harvest index (0.353**), number of spikelets/spike (0.315**), number of grains/spike (0.263**), spike length (0.255**), flag leaf length (0.215**), 1000 grain weight (0.193**) and biological yield/plant (0.486**), while non-significant association showed with days to heading (0.023) and negatively associated with plant height (-0.062). Nevertheless, the 1000 grain weight showed had positive and high significant correlation with spike length (0.388**), number of tillers/plant (0.244**), and flag leaf length (0.161**), while having significant association with plant height (0.106*) and non-significant association with days to heading (0.015) and number of grains/spike (0.548) in F_6 generation. [26] reported that grain yield is positively correlated with all characters except days to heading. [27] presented similar results where grain yield was positively correlated with the number of tillers per plant, number of spikelets per spike, number of grains per spike, and biological yield per plant. The positive correlation of grain yield with these characters implies that improving one or more of these traits could result in higher grain yield per plant.

3.6 Path Coefficients

The path coefficient analysis was done on genotypic correlation and results are presented below in Tables 10 and 11. The path coefficient is the measure of the direct and indirect effect of various independent (yield components) characters on dependent characters (yield) and it is interpreting in low, moderate, and high effects in this study for uncovering a realistic picture of a complex situation that exists at the correlation level. The residual effect (0.007 & 0.002) was low indicating a high contribution of independent traits to the dependent trait *i.e.* grain yield/plant

3.6.1 Direct effects on grain yield

In F_5 generation, the highest and positive direct effect on grain yield/plant was recorded by harvest index (0.985) and biological yield/plant (0.918) while the number of spikelets/spike (0.039) and the number of grains/spike (0.034) had a low positive direct effect. On the other hand, the low positive direct effect on grain yield/plant was shown by the 1000-grain weight (0.017), number of tillers/plant (0.017), flag leaf length (0.009), and spike length (0.008). The negative direct effect on grain yield was expressed by plant height (-0.001) and days to heading (-0.043). In F_6 generation, biological yield/plant (0.388) and harvest index (0.359) were as showed the highest direct effect on grain yield/plant and the number of tillers/plant (0.205) had a moderate positive direct effect. The low positive direct effect on grain yield/plant was recorded by flag leaf length (0.107) and 1000-grain weight (0.102). Furthermore, the negligible positive direct effect on grain yield/plant was shown by spike length (0.095), number of spikelets/spike (0.072), number of grains/spike (0.016), and days to heading (0.005) but plant height (-0.053) had a negative direct effect on grain yield. A similar result was obtained by [28, 29, 30, 31, 32, 33, 34, 35].

3.6.2 Indirect effects

In F_5 generation, the path coefficient analysis revealed that number of plant height (0.080) and days to heading (0.126) contributed towards grain yield per plot through harvest index and plant height. While, in F_6 generation, path correlation analysis revealed that plant height (0.034) contributed towards grain yield via biological yield/plant. [18, 36, 37, 38, 39] also obtained similar result.

Table 8. The estimation of Correlation coefficients among various traits of F_5 generation

Characters	DH	NT	PH	FLL	SL	GS	SS	TGW	BY	HI	GY
Days to heading	1										
Number of tillers/plant	-0.052	1									
Plant height (cm)	-0.028	0.043	1								
Flag leaf length (cm)	-0.055	-0.011	0.043	1							
Spike length (cm)	-0.021	-0.074	0.158**	0.141**	1						
Number of grains/spike	0.024	0.132**	0.062	0.122*	0.161**	1					
Number of spikelets/spike	-0.124*	0.004	0.134**	0.085	0.219**	0.522**	1				
1000 grain weight (g)	-0.066	0.142**	0.056	0.022	0.046	-0.0144	0.238**	1			
Biological yield/plant (g)	-0.083	0.028	0.124*	0.005	0.096*	0.056	0.012	0.057	1		
Harvest index (%)	0.069	0.05	-0.077	0.067	-0.012	0.079	0.009	0.177**	-0.602	1	
Grain yield/plant (g)	-0.043	0.111*	0.036	0.094	0.088	0.051*	0.001	0.168**	0.316**	0.529**	1

DH - Days to heading, NT - Number of tillers/plant, PH - Plant height (cm), FLL - Flag leaf length (cm), SL - Spike length (cm), GS - Number of grains/spike, SS - Number of spikelets/spike, TGW -1000 grain weight (g), BY -Biological yield/plant (g), HI - Harvest index (%), GY - Grain yield/plant

Table 9. The estimation of Correlation coefficients among various traits of F_6 generation

Characters	DH	NT	PH	FLL	SL	GS	SS	TGW	BY	HI	GY
Days to heading	1										
Number of tillers/plant	0.109*	1									
Plant height (cm)	-0.013	-0.042	1								
Flag leaf length (cm)	0.120*	0.198**	0.029	1							
Spike length (cm)	0.174**	0.283**	0.107*	0.243**	1						
Number of grains/spike	0.095	0.337**	-0.033	0.169**	0.441**	1					
Number of spikelets/spike	0.081	0.344**	-0.015	0.205**	0.487**	0.969**	1				
1000 grain weight (g)	0.015	0.244**	0.106*	0.161**	0.388**	0.0548	-0.529	1			
Biological yield/plant (g)	-0.047	0.029	0.087	0.029	0.394*	0.282**	.265**	-0.332	1		
Harvest index (%)	-0.05	0.153**	0.001	-0.009	0.250**	0.281**	0.275**	0.277**	-0.296**	1	
Grain yield/plant (g)	0.023	0.365**	-0.062	0.215**	0.255**	0.263**	0.315**	0.193**	0.486**	0.353**	1

DH - Days to heading, NT - Number of tillers/plant, PH - Plant height (cm), FLL - Flag leaf length (cm), SL - Spike length (cm), GS - Number of grains/spike, SS -Number of spikelets/spike, TGW -1000 grain weight (g), BY -Biological yield/plant (g), HI - Harvest index (%), GY - Grain yield/plant

Table 10. The estimation of path analysis among various traits of F_5 generation during 2018-2019

Characters	DH	NT	PH	FLL	SL	GS	SS	TGW	BY	HI	Correlation with GY
DH	-0.043	0.002	0.001	0.002	0.001	-0.001	0.005	0.003	0.004	-0.003	-0.043
NT	-0.001	0.017	0.001	0.000	-0.001	0.002	0.000	0.002	0.101	0.164	0.111*
PH	0.000	0.000	-0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.036
FLL	-0.001	0.000	0.000	0.009	0.001	0.001	0.001	0.000	0.000	0.001	0.094
SL	0.000	-0.001	0.001	0.001	0.008	0.001	0.002	0.000	0.001	0.000	0.088
GS	0.001	0.004	0.002	0.004	0.005	0.034	0.018	0.012	-0.002	0.003	0.051*
SS	0.006	0.000	-0.007	-0.004	-0.011	-0.027	0.039	-0.012	-0.001	-0.001	0.001
TGW	-0.001	0.002	0.001	0.000	0.001	0.006	0.004	0.017	-0.001	0.003	0.168**
BY	-0.084	0.028	0.126	0.005	0.098	-0.057	0.013	-0.058	0.918	-0.623	0.316**
HI	0.080	0.058	-0.088	0.077	-0.013	0.091	0.010	0.203	-0.703	0.985	0.529**

Residual Effect = 0.007. *DH - Days to heading, NT - Number of tillers/plant, PH - Plant height (cm), FLL - Flag leaf length (cm), SL - Spike length (cm), GS - Number of grains/spike, SS -Number of spikelets/spike, TGW -1000 grain weight (g), BY -Biological yield/plant (g), HI - Harvest index (%), GY - Grain yield/plant.*

Table 11. The estimation of Path analysis among various traits of F_6 generation during 2019-2020

Characters	DH	NT	PH	FLL	SL	GS	SS	TGW	BY	HI	Correlation with GY
DH	0.005	0.001	0.000	0.001	0.001	0.001	0.000	0.000	0.000	0.000	0.023
NT	0.022	0.205	-0.009	0.041	0.058	0.069	0.070	0.050	-0.006	0.031	0.365**
PH	0.001	0.002	-0.054	-0.002	-0.006	0.002	0.001	-0.006	0.005	0.001	-0.062
FLL	0.013	0.021	0.003	0.107	0.026	0.018	0.022	0.017	-0.003	-0.001	0.215**
SL	0.017	0.027	0.010	0.023	0.095	0.042	0.046	0.037	-0.032	0.024	0.255**
GS	-0.058	-0.205	0.020	-0.103	-0.268	0.016	-0.588	0.160	0.171	-0.170	0.263**
SS	0.058	0.245	-0.010	0.146	0.347	0.691	0.072	0.377	-0.189	0.196	0.315**
TGW	0.002	0.025	0.011	0.016	0.040	0.016	0.054	0.102	-0.040	0.028	0.193**
BY	-0.018	0.011	0.034	0.011	0.128	0.109	0.103	-0.153	0.388	-0.115	0.486**
HI	-0.018	0.055	0.001	-0.003	0.089	0.100	0.098	0.099	-0.106	0.359	0.353**

Residual Effect = 0.002. *DH - Days to heading, NT - Number of tillers/plant, PH - Plant height (cm), FLL - Flag leaf length (cm), SL - Spike length (cm), GS - Number of grains/spike , SS -Number of spikelets/spike, TGW -1000 grain weight (g), BY -Biological yield/plant (g), HI - Harvest index (%), GY - Grain yield/plant*

3.7 Reaction to yellow rust

To evaluate the presence of resistance in parents, F_5 and F_6 generation infector rows were planted between the blocks and artificial inoculations (using spray method) was carried out under field condition. The disease severity on leaves was evaluated by Modified Cobb's Scale in which rust severity was recorded as a percentage of leaf area infected.

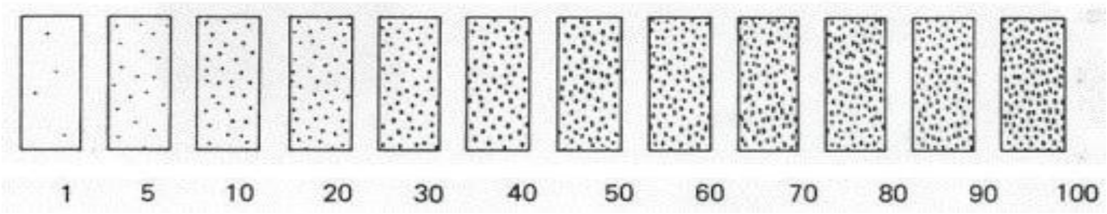

Figure 1. The modified Cobb-scale: severity of rust infection

The data on disease reaction of parents, F_5 and F_6 generation progenies revealed that all the plants of the resistant parents (PBW698) were free from the symptoms of yellow rust during both years, whereas, the susceptible parent (WH711) showed the symptoms of yellow rust. In the F_5 generation, 135 progenies including the resistance parent showed no infection, 25 showed traces of infection; 20MR was shown by 15 progenies, 40MS by 16 progenies, and 60S by 10 progenies including the susceptible parent. Highly susceptible reaction 100S to yellow rust was shown by 9 progenies. In the F_6 generation, 148 (including resistant parent) progenies showed no infection, 18 showed traces of infection 5-10R scale, only 15 plants showed 20 percent infection (MR), 14 progenies showed 40 percent infection (MS), 60 percent severity showed by 5 plants including WH711 and 100 percent susceptible reaction shown by 10 plants. [40] Evaluated the inheritance of stripe rust resistance and estimated the genetic components of resistance in wheat. The generation means analysis of F_1, F_2, BC_1, and BC_2 generations derived from a cross between MV17 (resistant) and Bolani (susceptible) parents with pathotypes 134E134A+ and 166E134A+ of stripe rust in two different experiments, showed that additive, dominant, and epistasis play a major role in increasing and decreasing the latent period and infection type, respectively. Despite the significant additive effect, dominance gene effect was the most important component in controlling these two characteristics [41, 42].

Table 12. Reaction to yellow rust of parents and progenies of F_5 generation

Modified Cobb's Scale	Yellow rust reaction	Progenies
0	HR	1, 2, 3, 5, 6, 7, 10, 12, 13, 14, 15, 16, 17, 21, 22, 25, 26, 27, 28, 29, 31, 32, 33, 38, 39, 40, 42, 43, 45, 46, 47, 48, 50, 52, 53, 54, 57, 58, 61, 63, 64, 66, 67, 69, 71, 72, 73, 74, 75, 78, 81, 83, 84, 85, 86, 87, 88, 125, 126, 128, 129, 131, 133, 134, 136, 137, 138, 139, 141, 143, 144, 145, 146, 147, 150, 151, 152, 153, 154, 157, 11, 158, 159, 160, 162, 165, 166, PBW-698, 167, 168, 171, 174, 175, 183, 188, 189, 191, 194, 196, 197, 199, 201, 202, 203, 206, 207, 209 and 210
TS	HR	90, 92, 94, 95, 97, 99, 100, 101, 102, 105, 107, 108, 111, 113, 114, 115, 116, 117, 119, 121, 122, 123 and 124
5S-10S	R	9, 11, 30, 37, 60, 62, 82, 89, 96, 106, 110, 118, 135, 148, 149, 156, 178, 179, 182, 187, 186, 195, 200, 204 and 208
20S	MR	23, 34, 49, 51, 68, 76, 104, 120, 130, 140, 163, 173, 176, 181 and 25
40S	MS	19, 55, 59, 70, 77, 79, 80, 93, 103, 109, 127, 142, 155, 169, 172, 185 and 192
60S	S	8, 18, 20, 36, 41, 98, 164, 170, 180, 190 and WH-711

100S	HS	4, 24, 35, 56, 65, 161, 177, 184 and 198

Table 13. Reaction to yellow rust of parents and progenies of F_6 generation

Modified Cobb's Scale	Yellow rust reaction	Progenies
0	HR	1, 2, 3, 5, 6, 7, 10, 12, 13, 14, 15, 16, 17, 21, 22, 25, 26, 27, 28, 29, 30, 31, 32, 33, 38, 39, 40, 42, 43, 44, 45, 46, 41, 72, 73, 74, 75, 78, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, PBW 698, 92, 94, 95, 96, 97, 125, 126, 128, 129, 131, 132, 133, 134, 135, 136, 137, 138, 139, 141, 143, 7, 48, 50, 52, 53, 54, 57, 58, 60, 61, 62, 63, 64, 66, 67, 69, , 7144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 156, 157, 11, 158, 159, 160, 162, 165, 166, 167, 168, 171, 174, 175, 183, 188, 189, 191, 192, 194, 196, 197, 199, 201, 202, 203, 206, 207, 209 and 210
TS	HR	99, 100, 101, 102, 105, 106, 107, 108, 110, 111, 112, , 113, 114, 115, 116, 117, 118, 119, 121, 122, 123 and 124
5S-10S	R	11, 23, 37, 34, 49, 51, 68, 76, 96, 103, 186, 178, 179, 182, 187, 186, 195, 200, 204 and 208
20S	MR	104, 120, 127, 130, 140, 155, 163, 169, 172, 173, 176, 181, 190, 193 and 205
40S	MS	19, 55, 59, 70, 77, 79, 80, 93, 109, 142, 164, 170, 180 and 185
60S	S	18, 20, 36, 41, 98 and WH-711
100S	HS	4, 8, 24, 35, 56, 65, 161, 177, 184 and 198

4. CONCLUSION

The study was conducted to estimate the genotypic and phenotypic variability, heritability, and genetic advance under selection between yield and yield contributes characters of 210 wheat lines including the parent. The result of ANOVA from all studied characters exhibited the presence of highly significant differences ($P<0.01$) among tested lines which indicates the presence of substantial variability among tested lines. The mean value of most of the characters was within the range of 20.28 to 55g, 17 to 48.15g, 7.17 to 20.30, 4.80 to 14.13, 1.75 to 6.40 g, 20 to 84 grain, 9.34 to 24.92, 6.67 to 10.92, 70.50 to 96.00 days, 79.84 to 108.00 cm, 13.33cm to 23.83cm for grain yield per plant, biological yield per plant, harvest index, productive tillers per meter, 1000 seed weight/g, number of grain per spike, number spikelets per spike, spike length, day of heading, plant height, flag leaf length. The result showed high phenotypic variance over the genotypic variance for the characters understudy (number of tillers per plant, plant height, flag leaf, spike length, number of grains per spike, number of spikelets per spike, 1000-grain weight, biological yield, grain yield, and harvest index). This shows environmental factors had a noticeable contribution to the phenotypic expression of these characters rather than the genotype factor. In this study, the phenotypic and genotypic variance was highly different for the characters i.e. days to heading, plant height, flag leaf, number of grains per spike, biological yield, and harvest index. High heritability estimates were observed for the number of grains per spike (97.82%), number of spikelets per spike (96.56%), number of tillers per plant (95.97%), grain yield/plant (85.19%) and 1000-grain weight (78.86%). This result indicates that it is reliable to improve yield through direct selection using these traits as major contributors to yield components. While low heritability was observed for flag leaf (28.11%), plant height (25.99%), and biological yield (21.18) characters. In F5 generation, the grain yield/plant had a positive and significant association with 1000 grain weight, biological yield/plant, harvest index, number of tillers/plant and grain yield/plant had a positive and high significant association with number of tillers/plant, flag leaf length, spike length, number of grains/spike, number of spikelets/spike, 1000 grain weight, biological yield/plant, harvest index in the F6 generation. The grain yield will be improved by direct selection of the aforementioned traits. In F5 and F6 generations harvest index, biological yield/plant, number of spikelets/spike, number of grains/spike, 1000 grain weight, number of tillers/plant, flag leaf length and spike length had the maximum direct contribution towards grain yield/ plant whereas, indirect effects of independent traits indicated that height and days to heading exhibited high contribution towards grain yield except for plant height. Hence, it would be rewarding to lay stress on these characters in the selection programme for increasing yield. The 135 and 148 progenies showed no infection in F5 and F6 generations. Finally, the result of the present study showed the presence of substantial variability existed among the tested wheat lines and the possibility of improving yield and other desirable traits through selection.

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