

# Genetic Evaluation of Bread Wheat's Grain Yield and Quality Traits

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## **Abstract**

Wheat is the most extensively grown cereal crop worldwide. It's second only to rice as a major staple crop in India. Wheat is a cereal plant that is a member of the Poaceae (Gramineae) family. Wheat is seen as the king of cereal crops because of its high nutritious content, high production, and the area it occupies, as well as its compatibility to all agro-climatic zones. Wheat, in contrast to other cereals, has a relatively high concentration of gluten, a protein that provides the elasticity required for producing high-quality bread. Researchers in this publication conduct a genetic analysis of the grain production and quality attributes of bread wheat.

**Keywords:** *Genetic Evaluation, Bread, Wheat, Quality Traits.*

**Tob Regul Sci.™ 2021;7(4): 561-581**

**DOI: <https://doi.org/10.52783/trs.v7i4.1309>**

## **Introduction**

Wheat is cultivated over an area of 224.27 million hectares, yielding roughly 732.31 million metric tonnes at a productivity of 3.27 tonnes per hectare. Some of the world's largest wheat exporters include: China, India, the United States, France, Russia, Canada, Australia, Pakistan, Turkey, the United Kingdom, Argentina, Iran, and Italy. These nations account for around 76% of global wheat output. With roughly 30.78 million hectares devoted to wheat production, yielding 98.5 million tonnes at an average productivity of 3.2 tonnes/hectare, wheat is a significant factor in India's food security system. <sup>1</sup>

Wheat is farmed over a 9.95 million hectare (ha) area in Uttar Pradesh, with a yield and productivity of 30.24 million tonnes and 3.04 tonnes/ha, respectively. In terms of landmass and output, the states of Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, and Rajasthan are crucial. To keep up with the rising demand for food in the country and to generate some foreign currency, a significant increase in production is essential. It is estimated that 100 million metric tonnes of wheat will be needed by 2030 to feed the country's expanding population. <sup>2-3</sup>

Increasing wheat production is necessary to meet this goal, and it can be done either horizontally, by expanding the amount of land used for farming, or vertically, by using varietal or hybrid improvement, one of the strongest tools for making dramatic increases in output and productivity

in different climates. Although our nation has become wheat self-sufficient since the discovery of the dwarfing gene, it is still need to make some serious efforts to tackle new hurdles.<sup>4-6</sup>

To meet the anticipated demand, the current yield gap must be reduced throughout the nation. In order to increase the yield of this vital commodity, researchers are focusing on developing cultivars that can withstand a wide range of biotic and abiotic stresses, use a minimum amount of inputs, and work well in a variety of crop rotations. Effective and long-term breeding initiatives are necessary to address these concerns.<sup>7-8</sup>

The physiological and genetic foundation for the sustained increase in wheat yields over the last 30 years is only poorly understood, despite the fact that this increase has been seen. In order to create and carry out an efficient breeding plan to generate high yielding and stress resistant varieties, genetic information about yield and other yield components contributes considerably in the selection of appropriate parents and the ensuing progenies. Researchers in the field of plant breeding often use the diallel cross approach to assess general combining ability, particular combining ability, variance components, and heritability, or to learn about the impacts of genetics on a predetermined set of parental lines.<sup>9-10</sup>

## **1. Material And Methods**

Ten different types of HUW varieties were used in this study: HUW 234, HUW 510, HUW 468, UP 2338, HD 2402, RAJ 1972, HD 2329, LOK-1, SONALIKA, and K 65. To maximize the incorporation of the most desirable agronomic characteristics in the constituted core material through a 10 parent diallel mating system, these materials were chosen on the basis of their wide variability in plant height, maturity, grain yield, and other developmental, morphological traits and quality too.

### **Production of F<sub>1</sub> seed:**

In order to complete a 10-parent diallel set during Rabi 2018- 19 at Experimental Farm, Integral College, Lucknow, Uttar Pradesh, India, and all feasible single crossings were made among 10 carefully chosen strains/varieties. Each cross yielded more than a hundred seeds.

### **Production of F<sub>2</sub>s:**

Half of the seeds from each of the 45 F<sub>1</sub> crosses were used to make F<sub>2</sub> seeds in the Rabi 2019–20 season at Experimental Farm, Integral College in Lucknow, Uttar Pradesh, India, while the other half were stored for further testing.

### **Design of an Experiment:**

Ten parents, 45 F<sub>1</sub>s, and 45 F<sub>2</sub>s were planted in a Randomized Complete Block Design with three replications during Rabi 2019–20. Each time, the parent and F<sub>1</sub> generation were planted in a single row, and the F<sub>2</sub> generation was planted in a dibble plot with two rows. The space

between rows was 30 centimetres and between rows was 15 centimetres, while the length of each row was 1.5 metres. It was fertilised at the appropriate rate (120 kilogrammes of nitrogen, sixty kilogrammes of phosphorus, and forty kilogrammes of potassium per hectare), and other cultural practises were implemented as needed to ensure the crop's continued health. Before planting, the soil was treated with Zinc sulphate at a rate of 25 kilogrammes per hectare. During the experiment, five light irrigations were delivered at different times. The 2015 harvest occurred during the last week of April and the first week of May.

Statistical and biometric evaluations of 14 different variables relating to development, morphology, physiology, and quality were recorded in the aforementioned experiment.

**Recording of experimental data:**

After 50 days after planting, the experimental plant was marked. Five plants from the parents and F1s, and ten from the F2s, were chosen at random for each replication, and data was collected for the following characteristics:

**(i) Number of tillers per plant:**

For each plant, we tallied the number of productive tillers that bore ears.

**(ii) Plant height:**

Plant height is defined as the distance in centimetres from the soil's surface to the bottom of the main spike, ear base, or panicle.

**(iii) Spike length per plant:**

The length of the spike was determined by measuring it from its base to its tip, awns not included.

**(iv) Number of spikelets per spike:**

Each spike or panicle of the chosen plants had its grain-bearing spikelet counted.

**(v) Leaf area index:**

The leaf area index is a non-metrical measure of the canopy size of a plant. It is the proportion of wide leaf canopies that are covered by green leaves relative to the total area of the ground below them.

**(vi) Day to maturity:**

The number of days till harvest will be determined by subtracting the date of sowing from the date of physiological maturity.

**(vii) Grain yield per plant:**

Using a weighing scale, we will determine the total weight of grain harvested from each replicated plant in each treatment.

**(viii) Protein Content:**

The Biuret technique will be used to calculate the percentage of protein in triplicate samples of grain flour from each treatment.

After dehydrating the sample in an oven at 50°C for 8-10 hours, it will be crushed using a grinder and sieved through a 20 mesh screen to ensure consistency. The protein content of the flour will be estimated using this powder.

**(ix) Gluten Content:**

Austin and Ran's (1971) approach was used to calculate gluten concentration. A standard dough ball requires 10 g of flour and the appropriate amount of water. To prevent the gluten from being washed away with the starch in the first step of washing, the dough ball was let to rest in a 100 ml beaker of tap water at room temperature for an hour while being carefully monitored and cleaned by hand under a moderate stream of tap water. The dough ball was baked at 100 degrees Celsius for 24 hours, during which time all of the starch was washed away. The weight after drying was determined using a physical balance.

**Statistical and biometrical analysis:**

**1. Analysis of variance**

The model served as the basis for the study of the experiment's variance.

$$P_{ij} = \mu + V_{ij} + r_k + e_{ijk} \quad (i, j = 1, \dots, t; k = 1, \dots, b \quad i \neq j)$$

Where,

$P_{ijk}$  = the phenotypic  $ijk^{\text{th}}$  observation

$\mu$  = the population mean

$V_{ij}$  = the effect of  $i^{\text{th}}$  variety at  $j^{\text{th}}$  progeny

$r_k$  = the effect of  $k^{\text{th}}$  replication

**2. Diallel analysis**

**(a) Genetic components analysis:**

Equation was used to determine the diallel cross variance components.

Assumptions for F1 diallel crossings:

$$V_p = D + E$$

$$V_r = (1/4) D + (1/4) H_1 - (1/4) F - [(n+1)/2n]$$

$$EW_r = (1/2) D - (1/4) F + (1/n) E$$

$$V_m = (1/4) D + (1/4) H_1 - (1/4) H_2 - (1/4) F + (1/2n) E$$

### 3. Estimation of heterosis and I.D:

#### (i) Heterosis:

To calculate the kind and extent of heterosis in F1 over the better parent, the midparent, and the economic parent, we use the following formulae:

$$\text{Heterosis over economic parent (EP) (\%)} = \frac{F1 - EP}{EP} \times 100$$

Where,

F1 = F1 mean

EP = Economic parent's mean

#### (ii) I.D:

This formula was used to determine the coefficient of I.D: Inbreeding depression (%) =  $\{(F_1 - F_2)/F_1\} \times 100$

Where,

F1 = Normalised F1 generation

F2 = F2 generational mean

### 4. Estimation of selection parameters:

Direct and indirect selection's viability was evaluated based on the selection characteristics (heritability, genetic progress, and correlations).

#### (i) Heritability:

Crumpacker and Allard (1962) suggested the following formula to determine the coefficient of heritability (in the limited sense) in the F1 generation:

Shashank Srivastav,

Genetic Evaluation of Bread Wheat's Grain Yield and Quality Traits

$$\text{Heritability (h}^2\text{)} = \frac{(1/4)D}{\left[ \frac{(-)}{4} D + \frac{(-)}{4} H_1 - \frac{(-)}{4} F + E \right]} \times 100$$

Verhalen and Murray (1969) provided the methods used to determine heritability in the F2 generation.

$$\text{Heritability (h}^2\text{)} = \frac{(1/4)D}{\left[ \left(\frac{1}{4}\right) D + \left(\frac{1}{16}\right) H_1 - \left(\frac{1}{8}\right) F + E \right]} \times 100$$

Where,

$h^2$ =Attempt at calculating the heritability.

D=Contribution to variation owing to the multiplicative action of genes.

$H_1$ =Variation that can be attributed to a few dominant genes.

F=Parental frequency distributions of dominant and recessive genes.

E=Variation attributable to the environment.

Heritability(inpercent)= $h^2$ (heritabilitycoefficient) $\times 100$

#### (i) Genetic advance:

The genetic improvement was figured up using the formula as:

Genetic advance(G.A.)=(K)( $h^2$ )( $\sigma_p^2$ )together with an estimated hereditary premium above the average personality trait of:

$$\text{G.A (\%)} = \text{(GA/X)} \times 100$$

Where,

GA = Prediction of Genomic Progress

K = Differential selection at a 5% selection rate

( $K=2.06$ ) $\sigma_p^2$ h = Dispersion of phenotypes

$h^2$  = Attempt at calculating the heritability

X = Typical of the involved character

### 3. Results

The 'F' test was used to analyze the variance between fourteen different variables: plant height, spike length per plant, number of spikelets per spike, peduncle length of main shoot, leaf area

index, days to maturity, grain yield per plant, 1000 grain weight, biological yield per plant, number of grains per spike, protein content, and gluten content.

Table 1:Wheat ancestry explored by an ANOVA on 14 characteristics across parents, F1s, F2s, crosses, and F1 vs. F2 generations.

Source of Variations	d.f.	Mean Sum of Squares				
		Number of tillers/ Plant	Plant height (cm)	Spike length /Plant (cm)	Peduncle length of main shoot (cm)	Leaf area index
Replication	2	1.34	16.43	0.11	11.56	0.31
Treatments	99	0.87	50.50	0.68	97.86	12.25
Parents	9	0.30	96.37	0.28	9.39	1.62
F1s	44	0.32	34.56	0.60	44.19	5.52
F2s	44	0.58	26.53	0.26	10.76	5.36
Parent vs. Crosses	1	8.22	9.30	2.58	1634.36	666.28
F1 vs. F2s	1	35.57	1434.75	24.87	5551.52	52.79
Error	198	0.29	8.50	0.15	8.28	2.43

  

Source of Variations	d.f.	Mean Sum of Squares			
		Grain yield/ Plant (g)	1000 grain weight (g)	Protein content (%)	Gluten content (%)
Replication	2	28.11	13.82	0.16	0.11
Treatments	99	38.13	15.89	0.41	0.49
Parents	9	57.83	8.25	0.14	0.27
F1	44	38.68	21.85	0.30	0.39
F2	44	25.83	6.51	0.36	0.64

Parent vs. Crosses	1	49.91	136.10	9.88	1.29
F1 Vs. F2s	1	365.64	114.60	0.52	0.06
Error	198	9.24	4.97	0.22	0.26

### Variance measures among parents, F1 offspring, and F2 progeny

In Table 3, we see the average and standard deviation for each of the fourteen characteristics throughout the ten-parent, 45-F1 hybrid, and 45-F2 segregating population. Variability in plant height (92.93 - 109.67), biological production per plant (96.00 - 112.00), grain yield per plant (33.53 - 47.73), peduncle length of main shoot (47.20 - 54.17), and 1000-grain weight (47.20 - 54.17) was rather high among the parents.

Plant height (92.93 - 107.97), peduncle length of main shoot (40.20 - 55.80), leaf area index (17.67 - 24.03), and days to maturity (111.00 - 116.33) showed the most variance across F1 hybrids, followed by biological yield per plant (87.73 - 112.83) and grain yield per plant (36.10 - 55.00). The biological yield per plant in the F2 generation showed the greatest range of variation (88.55 - 108.43), followed by the height of the plant (90.20 - 103.67), the grain yield per plant (32.13 - 43.57), the number of days to maturity (110.67 - 119.00), the peduncle length of the main shoot (34.00 - 42.37), and the leaf area index (17.75 - 23.22).

In all categories tested (number of tillers per plant, length of spikes per plant, number of spikelets per spike, peduncle length of main stem, weight of 1000 grains per plant, and biological yield per plant), the mean value of the parents was higher than that of the F1 and F2 progenies. When compared to both their parents and their F2 offspring, F1 hybrids had superior mean values for days to 50% blooming, plant height, leaf area index, grain production per plant, protein content, and gluten content. The average number of days to maturity of F2 descendants was also higher than that of their parents and F1 descendants.

Environmental factors had a minor impact on the expression of these traits, as estimated by the phenotypic coefficient of variance being larger than the corresponding genotypic coefficient of variation. From 2.19 (days to 50% flowering) to 13.47 (leaf area index), the phenotypic coefficient of variation (PCV) for all parameters in the F1 generation was rather large. PCV values of 7.32, 7.36, and 7.32 per thousand grains were found for leaf area index (plant), grain yield (plant), peduncle length (main shoot), spikelets per spike, and biological yield (plant). The coefficient of genetic variation (GCV) for the time it takes to reach 50% flowering was 1.50, whereas it was 11.28 for the leaf area index. The estimated phenotypic and genotypic coefficients of variation were both highest for the leaf area index. Characters like days to 50% blooming and days to maturity have low values for both the genotypic and phenotypic coefficients of variation



(GCV and PCV, respectively). Table 3 shows that in the F2 generation, the phenotypic coefficient of variation is greater than the genotypic coefficient of variance. PCV and GCV values of 13.36 and 12.46, respectively, were measured in the length of the primary shoot's peduncle.

**Table 2: Genotypic and phenotypic variances for 14 wheat traits were calculated among the parents, F1s, and F2s of a 10-parent diallel cross.**

Traits	Mean			Range			GCV		PCV	
	Parents	F1	F2	Parents	F1	F2	F1	F2	F1	F2
Number of tillers/ Plant	9.10	8.91	8.19	8.67-9.67	8.33-9.67	7.00-9.00	2.34	4.92	3.69	8.38
Plant height (cm)	98.74	100.45	95.84	92.93-109.67	92.93-107.97	90.20-103.67	3.51	3.47	4.57	4.54
Spike length/ Plant (cm)	10.59	10.58	9.97	10.07-11.03	9.93-12.55	9.36-10.50	3.30	3.17	5.08	4.71
Leaf area index	108.97	113.56	114.63	107.0-110.33	111.0-116.33	110.67-119.0	1.81	2.31	2.32	2.80
Day to maturity	39.75	42.27	39.95	33.53-47.73	36.10-55.00	32.13-43.57	8.15	6.62	10.89	10.26
Grain yield/ Plant (g)	44.89	43.30	41.99	47.20-54.17	36.43-47.47	39.03-45.0	5.17	3.27	7.32	6.05
Protein content (%)	8.53	8.76	8.73	8.0-8.96	8.10-9.60	7.85-9.69	2.40	3.89	6.30	6.83
Gluten content (%)										

Diallel Analysis

a) Genetic component analysis

The genetic component of variation in F1s and F2s was analysed using the variance component analysis method established. Except for the leaf area index and gluten content in both generations (F1s and F2s), which may have been the result of sampling error, non-significant values of  $t_2$  confirmed the validity of the hypothesis. Height, spike length, leaf area index, spike yield, and gluten content were all significantly different from 1.

Table 3:Wheat F1 and F2 generation b, Sb, (b-0)/Sb, (1-b)/Sb, and  $t_2$  estimation for 14 characteristics from a diallel cross of 10 parents.

S.No.	Attributes	G	b	Sb	(b-0)/Sb	(1-b)/Sb	$t_2$
1	Number of tillers/ Plant	F1	0.086	0.394	0.774	2.099	0.101
		F2	0.178	0.132	11.590	4.897	9.936
2	Plant height (cm)	F1	1.065	0.421	8.543	-2.683	3.390
		F2	0.195	0.326	2.395	1.887	0.032
3	Spike length /Plant (cm)	F1	0.004	0.130	0.276	7.626	11.050
		F2	0.231	0.251	4.585	2.139	0.771
4	Leaf area index	F1	0.266	0.122	20.122	3.843	11.074
		F2	0.288	0.102	30.490	4.142	16.637
5	Day to maturity	F1	0.473	0.124	34.699	0.441	6.966
		F2	0.057	0.170	3.329	5.200	5.034
6	Grain yield/ Plant (g)	F1	-0.150	0.176	5.704	7.397	4.321
		F2	0.875	0.340	10.144	-2.204	1.028
7	Protein content (%)	F1	0.284	0.151	14.304	2.850	5.913
		F2	0.105	0.196	3.265	4.029	3.019
8	Gluten content (%)	F1	0.360	0.126	25.439	2.219	8.694
		F2	0.159	0.167	6.455	4.150	5.110

Shashank Srivastav,

## Genetic Evaluation of Bread Wheat's Grain Yield and Quality Traits

Standard errors and associated parameters were calculated for each component of the F1 and F2 generations' analysis of variation. This included the variables D, H1, H2, F, h2, and E. The F1 generation had a significantly shorter time to 50% flowering (1.19 days) and shorter plants (0.03 metres) on average than the F2 generation (1.12 days), taller plants (0.05 metres) on average, and higher grain and biological yields (1.18 days) on average. Grain yield per plant in the F1 generation was the only character where the dominant component and their ratio (H1 and H2) did not display significant values. In all generations, H1 was shown to have a greater value for all qualities than H2 and the additive component (D). Days to 50% blooming were measured in both generations, and the F values were shown to be positively significant. In the F1 generation, a positive value of the F component was discovered for plant height, but in the F2 generation, a negative value was detected. Positive and insignificant values were shown for other characters. For all traits measured across generations, including days to tiller number per plant (0.59, 0.35), plant height (0.15, 2.71), spike length per plant (0.02, 0.06), leaf area index (0.02, 1.20), days to maturity (0.16, 0.04).

Number of tillers per plant (2.65), plant height (1.48), spike length per plant (3.86), , leaf area index (8.92), days to maturity (4.74), grain yield per plant (2.05), and number of grains per spike (9.17) all had estimates of mean degree of dominance (H Partial dominance was seen in gluten content, which was 0.5 from unity in both generations (0.23 and 0.22, respectively).

It was discovered that the ratio of positive to negative alleles in both generations ( $H2/4H1$ ) was lower than the expected value (0.25 for all the character). Characters such as number of tillers per plant (1.84), plant height (3.37), spike length per plant (1.15), leaf area index (1.06), grain yield per plant (3.31) were found to have a ratio of dominant to recessive gene greater than unity in the F1 generation. Days to 50% flowering (2.64), plant height (3.06), leaf area index (1.06), days to maturity (1.09), grain yield per plant (2.77), all showed ratios of dominant to recessive genes greater than unity in the F2 generation. While some traits displayed perfect unity, others showed deviations, suggesting that recessive genes are more common than dominant ones.

The  $h2/H2$  ratio, an approximation of the sets of genes responsible for a character's phenotype and dominant inheritance, was greater than 1 for days to 50% flowering and protein content in both generations. However, it was only greater than 1 in the F2 generation for plant height and leaf area index.

### Heterosis and I.D:

All fourteen traits evaluated in the experiment had their estimates of heterosis in percent over the economic parent (HD 2402) and I.D in the second generation tabulated and reported in Table.12. Below is a synopsis of my quick remarks on each character:

#### **Number of tillers per plant:**

If there is positive and considerable heterosis, it is expected that more productive tillers will be produced. For tillers per plant, heterosis over the economic parent ranged from -10.07 to 5.14%. Except for the cross combination HUWv468 UP 2338 (5.14), where positive and significant heterosis signalling towards the high tillering was seen, all of the other crosses exhibited negative and significant levels of heterosis over the economic parent.

In this research, 18 of 45 respective crossings exhibited substantial and positive expression of I.D, with values ranging from -4.80 to 20.08 percent, based on the number of productive tillers per plant.

#### **Plant height:**

Only six cross combinations demonstrated substantial and positive heterosis over economic parents for plant height, with the degree of heterosis ranging from -10.09 to 12.80 percent. The cross HD 2402 SONALIKA (-10.09) has the highest and most desirable heterosis for plant height with a negative value, followed by combinations like UP 2338 K 65 (07.46), HD 2402 K 65 (-6.22), SONALIKA K 65 (-5.89), HUW 234 SONALIKA (-5.69), and RAJ 1972 SONALIKA (-4.48). Heterosis was significantly favourable over the economic parent in 17 of the crosses. I.D was found to have a range of -14.54% to 14.58%. Nineteen out of 45 crosses showed statistically and positively significant I.D..

#### **Spike length per plant:**

The heterosis for spike length per plant ranged from -7.51 percent to 17.67 percent, relative to the economic parent. substantial positive heterosis was found in two crossings (UP 2338 RAJ 1972, 9.40), while substantial negative heterosis was found in five crosses (HD 2329, 17.67). Twenty different crossings showed substantial and positive expression of I.D for the characteristic of spike length per plant, with values ranging from -0.71 to 24.36 percent.

#### **Leaf area index:**

In terms of leaf area index, heterosis over the economic parent ranged from 8.63 percent to 55.70 percent. Except for two crosses, all cross combinations showed very substantial and positive heterosis over the economic parent. Two of the hybrids exhibited a significant negative I.D for leaf area index (-15.94%), whereas three of the crossovers showed a significant positive I.D (16.39%).

#### **Days to maturity:**

Days to maturity heterosis varied from 1.45% to 6.98%, with a median of 3%. In terms of days to maturity, all but one cross demonstrated considerable and favourable heterosis over the economic parent. Different values of I.D (from -7.24 to 2.92%) were observed for this feature.

Shashank Srivastav,

## Genetic Evaluation of Bread Wheat's Grain Yield and Quality Traits

Only three crossings out of 45 combinations indicated substantial I.D for the trait in question.

### Grain yield per plant:

For grain production per plant, heterosis was shown to vary from -13.21 percent to 53.42 percent, relative to the economic parent. There were fifteen cross combinations in which there was substantial positive heterosis over the economic parent, and three in which there was significant negative heterosis over the economic parent. For this feature, the I.D ranged from -11% to 39%. This characteristic was significantly and positively inbred in five different crossings.

### Protein content:

Protein content heterosis over the economically advantageous parent varied from a negative 3.35 percent to a positive 10.38 percent. For this feature, 23 out of 45 crosses exhibited statistically significant and positive heterosis over the economic parent. From a low of -6.43 to a high of 8.27%, the I.D score swung widely. For this feature, I.D was only detectable in one cross.

### Gluten content:

For gluten content, heterosis over the economically significant parent varied from a -6.61 percent decrease to a 12.16 percent increase. Only four cross combinations out of 45 demonstrated substantial and positive heterosis over economic parent for gluten content; these were HUW 510 K 65 (10.62), HUW 234 LOK-1 (11.24), HUW 468 RAJ 1972 (12.16), and LOK-1 K 65 (9.96).

This trait's I.D varied from -11.24 percentage points to 11.93 percentage points. I.D was only significantly positive for one possible cross.

Table 4:Wheat 10 × 10 diallel cross estimates for heterosis and I.D on 14 traits.

Cross	Number of tillers/ plant		Plant height (cm)		Spike length/ Plant (cm)	
	Heterosis	I.D	Heterosis	Heterosis	Heterosis	Inbreeding Depression
HUW510×HUW234	-3.97	10.150	1.76	8.26	12.66	7.965
HUW510×HUW468	2.94	9.646	-0.61	-0.91	25.31	0.634
HUW510×UP2338	-1.28	16.608	-2.51	-6.61	20.52	4.609
HUW510×HD2402	-0.72	9.091	-0.75	3.48	36.41	2.481
HUW510×RAJ1972	-1.82	4.815	1.24	-3.36	19.91	0.000

Shashank Srivastav,  
Genetic Evaluation of Bread Wheat's Grain Yield and Quality Traits

HUW510×HD2329	-1.81	11.073	4.01	-5.59	8.63	5.407
HUW510×LOK1	-4.48	5.639	0.87	-2.11	38.88	9.068
HUW510×SONALIKA	-3.91	10.370	-2.35	-1.83	35.05	7.009
HUW510×K65	-10.07	-4.796	-4.95	2.71	25.85	-0.705
HUW234×HUW468	-0.38	20.076	-7.51	-4.41	39.64	4.746
HUW234×UP2338	-3.55	12.403	-6.83	-13.02	36.96	0.559
HUW234×HD2402	-5.55	9.020	-6.03	-5.23	49.02	1.507
HUW234×RAJ1972	-0.75	16.538	2.32	2.60	37.89	4.010
HUW234×HD2329	-0.37	5.227	-2.17	-9.74	38.32	0.940
HUW234×LOK1	-5.70	0.395	-1.06	-11.44	23.57	0.000
HUW234×SONALIKA	-5.84	5.814	-4.02	-14.88	34.10	5.782
HUW234×K65	-3.32	5.344	2.27	-7.92	37.59	7.626
HUW468×UP2338	5.14	18.841	1.25	1.56	44.77	11.740
HUW468×HD2402	-2.26	13.514	2.27	2.74	54.51	8.116
HUW468×RAJ1972	2.66	8.889	-3.71	-8.60	37.19	1.523
HUW468×HD2329	-0.38	4.939	-0.58	-14.16	38.90	10.914
HUW468×LOK1	2.44	6.593	-5.77	-5.22	32.86	0.790
HUW468×SONALIKA	-2.97	10.345	-1.11	-14.71	55.70	1.903
HUW468×K65	0.38	4.869	-1.39	-14.20	46.85	0.474
UP2338×HD2402	-1.68	15.589	-5.59	-10.19	28.58	7.010
UP2338×RAJ1972	-3.20	8.949	9.40	-2.05	30.67	13.947
UP2338×HD2329	-2.44	-1.923	17.67	-16.97	36.46	24.356
UP2338×LOK1	1.49	9.890	0.65	-17.35	18.19	8.397
UP2338×SONALIKA	-6.44	0.787	-2.19	-15.59	42.35	2.955
UP2338×K65	-3.54	4.633	-2.36	-13.12	39.21	4.554

Shashank Srivastav,  
Genetic Evaluation of Bread Wheat's Grain Yield and Quality Traits

HD2402×RAJ1972	-2.61	-0.766	2.05	-1.42	30.92	2.240
HD2402×HD2329	-2.97	5.747	1.33	1.48	27.51	10.477
HD2402×LOK1	-2.03	8.647	-1.70	-5.45	29.26	5.372
HD2402×SONALIKA	-7.66	4.348	4.76	0.92	42.17	9.123
HD2402×K65	2.58	12.227	-2.09	-0.30	38.85	1.363
RAJ1972×HD2329	-5.99	-0.004	1.87	-12.63	30.42	4.884
RAJ1972×LOK1	0.19	12.593	-2.04	-17.59	35.04	1.116
RAJ1972×SONALIKA	-6.98	-2.367	5.11	-12.37	48.35	3.777
RAJ1972×K65	0.37	10.000	4.75	-9.17	38.01	9.966
HD2329×LOK1	-3.88	10.769	1.80	-12.99	23.20	8.062
HD2329×SONALIKA	-3.30	9.091	-0.93	-12.32	36.16	2.339
HD2329×K65	-1.48	8.647	2.53	-9.60	36.22	7.702
LOK1×SONALIKA	-4.54	6.844	0.08	-14.66	19.26	7.364
LOK1×K65	-4.95	9.266	-2.25	-12.43	30.57	6.847
SONALIKA×K65	-5.45	5.381	1.18	-7.92	40.72	8.702
SE±	0.178		0.289	0.547	1.058	
Cross	Leaf area index		Days to maturity		Grain yield/ Plant (g)	
	I.D	Heterosis	Heterosis	Heterosis	I.D	Heterosis
HUW510×HUW234	-0.158	3.40	41.63	2.50	4.600	2.45
HUW510×HUW468	2.022	3.27	53.42	6.60	7.093	1.20
HUW510×UP2338	-11.534	2.84	27.21	2.02	-4.199	-7.35
HUW510×HD2402	16.389	2.32	9.86	-9.08	-2.491	-0.61
HUW510×RAJ1972	-1.665	4.81	19.73	-7.06	-11.832	-5.62
HUW510×HD2329	-0.585	4.61	31.01	0.45	-4.136	-8.25
HUW510×LOK1	3.127	4.83	4.19	3.17	6.897	-0.38

HUW510×SONALIKA	-1.530	5.23	9.73	-8.84	-9.141	-9.83
HUW510×K65	-15.942	6.39	9.68	6.07	10.952	-2.04
HUW234×HUW468	1.061	4.92	13.23	0.70	-1.230	-3.41
HUW234×UP2338	10.820	2.29	13.56	5.16	6.727	-3.95
HUW234×HD2402	9.538	5.12	-2.90	-6.91	-3.257	-8.95
HUW234×RAJ1972	10.512	6.98	14.36	-8.42	2.586	-4.27
HUW234×HD2329	11.215	5.58	15.00	-1.42	4.107	-6.03
HUW234×LOK1	4.154	5.41	9.23	-2.02	-2.012	-5.99
HUW234×SONALIKA	4.284	6.45	10.66	-9.46	-9.004	-6.78
HUW234×K65	-6.261	2.89	3.34	1.05	12.764	0.55
HUW468×UP2338	9.345	2.90	-7.44	0.61	5.605	-0.46
HUW468×HD2402	6.160	3.42	-5.46	-5.49	-3.656	-12.90
HUW468×RAJ1972	8.683	3.99	18.20	0.35	-0.037	-7.46
HUW468×HD2329	-0.735	3.44	12.34	1.35	4.025	-4.99
HUW468×LOK1	6.015	3.33	11.51	9.98	17.839	-2.51
HUW468×SONALIKA	7.710	5.82	11.49	12.51	18.597	-10.51
HUW468×K65	-1.067	6.39	-12.30	-0.22	1.383	-9.24
UP2338×HD2402	6.090	4.46	-6.07	-9.89	-7.336	6.58
UP2338×RAJ1972	8.465	5.75	3.00	-5.69	-2.451	-8.68
UP2338×HD2329	13.836	3.36	3.68	-6.14	-4.908	-5.25
UP2338×LOK1	-6.942	3.06	9.26	5.92	6.384	-10.33
UP2338×SONALIKA	12.631	1.45	-4.52	1.67	6.281	-10.57
UP2338×K65	4.732	2.90	-13.21	-6.20	0.486	0.86
HD2402×RAJ1972	-1.381	3.81	4.37	-8.17	3.795	-7.41
HD2402×HD2329	1.885	3.33	5.65	-1.90	5.590	-3.99



**Shashank Srivastav,**  
**Genetic Evaluation of Bread Wheat's Grain Yield and Quality Traits**

HD2402×LOK1	5.808	4.43	-6.43	-5.70	4.442	-3.01
HD2402×SONALIKA	12.789	4.19	-9.23	-5.52	-1.989	2.80
HD2402×K65	1.746	4.19	-10.59	-6.52	5.452	-4.26
RAJ1972×HD2329	11.695	2.30	10.73	-4.42	3.177	-3.13
RAJ1972×LOK1	11.217	5.34	16.13	9.45	11.948	-8.78
RAJ1972×SONALIKA	9.978	4.79	-7.04	-11.66	1.835	-13.59
RAJ1972×K65	-1.103	4.21	1.03	7.31	14.373	-8.50
HD2329×LOK1	-0.613	3.39	-1.21	-11.53	-11.185	-9.66
HD2329×SONALIKA	15.493	3.15	-4.22	-1.82	6.786	-0.82
HD2329×K65	3.819	5.49	16.17	15.12	9.656	-0.84
LOK1×SONALIKA	-2.602	5.76	0.83	10.12	18.663	-10.94
LOK1×K65	-9.700	4.15	-5.26	5.54	5.630	-0.46
SONALIKA×K65	3.603	4.52	1.49	-7.59	-2.307	3.76
SE±		1.154	2.133	4.044		0.670
<b>Cross</b>	<b>Gluten content (%)</b>			<b>Protein content (%)</b>		
	<b>Heterosis</b>	<b>I.D</b>		<b>Heterosis</b>	<b>I.D</b>	
HUW510×HUW234	5.21	-3.733		3.46	0.084	
HUW510×HD2402	-1.19	-2.133		6.12	-1.226	
HUW510×HD2329	-2.53	0.000		7.10	-0.077	
HUW510×UP2338	-0.21	0.034		-3.35	0.000	
HUW510×K65	10.62	0.000		6.62	-0.844	
HUW510×RAJ1972	-2.03	0.000		6.23	3.000	
HUW510×HUW468	3.19	-2.226		8.48	3.594	
HUW510×LOK1	2.20	0.000		5.64	0.308	
HUW510×SONALIKA	-1.29	0.000		7.90	2.492	

Shashank Srivastav,  
Genetic Evaluation of Bread Wheat's Grain Yield and Quality Traits

HUW234×HUW468	0.29	0.000	8.69	0.000
HUW234×UP2338	8.12	0.035	3.49	0.000
HUW234×HD2402	0.12	-6.529	3.19	-3.765
HUW234×RAJ1972	5.06	4.211	8.05	2.137
HUW234×HD2329	-6.61	-11.242	2.92	-3.406
HUW234×LOK1	11.24	11.555	4.87	1.150
HUW234×SONALIKA	4.47	-6.468	3.08	-0.905
HUW234×K65	5.61	-0.301	6.16	2.675
HUW468×UP2338	6.51	-1.341	3.82	-0.556
HUW468×HD2402	-2.17	0.000	4.15	0.000
HUW468×RAJ1972	12.16	-0.486	2.78	0.000
HUW468×HD2329	-3.22	-9.881	1.86	-4.537
HUW468×LOK1	4.73	3.177	8.14	3.087
HUW468×SONALIKA	5.25	0.504	9.46	2.023
HUW468×K65	1.71	-4.933	4.82	-2.879
UP2338×HD2402	-1.99	3.990	5.41	3.140
UP2338×RAJ1972	0.10	0.781	2.64	-3.923
UP2338×HD2329	-5.77	-5.031	4.38	3.083
UP2338×LOK1	6.62	9.549	8.83	3.441
UP2338×SONALIKA	5.23	-1.310	9.03	1.946
UP2338×K65	1.76	-10.172	4.43	-5.678
HD2402×RAJ1972	6.05	6.525	10.38	0.247
HD2402×HD2329	1.18	10.247	8.46	8.077
HD2402×LOK1	2.97	-0.765	6.74	4.263
HD2402×SONALIKA	0.86	-4.627	1.58	-0.115

Shashank Srivastav,  
Genetic Evaluation of Bread Wheat's Grain Yield and Quality Traits

HD2402×K65	7.93	11.927	9.47	8.272
RAJ1972×HD2329	1.26	7.236	8.99	6.127
RAJ1972×LOK1	-0.88	-0.170	7.01	-1.395
RAJ1972×SONALIKA	-1.43	-1.317	2.64	-0.761
RAJ1972×K65	7.16	2.958	10.35	4.754
HD2329×LOK1	2.15	-0.562	4.87	3.573
HD2329×SONALIKA	2.91	1.601	0.64	-6.432
HD2329×K65	-2.40	-3.408	3.85	-1.926
LOK1×SONALIKA	5.30	2.571	8.25	2.075
LOK1×K65	9.96	5.350	6.46	-3.785
SONALIKA×K65	8.47	5.238	8.03	5.249
SE±	0.359		0.331	

### Selection parameter

#### Heritability and the progression of genetics

For both generations, the estimated heritability (in the narrow sense) and genetic gain (in terms of genetic advance in percentage above the mean) for fourteen characteristics are listed in Table.

“Table shows that no exceptional value of genetic progress in percent above mean in F1 generation was ever documented. Only moderate to low value were confined for plant height (7.12), grain yield per plant (6.74), leaf area index (5.07), day to maturity (4.22), 1000-grain weight (4.19), number of grains per spike (1.52), spikelet's per spike (0.75), , protein content (0.39), number of tillers per plant (0.35) and gluten content (0.21).

Plant height (6.74), day to maturity (5.70), grain yield per plant (4.50), leaf area index (4.04), days to 50% flowering (1.99), 1000-grain weight (1.99), num number of tillers per plant (0.63), spikelet's per spike (0.63), gluten content (0.51), and protein content (0.41) were all moderate to low in the F.”

Table 5: Heritability and genetic progress estimates for 14 wheat traits throughout generations F1 and F2.

Characters	Grand Mean (X)			Heritability % (h <sup>2</sup> )		Genetic Advance at 5%		Genetic Advance at 1%	
	Parents	F1	F2	F1	F2	F1	F2	F1	F2
Number of tillers/Plant	9.02	8.84	8.27	40.0	35.0	0.27	0.49	0.35	0.63
Plant height (cm)	98.74	100.14	96.37	59.0	58.0	5.55	5.26	7.12	6.74
Spike length /Plant (cm)	10.59	10.58	10.08	42.0	45.0	0.47	0.44	0.60	0.57
Leaf area index	15.92	20.34	19.63	60.0	61.0	3.96	3.15	5.07	4.04
Day to maturity	39.01	112.70	113.59	61.0	68.0	3.29	4.45	4.22	5.70
Grain yield/ Plant (g)	39.75	41.81	39.91	56.0	42.0	5.26	3.51	6.74	4.50
Protein content (%)	11.42	11.95	11.87	27.0	29.0	0.30	0.32	0.39	0.41
Gluten content (%)	8.53	8.72	8.70	15.0	32.0	0.16	0.40	0.21	0.51

#### 4. Conclusion

After sifting through all of the data, we can say that the hypotheses put forth by the various scientists in the manuscript have been confirmed by our research, and that in a population as diverse as this one, the pedigree method of selection, in combination with the recurrent modified technique, will be the best strategy for increasing crop yield by selecting for desirable traits.

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