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Studies on genetic variability in F5 segregating generation of wheat (*Triticum aestivum* L.)

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Abstract
The current investigation involved the analysis of 90 wheat genotypes from an F5 segregating population to assess variability, heritability, and genetic advance. The analysis of variance demonstrated significant variability among the genotypes for 13 traits. The F5 progeny resulting from the cross DBW-110 X MP-3382 exhibited the highest grain yield per plant based on mean performance. Among the traits, high percent coefficient of variation (PCV) was observed in biological yield (34.51), followed by harvest index (33.01), grain yield per plant (30.23), ear weight (22.74), number of productive tillers per plant (21.81), chlorophyll content (18.45), test weight (15.1), number of grains per ear (13.67), number of spikelets per ear (13.54), ear length (11.9), plant height (10.52), days to maturity (6.98), and days to 50% heading (5.3). Similarly, high genetic coefficient of variation (GCV) was observed in biological yield (34.28), followed by chlorophyll index (32.99), harvest index (30.28), ear weight (20.53), number of productive tillers per plant (20.25), grain yield per plant (18.28), grain weight (14.44), number of spikelets per ear (13.18), number of grains per plant (12.91), ear length (11.21), plant height (10.18), days to maturity (6.9), and days to flowering (5.06). Furthermore, all the traits exhibited high broad sense heritability estimates. In particular, plant height, number of productive tillers per plant, ear length, number of spikelets per ear, ear weight, number of grains per ear, test weight, biological yield per plant, grain yield per plant, harvest index, and chlorophyll content demonstrated high heritability along with significant genetic advance. These results indicate that these traits can be effectively improved through direct selection.

Keywords: Genetic, segregating, wheat, population, *Triticum aestivum* L.

1. Introduction
Wheat (*Triticum aestivum* L.) is the second most cultivated crop in India, following rice (*Oryza sativa* L.). It serves as the staple food for approximately 40% of the global population. With India's population growing at a rate of 1.2%, ensuring sufficient food supply becomes a challenging task for plant breeders. Their goal is to enhance productivity and overall crop production, particularly of staple crops, to meet the increasing demand and achieve food security. Since the cultivable land area cannot be expanded indefinitely, the focus lies on augmenting production through the utilization of superior varieties, hybrids, efficient resource management, and effective management of biotic and abiotic stresses. These approaches provide the best available options to enhance agricultural output and sustainably address the food requirements of the country.

The initial and authentic form of cultivated bread wheat was primarily comprised of landraces. These landraces were chosen by farmers from diverse and wild wheat populations based on their exceptional performance, particularly in terms of yield and other favorable traits. This early method of selection was non-scientific in nature. However, during the process of domestication and the introduction of new wheat varieties to local environments, specific genetic characteristics were favored, causing them to diverge from their wild counterparts. This divergence was driven by the need to meet the increasing food demands of a rapidly growing population. To address the challenge of feeding a growing population and ensuring food security, it became crucial to develop novel and improved wheat varieties that exhibited high resistance to both biotic stresses (Such as diseases, insects, and pests) and abiotic stresses (such as drought, nutrient deficiencies, and heat). This necessitated the development of innovative breeding methods and approaches to unlock the genetic potential of wheat crops.

The success of crop improvement depends significantly on the extent of genetic variability and the heritability of desirable traits. Genetic variability is a crucial factor in the process of evolution, as it determines how individuals respond to environmental stresses.

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This, in turn, leads to the differential survival of organisms within a population, favoring the selection of the most suitable variants through natural selection. In crop breeding, heritability and genetic advance are two important parameters for selection.

Breeders are interested in selecting superior genotypes based on their phenotypic expressions. Heritability estimates serve two primary purposes in this context. Firstly, they provide information about the phenotypic expression of traits, helping breeders understand how these traits manifest themselves. Secondly, heritability estimates offer insights into the transmission of traits from parent to progeny, aiding breeders in predicting the inheritance patterns of desired traits.

Yield and its component traits are influenced by multiple genes, and their expression is greatly influenced by environmental factors. Traits controlled by non-additive gene action tend to have high heritability but low genetic advance. On the other hand, traits controlled by additive gene action exhibit both high heritability and genetic advance.

Grain yield is a multifaceted trait that is influenced by a multitude of genetic factors and environmental fluctuations. To develop high-yielding varieties, it is crucial to have a comprehensive understanding of the existing genetic variation for yield and its various components. The observed variability in yield is a result of both genetic and environmental factors, although only the genetic component is heritable. However, relying solely on estimates of heritability does not provide insight into the expected improvement in the next generation. It is necessary to consider these estimates in conjunction with measures of genetic advance and the change in mean value between generations to gain a more accurate understanding of the potential progress (Shukla et al., 2006) [41].

2. Materials and Methods
The study utilized a total of 90 genetically diverse genotypes of F5 segregating generation of wheat (Triticum aestivum) along with four local check varieties. The evaluation was conducted at the Department of Plant Breeding and Genetics field, located within Lovely Professional University in Phagwara, Punjab. The climate in this area follows a seasonal pattern, with summers occurring between April and June and winters prevailing from November to February. The district where the university is situated primarily consists of alluvial deposits from the Indus-Ganga River system, covering approximately 18,000 square kilometers and accounting for 36% of Punjab's total area. The specific geographical coordinates of the location are approximately 31.2446771° north latitude and 75.695430° east longitude, with an altitude of around 300 feet above sea level.

The study recorded observations on 13 traits namely days to 50% flowering, days to maturity, plant height, no. of productive tillers per plant, ear length, ear weight, number of spikelets per ear, no. of grains per ear, grain weight, biological yield per plant, harvest index, grain yield per plant and chlorophyll index using an augmented design of experimentation. The planting of the material took place during the Rabi season of 2021-22, with a row-to-row spacing

of 22.5 cm. All recommended agronomic field practices were followed throughout the crop growth period. The analysis of variance was performed to partition the total variation into components attributed to treatments and replications, following the procedure outlined by Panse and Sukhatme (1957) [32]. The current study involved the estimation of three types of coefficients of variation, namely phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), and error/environmental coefficient of variation (ECV), as well as heritability. These coefficients were calculated using the formulas provided by Burton (1952) [7] and Burton and Devane (1953) [8]. The estimates of genetic advance were obtained using the formula given by Johnson et al. (1953) [14].

3. Results and Discussion
The mean sum of square was highly significant for Days to maturity, plant height, no. of productive tillers per plant, ear length, no. of spikelets per ear, ear weight, grain weight, biological yield per plant grain yield per plant, harvest index and chlorophyll index however it was not significant for remaining characters indicates that there is an ample scope for selection of promising genotype from present genotypes for yield improvement. The wide range of variation observed in all the characters offer scope of selection for development of desirable type of wheat. The presence of large amount of variability might be due to diverse source of material as well as environmental influence affecting the phenotypes. Similar findings in wheat were also reported by Mahmood et al. (2005) [28]; Nagireddy and Jyothula (2009) [30]; Nayeem et al. (2002) [31]; Ahmad et al., (2003) [40] and Khiziri et al. (2010) [15] Kumar et al. (2014) [19].

The heritability estimates for various traits in a study showed high values, high heritability was recorded for the harvest index(99.9%) followed by grain yield per plant (99%), biological yield (98.67%), chlorophyll content (98.1%), days to maturity (97.63%), no. of spikelets per ear (94.8%), plant height (93.71%), days to 50% flowering (91.04), no. of grains per ear (89.25%), ear length (88.72%), no. of productive tillers per plant (86.2%), ear weight (81.48%), test weight (80.41%). Similar findings were reported in studies conducted by Kumar et al. in 2018 [42], Bayisa et al. in 2020 [6], Kumar et al. in 2021 [20], and Prasad et al. in 2021 [43] for days to 50% flowering, days to maturity and number of spikelets per ear. The high heritability observed in these traits suggests that selecting individuals based on their phenotypic characteristics could be an effective approach.

The genetic advance percent per mean varied across different traits, highest for biological yield (70.25) followed by harvest index (68.03%), grain yield per plant (61.75%), no. of productive tillers per plant (38.78%), ear weight (38.22%), chlorophyll content (37.35%), test weight (26.71%), no. of spikelets per ear (26.48%), no. of grains per ear (25.16%), ear length (21.78%), plant height (20.34%), days to maturity (14.06%) and days to 50% heading (9.96%).Similar results were observed by Kumar et al., 2018 [42], Bayisa et al., (2020) [6] Kumar et al., (2021) [20].

Table 1: Analysis of variance

Source	DF	DTF	DM	PH	NPT/P	EL	NS/E	EW	NG/P	GW	BY/P	GY/P	HI	CI
Treatment (ignoring Blocks)	93	39.02**	83.14**	136.08**	1.17**	1.39**	6.79**	0.45**	32.48**	56.26**	56.4**	6.48**	159.3**	46.8**
Treatment: Check	3	147.11**	240.6**	39.63**	1.8**	2.95**	0.71*	0.06 ns	37.46**	121.7**	76.2**	1.57**	139.9**	47.6**
Treatment: Test	89	24.31**	77.8**	108.51**	1.01**	1.13**	3.27**	0.2**	29.46**	54.1**	56.2**	6.3**	161.3**	47**
Treatment: Test vs. Check	1	1023.6**	86.23**	2878.7**	13.7**	20.3**	338**	23.8**	286.4**	52.14*	10.8**	37.1**	40.66**	28.9**
Block (eliminating Treatments)	5	4.57 ns	8.57**	38.08**	7.77**	7.87**	6.28**	7.51**	7.13 ns	36.77*	12.8**	7.46**	7.29**	6.9**
Residuals	15	2.18	1.84	6.83	0.14	0.13	0.17	0.04	3.17	10.6	0.75	0.06	0.17	0.89
CV(%)	-	1.61	1.08	2.69	7.86	3.92	2.93	9.09	4.41	7.17	3.96	2.94	1.07	2.53

*, **=significant at 5% and 1% probability levels, respectively.

ns $p>0.05$; * $p<= 0.05$; ** $p<= 0.01$

Table 2: Estimates of variability, heritability and genetic advance as percent of mean in wheat (Segregating F5 generation population)

Characters	Range		Mean	Co-Variance		Heritability (BS) %	Genetic advance	GA %
	Min.	Max.		GCV%	PCV%			mean
Days to 50% heading	80.58	104.42	92.95	5.06	5.3	91.04	9.26	9.96
Days to maturity	94.33	135.33	126.38	6.9	6.98	97.63	17.77	14.06
Plant height (cm)	78.31	124.71	99.01	10.18	10.52	93.71	20.14	20.34
No. of productive tillers per plant	1.13	7.96	4.61	20.25	21.81	86.2	1.79	38.78
Ear length(cm)	4.79	12.96	8.92	11.21	11.9	88.72	1.94	21.78
No. of spikelets per ear	8.16	19.7	13.36	13.18	13.54	94.8	3.54	26.48
Ear weight(g)	0	4	1.98	20.53	22.74	81.48	0.76	38.22
Number of grains per ear	28.21	57.21	39.72	12.91	13.67	89.25	9.99	25.16
Test-weight(g)	29.13	66.93	45.67	14.44	16.1	80.41	12.2	26.71
Biological yield	8.96	42.58	21.72	34.28	34.51	98.67	15.26	70.25
Grain yield per plant (g)	2.27	19.86	8.31	30.08	30.23	99	5.13	61.75
Harvest index (%)	11.99	78.07	38.47	32.99	33.01	99.9	26.17	68.03
Chlorophyll content	21.05	52.66	37.15	18.28	18.45	98.1	13.88	37.35

Table 3: Crosses showing high mean performance in F5 segregating population

Sr. no	Character	Genotypes
1	Days to 50% flowering	GW- 273 X LOK-1
2	Days to maturity	MP-1203 X GW-273
3	Plant height (cm)	MP-1203 X GW-273
4	No. of productive tillers/plant	DBW-110 X MP-3382
5	No. of spikelets/ear	DBW-110 X MP-3382
6	No. of grains/ear	DBW-110 X MP-3382
7	Ear length (cm)	DBW-110 X MP-3382
8	Ear weight (g)	DBW-110 X MP-3382
9	1000 grain weight (g)	DBW-110 X MP-3382
10	Biological yield/ plant (g)	MP-1203 X GW-273
11	Grain yield/ plant (g)	DBW-110 X MP-3382
12	Harvest index (%)	DBW-110 X MP-3382
13	Chlorophyll index	DBW 110 X MP-3382

4. Conclusion

As per the traits, high mean performance for the characters along with high performing crosses has been given in the table no.3. In the evaluation of F5 segregating population plant height, number of productive tillers per plant, ear length, number of spikelets per ear, ear weight, number of grains per ear, test weight, biological yield per plant, grain yield per plant, harvest index, and chlorophyll content exhibited high heritability along with high genetic advance. These findings indicate that direct selection can effectively improve these traits. Furthermore, the number of days to maturity displayed high heritability along with a moderate genetic advance, suggesting the presence of additive gene action in determining this trait. In contrast, high heritability with low genetic advance was observed for days to 50% flowering, indicating the influence of non-additive gene action on this particular trait.

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