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## Genetic variability studies of newly developed lines in bread wheat (*Triticum aestivum* L.)

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### Abstract

Genetic variability was assessed in newly developed lines in bread wheat (*Triticum aestivum* L.) germplasm with 50 genotypes of wheat collected from office of Wheat Specialist, Agricultural Research Station, Niphad (MPKV, Rahuri) during *Rabi*, 2019-20. The analysis of variance for eight characters indicated the appreciable amount of variability was present in the material under study. Genotypic coefficient of variation (GCV) was lower than the phenotypic coefficient of variation (PCV) for all the characters under study. The high GCV and PCV was observed for grain yield per plot, number of spikelets per earhead, 1000 grain weight, number of grains per earhead, spike length and plant height. The characters such as grain yield per plot, 1000 grain weight, number of spikelets per earhead, and number of grains per earhead exhibited high heritability coupled with high genetic advance indicating that most likely heritability is due to additive gene effect and selection may be effective for these characters. High heritability coupled with moderate genetic advance was observed in plant height, spike length, days to 50 percent flowering indicating that additive and non-additive both gene action were present.

**Keywords:** Wheat, genetic variability, heritability, genetic advance

### Introduction

Wheat (*Triticum aestivum* L.) is one of the most important staple food crops of the world population and it has been the cheapest source of food, energy and protein. It belongs to family Poaceae (Gramineae) that includes other cereals such as rice and corn. It provides provides 20 percent of a person's total calorie intake (Anonymous, 2018-a) [1]. Wheat has a protein concentration of roughly 12 percent, which is rather high when compared to other major cereals. Wheat contains 70 percent carbohydrates, 2 percent fiber, 2 percent vitamins, 1-1.5 percent fat and a variety of minerals (Anonymous, 2018-b) [2]. Wheat is a low-cost supply of amino acids, as well as a good source of P, Fe, Cu, Mn, Mg, Zn and vitamin B.

In India, wheat is cultivated in an area of 30.56 mha with the production level of 109.24 Mt (Anonymous, 2020) [4], while in Maharashtra, wheat is cultivated in an area of 1.38 m ha. with the production of 2.30 Mt (Anonymous, 2019) [3].

Any breeding programme to be successful it depends upon the degree of genetic variability available in the crop species, the efficiency of selection technique implemented by plant breeder. Grain yield is a complex phenotypic character which gets influenced by several quantitative traits, these are governed by polygenes. An implementation of biometrical techniques in plant breeding has helped to better understand the genetics of quantitative characters and has proved useful to the plant breeder for systematic analysis at genetic level. Robinson *et al.* (1949) [15] stated that heritability is the main concern to breeder, since it indicates that improvement can be achieved through selection. Heritability together with genetic advance would bring out the genetic gain expected from selection (Johnson *et al.*, 1955) [9]. The knowledge of the source of genetic variability for the different characters is considered of great importance, since the target of the plant breeder is to improve the yield and the quality by evolving superior varieties. With this available background information, the present studies have been initiated with an objective to understand the variability for grain yield and yield contributing characters in wheat.

### Materials and Methods

For the present study, 50 genotypes of wheat (*Triticum aestivum* L.) collected from office of Wheat Specialist, Agricultural Research Station, Niphad (MPKV, Rahuri). The genotypes were sown in *Rabi*, 2019-20 in a Randomized Block Design with two replications.

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Dibbling was used to sow the grains. Each entry was represented by two rows of 6.0 meters each with a 40-centimeter space between them. Observations were recorded on randomly selected five plants for eight characters *viz.* days to 50 percent flowering, days to maturity, plant height (cm), spike length (cm), number of spikelets per earhead, number of grains per earhead, 1000 grain weight (g) and grain yield per plot (g).

The analysis of variance was done as suggested by Panse and Sukhatme (1985) [13]. The genotypic and phenotypic variance was calculated as per the formulae (Burton and Devane, 1953) [6]. Genotypic coefficient of variation (GCV) was estimated by formula suggested by Burton (1952) [7].

$$GCV (\%) = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where,  $\sigma_g^2 = V_g =$  Genotypic variance,  $\bar{X} =$  General mean of the character

Phenotypic coefficient of variation (PCV) was also estimated by the formula suggested by Burton (1952) [7].

$$PCV (\%) = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

Where,  $\sigma_p^2 = V_p =$  Phenotypic variance

GCV and PCV were classified as suggested by Robinson *et al.* (1949) [15]

Heritability estimates in broad sense ( $h^2$ ) were computed by the formula suggested by Burton (1952) [7]. Heritability was classified as, (Robinson *et al.* 1949) [15]. From heritability estimates the genetic advance was estimated by the formula given by Burton (1952) [7]. In order to estimate the relative utility of genetic advance among characters, genetic advance as percent for mean is usually calculated. The range of genetic advance as percent of mean was classified as per suggestion by Johnson *et al.* (1955) [9].

## Results and Discussion

The analysis of variance for eight characters has been presented in Table 1. It revealed that, the mean sum of square due to treatments for all characters studied is found to be significant. It indicated that appreciable amount of diversity is present in the material under study. The parameters range, GCV and PCV, heritability in broad sense and genetic advance as percent of mean have been presented in the Table 2.

The estimates for genotypic coefficients of variation (GCV) were lower than the phenotypic coefficients of variation (PCV) for all characters under trial. The character grain yield per plot exhibited the highest GCV (27.31) and PCV (28.51). The high GCV and PCV was observed for grain yield per plot indicating the presence of large variation among the genotypes for this character. The characters number of spikelets per earhead, 1000 grain weight and number of grains

per earhead exhibited moderate GCV and PCV. One character exhibited high GCV and PCV, three characters recorded moderate GCV and PCV, while four characters recorded low GCV and PCV. Similar results were obtained for grain yield per plant, number of tillers per plant and number of grains per spike by Yousaf Ali *et al.* (2008) [17], Kumar *et al.* (2009) [10] and Devi *et al.* (2014) [8].

The characters *viz.* spike length, plant height, days to 50 percent flowering and days to maturity registered low estimate of GCV and PCV which indicate that low degree of variation found in these characters in the present experimental material, thus gives little scope for future improvement of these characters. Similar types of findings were reported by Kumar *et al.* (2009) [10] for days to 50 percent flowering and days to maturity; Mohammed *et al.* (2011) [12] for days to maturity and 1000 grain weight; Asayeet *et al.* (2013) [5] for days to maturity.

All heritability figures were more than 60% so all characters have been classified under high heritability. Heritability as well as genetic advance are regarded as an important selection parameter. Burton (1952) [7] suggested that "genetic variation along with heritability estimate would give a better idea about the efficiency of selection." From the present study, it can be concluded that high heritability values were recorded for all the characters; these estimates indicate the least effect of environment on these characters.

Grain yield per plot, 1000 grain weight, number of spikelets per earhead, and number of grains per earhead exhibited high heritability with high genetic advance indicating that probably heritability is due to additive gene effect and selection could be effective for these characters. High heritability with moderate genetic advance was observed in plant height, spike length, days to 50 percent flowering which indicate that additive and non-additive both gene actions were present. Similar results were obtained by Rebetzke (1999) [14] found high heritability with moderate genetic advance for plant height and Subhashchandra (2009) [16] reported high heritability with moderate genetic advance for plant height and sedimentation value. In the case of days to maturity, Kumar *et al.* (2013) [11] observed substantial heritability with low genetic advance.

**Table 1:** Analysis of variance for eight characters of 50 wheat genotypes

Sr. No.	Character	Replication	Genotypes	Error
	DF	1	49	49
1	Days to 50% flowering	1.69	45.52**	0.51
2	Days to maturity	0.25	53.48**	0.68
3	Plant height (cm)	2.86	133.72**	2.03
4	Spike length (cm)	0.42	2.37**	0.23
5	No. of spikelets per earhead	3.57	9.16**	0.11
6	No. of grains per earhead	47.33	46.35**	1.86
7	1000 grain weight (g)	39.31	47.26**	5.29
8	Grain yield per plot (g)	221841.00	138891.47**	13250.33

\*Significant at 5% level

\*\*Significant at 1% level

**Table 2:** Different parameters of variability in 50 genotypes of wheat

Sr. No.	Characters	Mean	Range	Genotypic variance	Phenotypic variance	PCV (%)	GCV (%)	h <sup>2</sup> % (b.s.)	GA	GA as % mean
1	Days to 50% flowering	67.37	59.50 - 79.00	22.51	23.02	7.12	7.04	97.78	9.66	14.34
2	Days to maturity	112.41	103.50 - 122.00	26.40	27.08	4.62	4.57	97.49	10.45	9.29
3	Plant height (cm)	96.51	83.20 - 123.00	65.84	67.87	8.53	8.41	97.00	16.46	17.05
4	Spike length (cm)	11.22	8.95 - 14.30	1.08	1.31	10.20	9.26	82.44	1.74	17.32
5	No. of spikelets per earhead	16.08	13.50 - 21.40	4.52	4.64	13.39	13.23	97.41	4.35	26.88
6	No. of grains per earhead	44.76	35.10 - 58.40	22.25	24.11	10.97	10.53	92.28	9.33	20.85
7	1000 grain weight(g)	39.23	31.40 - 53.10	20.99	26.27	13.06	11.67	79.86	8.43	21.49
8	Grain yield per plot(g)	924.22	479.00 - 1644.00	62820.57	76070.90	29.84	27.11	82.58	469.20	50.76

### Conclusion

The analysis of variance indicated that appreciable amount of variability is present in the material under study. High estimate of GCV and PCV indicate that high degree of variation found in these characters in the present experimental material, thus gives large scope for future improvement of these characters. It can also be seen that high heritability values were recorded for all the characters; these estimates indicate the least effect of environment on these characters. All high heritability values indicate transmission of characters from parents to their offspring which will be helpful for selection in future hybridization programme. High heritability coupled with moderate genetic advance as percent of mean indicating additive gene action and selection would be effective for these characters.

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