

Heritability of Some Important Quantitative Characters in Wheat (*Triticum aestivum* L.)

by

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One of the most important properties of a metric character is the heritability. It is expressed as the proportion of total variance that is attributable to the average effect of genes and it determines the degree of resemblance between relatives. But the most important function of the heritability in the genetic studies of quantitative characters is its predictive role. It expresses the reliability of the phenotypic value as a guide to the breeding value. We can only measure phenotypic values of the individuals and the performance in the following generation will be determined by the breeding value. The possible advance through selection based on phenotypic values can, therefore, be predicted only from knowledge of the degree of correspondence between phenotypic value and breeding values. This degree of correspondence is measured by the heritability estimates. The heritability estimates enter into almost every formula connected with breeding methods and many practical decisions about the techniques to be followed depend on its magnitude.

Materials and Methods: The materials consisted of eleven geographically diverse wheat varieties viz., NP 825 and NP 847 from Delhi, C 306, C 303 and C 273 from Punjab and S 227, S 210, S 354, S 355, S 409 and Mayo-64 from Mexico, and their nine F_2 hybrid populations. Punjab and Delhi wheats are tall growing while all the Mexican wheats, except S 409 which is triple dwarf, are double dwarf. The F_2 cross combinations studied were, C 273 \times S 354, C 273 \times S 355, C 306 \times S 409, C 303 \times 210, C 303 \times Mayo 64, C 303 \times S 227, C 303 \times S 409, NP 825 \times C 306, NP 847 \times C 303.

All the twenty populations were grown in a randomised block design with six replications at Punjab Agricultural University, Ludhiana during *rabi* 1965-66. Each population was provided two 3.45 metres long rows in each replication. The row to row and plant to plant spacings were 22.5 and 15 cm, respectively. The data were recorded on ten randomly selected plants from 2-row plots of each parent variety and on twenty similarly selected plants of each F_2 cross. Individual plant observations were recorded for nine characters i. e. days to flowering, plant height, spike length, number of spikelets per plant, number of grains per spike, 100-grain weight and grain yield.

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The mean progeny values were used in the statistical analyses. The genotypic and phenotypic coefficients of variation were estimated by the following formulae :

$$\text{Phenotypic coefficient of variation} = \frac{\sqrt{\text{Phenotypic variance}}}{\bar{x}} \times 100$$

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where, \bar{x} = mean of the character

The genotypic variance was estimated by the formula :

$$\text{Genotypic variance} = \frac{(\text{Mean squares for progenies} - \text{Mean squares for error})}{\text{number of replications}}$$

The phenotypic variance was calculated by adding genotypic and error variances.

Heritability for different characters was determined by the following two methods :-

- 1) Heritability from variance components (Hanson *et al.* 1956) :-

$$H_1 = \frac{S^2_g}{S^2_P} \times 100 \text{ where, } S^2_g = \text{genotypic variance and } S^2_P = \text{phenotypic variance}$$

- 2) Heritability by parent-offspring correlation method :-

Parent-offspring correlations were worked out by using the formula :

$$r_{\text{MP/OFF}} = \frac{\text{Covariance MP/OFF}}{\sqrt{(\text{Variance MP}) \times (\text{Variance OFF})}}$$

where MP = Mid-parent $\frac{(\text{Parent}_1 + \text{Parent}_2)}{2}$ and

OFF = Offspring i.e. F_2 hybrid

The degree of determination was worked out by squaring the correlation coefficient, which gives the estimate of true heritability (H_2) of a character. It was converted into percentage but multiplying with hundred.

Results : The heritability estimates determined by two different methods and the phenotypic and genotypic variances are given in Table I. The heritability estimates worked out by variance component method (H_1) i.e. heritability in broad sense were high for plant height, days to flowering,

number of spikelets per spike, number of grains per spike and 100-grain weight. It was moderate for spike length and comparatively low for spikes per plant and grain yield. The heritability estimates (H_2) by the parent-offspring correlation method (heritability in narrow sense) were high for plant height, grains per spike and spikelets per spike; moderate for spikes per plant, spike length and days to flowering; and very low for grain yield. The coefficient of phenotypic variation was highest for grain yield followed by number of spikes per plant and number of grains per spike but as regards genotypic co-efficient of variation, grain yield was regulated to the fourth position. Error variance was comparatively higher for grain yield and spikes per plant.

TABLE. *Estimates of heritability, variances and coefficients of variability*

Character	Range	Variances			Phenotypic coefficient of variation	Genotypic coefficient of variation	Heritability (percent)	
		Phenotypic	Genotypic	Error			H ₁	H ₂
Days to flowering	97-111	23.34	19.52	3.82	4.73	4.32	83.64	23.31
Plant height (cm)	67-143	335.20	312.97	22.23	15.82	15.35	93.36	91.85
Spike length (cm)	9.8-12.0	0.37	0.20	0.16	5.15	4.01	55.31	26.44
Spikelets per spike	19.1-25.1	2.45	2.02	0.44	7.48	6.81	82.21	61.11
Grains per spike	44.4-75.9	87.26	76.56	10.70	16.96	15.89	87.73	85.26
100-grain weight (g)	2.82-4.79	0.43	0.38	0.05	16.22	15.06	87.50	15.78
Spikes per plant	8.6-15.2	4.34	1.26	2.72	18.08	11.04	37.43	45.45
Grain yield (g)	15.8-28.7	25.74	11.21	14.53	21.72	14.31	43.55	4.29

Discussion: The heritability estimates varied largely for the different quantitative characters studied. It may, however, be mentioned that heritability is a property, not only of a character but also the population under study and the environmental conditions to which it is subjected. The heritability depends upon the magnitude of all the components of variance and a change in any one of these will affect it. The populations selected for this study are quite representative of the wheat breeding material being handled these days by the wheat breeders for the development of short statured superior varieties.

The magnitude of heritability estimates worked out by following first method (H_1) will depend largely on variability between the populations and the extent to which a particular character is influenced by the environments. The low heritability observed for grain yield and number of spikes per plant is largely because of greater influence of the environment which reduces the degree of correspondence between phenotypic and the breeding values. Weibel (1956) and Sikka and Jain (1958) also reported low heritability for grain yield while Gandhi *et al.* (1964) observed moderate value.

The heritability estimate by the parent-offspring correlation method also varied greatly for different characters. The differences are largely due to differential gene interaction for the various characters in the F_2 populations under study. These are estimates of narrow sense heritability and give better picture of the true breeding values. The comparison between the two heritability estimates revealed lower values for the grain yield, 100-grain weight, days to flowering and spike length in the parent-offspring correlation method. This might be because of dominance and epistatic gene actions involved in these characters. Whitehouse *et al.* (1958), Tandon (1961) and Singh (1968) have reported that gene interaction is important in manifestation of grain yield. Partial to full dominance for grain weight had been observed by Weibel (1956), Johnson and Aksel (1959) and Singh (1967). Dominance effects had also been reported for spike length and heading date (Selim, 1960 and Nandpuri, 1959).

The estimation of heritability alone is not sufficient to predict genetic advance in a population. Besides heritability it will depend upon phenotypic variability in the population and intensity of selection. However, the heritability estimates clearly guide in the procedures to be adopted. The results of the present study reveal that the grains per spike and the spikelets per spike are the two important yield components which should be looked into while selecting the parents for hybridisation as these are greatly transmitted to the offsprings and are less influenced by the environments. Grain weight is also less influenced by environment but because of gene interactions involved, the selections in early generations may be little less effective. Spikes per plant, an important yield component, largely depend on the parental choice, but because of greater environmental influences, more precise techniques are required to discern the heritable differences. The grain yield does not seem to depend much on the parental choice and is also highly influenced by the environments. The selection directly for grain yield may be more effective in the advanced generations tested in replicated trials and if possible repeated over different environments. The masking effect of the gene interactions will also get considerably reduced in the advanced generations. In the early generations like F_2 , selection for yield components may be more rewarding.

Summary: Heritability estimates were worked out by variance component method and parent-offspring correlation method from F_2 cross combinations and their parents. Out of 11 parent varieties, 5 are tall growing. 5 are 2-gene dwarf and one is 3-gene dwarf. The estimates by variance component method (heritability in broad sense) revealed high heritability for plant height, days to flowering, number of spikelets per spike and 100-grain weight; moderate for spike length and comparatively low for spikes per plant and grain yield. The narrow sense estimates of heritability (parent-offspring correlation

method) were lower than the estimates in broad sense for grain yield, 100-grain weight, days to flowering and spike length which indicate the influence of dominance and/or epistasis in genetic control of these characters. The implications of heritability estimates in the breeding programmes have been discussed.

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