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Inheritance of Five Quantitative Characters of Bread Wheat

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Summary. Heritability estimates of five characters of the wheat plant were studied in five crosses involving six cultivars of bread wheat. Parents, F_1, F_2 and backcrosses to both parents were used in the estimation of the genetic parameters.

Heritability was low for number of fertile spikes/plant, moderate for number of spikelets/spike, number of kernels/spike, 1000-kernel weight and moderately high for number of kernels/spike. Evidence for mainly nonadditive gene effects were observed in the expression of number of fertile spikes and 1000-kernel weight. Although nonadditives contributed to a lesser degree to the gene action, additives seemed to be the most important genetic expression regulating number of spikelets/spike, number of kernels/spike, and number of kernels/spikelet. Except for number of fertile spikes/plant, selection in F_2-populations seems to be promising.

Keywords: Heritability – Bread wheat

Introduction

The pronounced attention given to the improvement of wheat production in Saudi Arabia promoted the need for local wheat breeding programs. The most efficient breeding procedures and the expected gains from selection depend upon the degree to which the phenotype reflects the genotype (heritability), the magnitude of gene effects and the mode of their action. Little information is available as to possible improvement or importance of genotypic and environmental effects on local as well as new introductions.

The present study was designed to obtain estimates of heritability for five characters using five crosses which involved six different parental lines of local and introduced cultivars.

Material and Methods

The five crosses used in the present study were derived from six parental wheat cultivars: "Mexipak" (M, Mexican), "Florence" (F, France), "Giza 150" (G, Egypt), "Agiba" (A, Iraq), "Samma" (S, Local) and "Khoulani" (K, Local). These five crosses were: M×F, M×K, M×S, F×G and A×G. The original crosses were made in the winter of 1974 and F_1's were grown later in the Fall of the same year along with the parents. Each F_1 was reciprocally crossed to both parents. In the Fall of 1975, parents, F_1, F_2 and BC populations were all sown at the College of Agriculture, Riyadh, in a randomized block design. Parental, F_1 and BC populations each occupied 4 rows while each of the F_2– populations occupied 30 rows. Twenty plants, spaced 15 cm apart, comprised each row and the distance between rows was 30 cm.

Data was collected from individual plants for the following characters:

(1) Number of fertile spikes/plant
(2) Number of spikelets/spike (average of 3 spikes/plant)
(3) Number of kernels/spike (average of 3 spikes/plant)
(4) Number of kernels/spikelet (obtained by dividing (3) by (2))
(5) 1000-kernel weight

A regular analysis of variance was conducted on the 5 characters. Heritability in the broad-sense (Hb) was calculated as the ratio of genetic to F_2 phenotypic variance. The genetic variance was obtained by subtracting the environmental variance, average of the P_1, P_2 and F_1 variance, from the F_2 phenotypic variance. Heritability in the narrow-sense (Hn) was calculated using the F_2 and backcross variances according to Allard (1960). The narrow to broad sense heritability ratio was obtained by dividing Hn by Hb estimates x 100. The data did not include BC_1 for cross 5 since few guarded plants existed at harvest. However, in order to complete the set of means required for the genetic parameters estimation, values were obtained using Mather and Jinks (1971) formula, $P_1F_1 = \frac{1}{2} P_1 + \frac{1}{2} F_1$, although it does contain some bias due to the assumption of only additive gene action.

Results and Discussion

Number of Fertile Spikes/plant

Means, heritability estimates and ratios from the five crosses are shown in Table 1. Broad-sense heritability (Hb)

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Table 1. Means, Heritability Estimates and Ratios for the Number of Fertile Spikes/Plant

Population	Crosses					Avg.
	1	2	3	4	5	
P_1	16.8	16.8	16.8	15.9	21.9	
P_2	15.93	23.25	27.8	16.9	16.9	
MP	16.4	20	19.8	16.8	19.4	
F_1	14.43	15.1	14.4	22	23.2	
F_2	15.9	16.52	15.4	14.5	19.2	
BC_1	10.6	24.8	10.3	14.1	–	
BC_2	18.75	14.3	15.9	17.3	17.8	
Hb	.41	.46	.3	.26	.31	.35
Hn	.10	.09	.14	.13	.17	.13
Hn/Hb %	24	20	47	50	55	39.2

MP = Mid parent, BC1 = $F_1 \times P_1$, $BC_2 = F_1 \times P_2$

Table 2. Means, Heritability Estimates and Ratios for the Number of Spikelets/Spike

Population	Crosses					Avg.
	1	2	3	4	5	
P_1	19.	19.	19.	17.1	18.2	
P_2	17.1	18.7	21.8	16.5	16.5	
MP	18.	18.8	20.4	17.	17.4	
F_1	18.58	19.9	20.9	18.3	18.	
F_2	19.4	19.7	18.5	16.7	16.7	
BC_1	19.8	17.6	18.0	18.8	–	
BC_2	20.25	21.5	18.6	16.3	17.1	
H_b	.56	.53	.42	.42	.41	.47
H_n	.16	.52	.28	.41	.34	.34
H_n/H_b %	28	98	67	98	83	74.8

estimates were low (Avg. .35) and indicated a strong environmental effect. The smallest Hb estimate occurred in cross 4 which involved two non-proliferating parents (F and G). These low heritability estimates are in contrast to Kaltsikes and Lee's (1971) findings in durum wheat of high heritability estimate of this character. The narrow sense-heritability (Hn) estimates were also low (Avg. .13) and together with the ratio of narrow to broad-sense heritability (Hn/Hb) suggest that a nonadditive genetic system is operating in the character.

F_1-population means for crosses 1, 2 and 3 were lower than those of their midparents but closely related to that of the respective lower parent. Most of the segregating populations (F_2, BC_1 and BC_2) had greater means than the respective F_1-values. Crosses 4 and 5 contrasted the above mentioned situation with high non-segregating population means vs. lower segregating population means. Such behaviour was seen as mere evidence for a substantial dominance effect which agrees with previous studies by Johnson et al. (1966). The extreme influence of environment on the number of fertile spikes/plant, even under precise plant spacing, coupled with very small additive gene effects, makes single plant selection in segregating populations futile.

Number of Spikelets/spike

The means of the different populations, along with heritability estimates for all crosses, appear in Table 2. With respect to the midparent means, F_1-population means for the number of spikelets were higher in all crosses. F_2-means for crosses 1 and 2 exceeded the respective midparent value. Similarly, values for the backcrosses of crosses 1, 2 and 4 were higher than the F_1-means and that of the parent involved in the backcross. These results suggested that lack of dominance seems to be the case and indicated an additive genetic expression for this trait similar to the observation made by Ketata et al. (1976) and Edwards et al. (1976). Further support for this conclusion is seen in the observed heritability estimates. Broad-sense heritability estimates ranged from .41 to .56 (Avg. .47) while the narrow-sense heritability estimates were closely related (Avg. .34) and was reflected in a high ratio of narrow to broad-sense heritability. The low-moderate heritability estimates indicate that number of spikelets is strongly dependent on environmental conditions as was reported by Rahman et al. (1977).

Number of Kernels/spike

Population means for the five crosses (Table 3) clearly show higher F_1-values than those of their respective midparent. These F_1-means closely approximated the parent with a greater number of kernels/spike. The F_2-population means were always lower than the midparent means

Table 3. Means, Heritability Estimates and Ratios for the Number of Kernels/Spike

Population	Crosses					Avg.
	1	2	3	4	5	
P_1	64.2	64.2	64.2	45	50.3	
P_2	45	46.8	60.7	49.3	49.3	
MP	45.6	55.5	62.5	47.2	49.8	
F_1	56.24	62.3	64.3	51.3	52.8	
F_2	53.1	51.8	54.4	37.73	38.	
BC_1	58.7	47.7	43.2	54.18	–	
BC_2	37.8	58.6	41.3	36.8	39.3	
H_b	.68	.56	.57	.57	.45	.57
H_n	.45	.17	.38	.32	.14	.29
H_n/H_b %	66	30	67	56	31	50

and the values from crosses 4 and 5 were still less than the lower parent value. The eminant dominance expression for greater number of kernels/spike was supported by high means of backcrosses to parents with greater means in crosses 1, 2 and 4.

Estimates of broad-sense heritability were moderately high, ranging from .45 to .68 (Avg. .57). Since broad-sense heritability is based on the analysis of F_2 and non-segregating generations, heritability estimates will depend primarily on the amount of variation available in the F_2 population. Parents with a greater difference in the expression of the trait under study will induce greater variation in their F_2-population than those with a smaller difference, unless different mechanisms operate in each parent. In the present study, the highest and lowest heritability estimates were obtained from cross 1 and cross 5, which involved the two parents with the greatest difference and the two parents with the smallest difference, respectively.

The exploitation of the moderately high heritability estimates obtained for this trait seemed to be hampered by the presence of nonadditives, (presumably dominant) since it was reflected in the narrow-sense heritability estimates (Avg. .29) and the ratio of narrow to broad-sense heritability.

Number of Kernels/spikelet

Means, heritability estimates and ratios are shown in Table 4. Heritability in the broad-sense was generally high for all crosses and on the average was the highest (Avg. .60) among the characters investigated in the present-study. Crosses 1 and 2, with cultivar M as a common parent, recorded the highest estimates (.74 and .65 respectively). F_1-means exceeded their mid-parent values in all cases but the higher parent means in crosses 3 and 5 only. Similarly, F_2-means closely approximated the mid-parent values in a pattern suggesting partial or absent dominance. The high means of backcrosses to parents with higher means (except for cross 4) is further evidence for the presence of additive gene effects. These results were expected in view of the high narrow-sense heritability estimates and Hn/Hb ratio which reflect higher additive portion relative to nonadditive one.

Based on the high heritability estimates, mass selection should be effective to improve this trait.

1000-Kernel Weight

Means, heritability estimates and ratios for all crosses are presented in Table 5. It is noteworthy that the single plant thresher used in the present study caused a mechanical bias due to the fact that light weight seeds were blown out with the chaff, resulting generally in a higher 1000-kernel weight than expected. Broad-sense heritability estimates were consistently moderate (range .46 – .58, Avg. .53) for this character. In all crosses, F_1-population means conspicously deviated from the midparent values and from the respective parents with heavier kernel weight, indicating that sizable amount of nonadditive gene action is involved in the expression of this character. Similarly, F_2-means for crosses 1, 4 and 5 exceeded the high parent means whereas cross 3 exceeded only the midparent. Examination of other segregating populations (BC's) showed a tendency of parents with higher means to transfer to their backcross populations means that closely related to their average, suggesting the presence of some additive effects. These results were enforced by the observed narrow-sense heritability estimates. Moreover, the ratio of narrow to broad-sense heritability showed that a good third of the genetic variation was due to additive effects. It seems that in the current material, dominance and additives contributed to the inheritance of 1000-kernel weight, a conclusion previously reported by Johnson

Table 4. Means, Heritability Estimates and Ratios for the Number of Kernels/Spikelet

Population	Crosses 1	2	3	4	5	Avg.
P_1	3.2	3.2	3.2	2.6	2.7	
P_2	2.6	2.5	2.8	2.9	2.9	
M_p	2.9	2.75	3.0	2.75	2.8	
F_1	3.	3.1	3.6	2.8	3.4	
F_2	2.74	2.6	2.9	2.3	2.9	
BC_1	3.0	2.8	2.4	2.9		
BC_2	2.28	2.7	2.2	2.3	2.8	
H_b	.74	.65	.56	.48	.57	.6
H_n	.55	.5	.42	.27	.39	.43
H_n/H_b %	74	75	75	56	68	70

Table 5. Means, Heritability Estimates and Ratios for the 1000 Kernel Weight

Population	Crosses 1	2	3	4	5	Avg.
P_1	38.7	38.7	38.7	43.7	38.3	
P_2	43.7	35.4	35.1	35.3	35.3	
MP	41.2	37.1	36.9	39.5	36.8	
F_1	44.36	42.4	40.0	36.9	41.5	
F_2	45.9	36.1	37.7	48.5	39.5	
BC_1	41.53	40.6	39.35	45.3	–	
BC_2	44.03	38.9	38.85	41.1	38.4	
H_b	.57	.57	.58	.49	.46	.53
H_n	.22	.18	.24	.13	.20	.19
H_n/H_b %	39	32	41	27	43	36.4

et al. (1966) for bread wheat and Lebsock and Amaya (1969) in *Durum* wheat.

In general, the heritability estimates obtained in this study were similar to those mentioned in previous reports by other workers. It is also worth noting that high heritability estimates in the present material occurred for characters exhibiting wide differences between the parental means. The failure to detect significant differences between generations could be attributed to close parental means and or sampling error.

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