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Estimation of Heritability and Genetic Gain of Some Metric Traits in Six Hybrid Population of Spring Wheat

Abdul Sattar, Muhammad Aslam Chowdhry and Muhammad Kashif
Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan

Abstract: Broad-sense heritability and genetic advance value were computed for flag leaf area, flag leaf weight, specific flag leaf area, specific flag leaf weight, plant height, tillers per plant, spike length, spikelets per spike, grains per spike, 1000-grains weight and grain yield per plant involving six bread wheat crosses viz., WLRG-6 x 5039, WLRG-7 x 5039, WLRG-6 x LU26S, WLRG-1 x LU26S and WLRG-1 x 5039. Most of these traits showed moderate to high estimates of heritability with appreciable genetic advance values. Crosses WLRG-7 x LU26S, WLRG-1 x 5039 and WLRG-7 x 5039 are of considerable interest showing high heritability estimates for all the characters studied.

Key words: Wheat genotypes, F₂ population, broad-sense heritability

Introduction

Wheat being the major food grain of Pakistan invites the attention of breeder/researcher and grower to raise the level of production so that hungry bellies of increasing population be filled and farmer could grow it economically. Wheat is the most widely grown crop in the world and approximately one sixth of the total arable land in the world is cultivated with it. In Pakistan wheat is grown over the area of 8.18 million hectares with production of 19.02 million tons with average yield of 2325 kg per hectare (Anonymous, 2002). It is dietary main for millions of people. The concerned breeders and geneticists have always been making efforts to improve its population to the level of self-sufficiency. However, the success of any breeding programme depends on the presence of genetic variation in the breeding material. High heritable character can easily be fixed with simpler selection procedure resulting in quick progress. Heritable, character can easily be fixed with simpler selection procedure resulting in quick progress. Heritability of a character describes the extent to which it is transmitted from one generation to the next generation. The knowledge of heritability thus guides the plant breeder to predict the behavior of the succeeding generation, making describable selection and accessing the magnitude of genetic advance improvement which is possible through selection. Considerable research on this aspect has already been reported by many researchers. High heritability with high genetic advance have been reported for plant height, tillers per plant, spikelets per spike, grains per spike (Kisana *et al.*, 1982; Masood *et al.*, 1986), 1000-grain weight, grain yield per plant, spike length and flag leaf area. (Chowdhry *et al.*, 1993; Awaad *et al.*, 1996). While moderate to high heritability and genetic advance were observed for plant height, grain yield per plant, spikelets per spike, spike length, 1000-grain weight and grain per spike (Pathak and Nema 1985; Chowdhry *et al.*, 1997), flag leaf weight, specific flag leaf area and specific flag weight (Riaz, 1990; Rehman, 1995).

Materials and Methods

F₁ seeds of six crosses involving five strains/varieties of bread wheat namely WLRG-6 x 5039, WLRG-7 x 5039, WLRG-6 x LU26S, WLRG-1 x LU26S, WLRG-7 x LU26S and WLRG-1 x 5039 alongwith their parents were space planted in the experimental area of the University of Agriculture, Faisalabad to which the F₂ population during the crop season 2001-2002. The seed were sown with a dibble keeping plant to plant and row to row distance of 15 and 30 cm, respectively. At maturity 200 plants from each F₂ population of each cross and 20 plants from each parent were taken randomly and data were recorded on flag leaf area (cm²), flag leaf weight (mg), specific flag leaf area, specific flag leaf weight, plant height (cm), tillers per plant, spike length (cm), spikelets per spike, 1000-grain weight(g) and grain yield per plant(g).

Heritability estimates in broad-sense were calculated by using the formula proposed by Mahmud and Kramer (1951). Genetic advance was computed by the following formula at 10 percent selection intensity.

- GA = $SDF_2 \times h^2 \times I$
GA = The genetic advance
SDF₂ = The phenotypic standard deviation of F₂ population
h₂ = The estimates of broad-sense heritability in fraction
I = Constant value that reflects the selection intensity
I = 1.775 in this study at 10% selection pressure

Results and Discussion

Heritability estimates and genetic advance are given in Table 1. It is obvious from the table that the highest heritability (92.22%) occurred in cross combination WLRG-7 x LU26S with highest genetic advance (12.17) while the lowest heritability

estimates (64.64%) along with lowest genetic advance (5.73) was observed in the cross WLRG x LU26S for flag leaf area. Moderate to high heritability and genetic advance in F_2 population showed that an appropriate cross combination and new strain may be developed by possessing desired level of flag leaf area. The results given in the table are also in agreement the findings of Mornhinweg (1985) and Chowdhry (1997). For Flag leaf weight the highest heritability estimates (76.35%) coupled with highest genetic advance (42.61) was recorded in the cross WLRG-1 x 5039 while the lowest heritability estimates (51.79%) coupled with low genetic advance (20.57) was noted in the cross WLRG-1 x LU26S. Flag leaf weight plays an important role in proper grain development and filling. High heritability for this trait shows that effective selection can be made from the F_2 population and new strains may be developed with desired level of flag leaf weight. These results are in accordance with the results of Riaz (1990) and Rehman (1995). Moderate to high heritability estimates in F_2 population varying from 52.39 (WLRG-6 x 5039) to 83.96 percent (WLRG-1 x LU26S) were calculated for specific flag leaf area. However the values of genetic advance ranged from 0.044 to 0.10 for the crosses WLRG-1 x 5039 and WLRG-1 x LU26S, respectively. The highest heritability and genetic advance values were recorded for the cross combination WLRG-1 x LU26S which reflects that effective selection is possible for this character. Similar results were obtained by Raiz (1990) and Rehman (1995). In case of specific flag leaf weight highest value of heritability 88.41 percent with genetic advance 2.99 was exhibited by the cross WLRG-1 x 5039 whereas lowest heritability 28.12% along with genetic advance 0.43 was observed in the cross WLRG-7 x 5039. Low to high heritability indicate that variability as present in much extent for this trait and though appropriate combinations improvement is possible for this character. Rehman (1995) also reported similar results. It is clear from the table that heritability estimate (91.94%) coupled with genetic advance 25.09 was obtained from the cross WLRG-1 x 5039 while lowest heritability value (57.24%) along with genetic advance (6.69) was found in the cross WLRG-6 x 5039. Transgressive segregation with high heritability and genetic advance for plant height in most crosses indicate that genetic variability was present in the F_2 populations and different high levels can be selected from those crosses. These results are in conformity with those of Masood *et al.* (1986), Awaad (1996) and Fida *et al.* (2001). For tillers per plant the heritability values ranged from 36.07 to 73.83% with genetic advance ranging from 1.51 to 3.87, for the crosses WLRG-6 x 5039 and WLRG-7 x LU26S, respectively. Heritability and genetic advance were moderate for most of the crosses and their magnitude showed that considerable progress is possible. The present results are in closely agreement with the findings of Pathak and Nema (1985) and Chowdhry *et al.* (1997). As regard the spike length heritability estimates in

Table 1: Estimation of heritability and genetic gain of some metric traits in six hybrid populations of spring wheat

Characters	Crosses	h ² %	GA
Flag leaf area	WLRG-6 x 5039	79.18	8.21
	WLRG-7 x 5039	90.07	9.44
	WLRG-6 x LU26S	64.64	5.73
	WLRG-1 x LU26S	71.46	6.55
Flag leaf weight	WLRG-7 x LU26S	92.22	12.17
	WLRG-1 x 5039	82.06	8.51
	WLRG-6 x 5039	53.41	22.27
	WLRG-7 x 5039	54.98	21.23
	WLRG-6 x LU26S	51.79	20.57
	WLRG-1 x LU26S	69.03	32.62
	WLRG-7 x LU26S	71.26	42.61
Specific flag leaf area	WLRG-1 x 5039	76.35	42.61
	WLRG-6 x 5039	52.93	0.05
	WLRG-7 x 5039	72.82	0.07
	WLRG-6 x LU26S	66.49	0.07
	WLRG-1 x LU26S	83.96	0.01
	WLRG-7 x LU26S	74.88	0.08
	WLRG-1 x 5039	61.17	0.04
Specific flag leaf weight	WLRG-6 x 5039	69.94	1.77
	WLRG-7 x 5039	28.12	0.43
	WLRG-6 x LU26S	69.51	1.64
	WLRG-1 x LU26S	83.49	2.23
	WLRG-7 x LU26S	81.06	2.28
	WLRG-1 x 5039	88.41	2.99
	WLRG-6 x 5039	57.24	6.69
Plant height	WLRG-7 x 5039	82.90	15.54
	WLRG-6 x LU26S	74.29	14.75
	WLRG-1 x LU26S	81.45	19.30
	WLRG-7 x LU26S	61.38	10.08
	WLRG-1 x 5039	91.94	25.09
	WLRG-6 x 5039	36.07	1.51
	WLRG-7 x 5039	49.85	2.20
Tillers per plant	WLRG-6 x LU26S	66.05	3.24
	WLRG-1 x LU26S	54.67	2.41
	WLRG-7 x LU26S	73.84	3.87
	WLRG-1 x 5039	45.44	2.13
	WLRG-6 x 5039	79.54	1.64
	WLRG-7 x 5039	85.46	1.97
	WLRG-6 x LU26S	61.81	1.01
Spike length	WLRG-1 x LU26S	65.29	1.23
	WLRG-7 x LU26S	77.30	1.55
	WLRG-1 x 5039	79.58	1.80
	WLRG-6 x 5039	72.81	2.15
	WLRG-7 x 5039	82.26	2.82
	WLRG-6 x LU26S	79.64	2.38
	WLRG-1 x LU26S	77.91	2.24
Spikelets per spike	WLRG-7 x LU26S	85.14	2.79
	WLRG-1 x 5039	79.55	2.71
	WLRG-6 x 5039	51.51	7.15
	WLRG-7 x 5039	58.58	8.75
	WLRG-6 x LU26S	72.23	11.19
	WLRG-1 x LU26S	61.38	8.74
	WLRG-7 x LU26S	82.42	15.96
Grains per spike	WLRG-1 x 5039	46.53	6.67
	WLRG-6 x 5039	36.75	2.39
	WLRG-7 x 5039	67.88	6.15
	WLRG-6 x LU26S	30.30	2.19
	WLRG-1 x LU26S	32.91	2.04
	WLRG-7 x LU26S	45.06	3.64
	WLRG-1 x 5039	44.91	2.64
Grain yield per plant	WLRG-6 x 5039	32.75	3.63
	WLRG-7 x 5039	25.60	2.53
	WLRG-6 x LU26S	15.35	1.51
	WLRG-1 x LU26S	62.69	6.27
	WLRG-7 x LU26S	42.05	4.70
	WLRG-1 x 5039	65.67	6.87

broad-sense ranged from 61.81 (WLRG-6 x LU26S) to 85.46% (WLRG-7 x 5039). These crosses indicated the genetic advance of 1.01 to 1.97, respectively. The results indicated moderate to high heritability for most of the crosses for spike length. So that spike length can be exploited for selecting high yielding genotypes of bread wheat. Similar results have also been reported by Khan *et al.* (1985), Chowdhry (1997) and Thakur *et al.* (1999).

Highest values of heritability were observed for number of spikelets per spike which ranged from 72.81 to 85.14% coupled with genetic advance 2.15 to 2.79 for the crosses WLRG-6 x 5039 and WLRG-7 x LU26S, respectively. Number of spikelets per spike is a character of great interest for wheat breeder as it determined the yield. High heritability showed that there is a scope for improvement in this trait with appropriate cross combination. Results obtained are in conformity with the findings obtained by Kisana *et al.* (1982), Pathak and Nema (1985), Maseed *et al.* (1986), Singh *et al.* (1999) and Riaz (1990). In case of grains per spike broad sense heritability estimates varied from 46.53 to 82.42% and genetic advance ranged from 6.67 to 15.96 for the cross combinations WLRG-1 x 5039 and WLRG-7 x LU26S, respectively. High heritability coupled with genetic advance values indicated that effective selection for grains per spike can be through an efficient hybridization programme. The results of the present study regarding grains per spike are supported by the findings of Khan *et al.* (1985), Subhani *et al.* (1995) and Fida *et al.* (2001). As regards 1000-grain weight moderate heritability (67.88%) along with genetic advance 6.15 observed for cross WLRG-7 x 5039. The heritability estimates for 1000-grain weight ranged from 30.30 to 67.88 and genetic advance 2.04 to 6.15. These findings are in accordance with those of Ansari *et al.* (1991) and Gupta and Verma (2000). The heritability estimates in broad-sense ranged from 15.35 to 65.67% and genetic advance varied from 1.51 to 6.87 for grain yield per plant. Grain yield per plant is a character of prime importance and special interest to the plant breeders. Moderate heritability with genetic advance indicate that effective selection is possible for the improvement in this character. The present results are in collaboration with the findings of Fida *et al.* (2001). The crosses of F₂ population WLRG-1 x LU26S, WLRG-7 x LU26S, WLRG-1 x 5039 and WLRG-7 x 5039 are of considerable interest showing interest showing high heritability estimates and high genetic gain for almost all the characters. It is concluded that varieties/lines like WLRG-1, WLRG-7, LU26S and 5039 possess high heritable characters for almost all traits. So these varieties/lines should be given due importance in future breeding programme.

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