

Response to Selection under Sib-mated and Selfing Progeny in Wheat (*Triticum aestivum* L.)

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The relative efficiency of the biparental mating system and selfing series was evaluated in terms of response to selection for grain yield following phenotypic and geno-phenotypic selection procedures in two crosses of wheat. The variability and the response to selection for grain yield was more under biparental mating system than under selfing series. The realized response due to the first cycle of selection and predicted response due to second cycle of selection indicated that geno-phenotypic procedure of selection was more efficient than phenotypic selection procedure. An index comprising grain yield, tiller number and biological yield could be used for selecting high yielding genotypes.

Key Words: Phenotypic and Geno-phenotypic Selection, Predicted and Realized Response, Sib-mating/Biparental Mating

The occurrence of recombinants in the traditional method of breeding is not only restricted by the limited recombination potential but also by the possible character associations resulting due to linkage and/or pleiotropism (Anderson, 1939; Dempster, 1949). The consequences of linkage and pleiotropism in relation to the potential breeding value of the material are different and are of critical importance. Hanson (1959) and Miller and Rawlings (1967) proposed that intermating in segregating generation might tend to break up linkages. Further this approach is also expected to retain greater variability for several cycles of selection, to elevate the population mean and to improve the chances of assembling the maximum number of potentially important genes leading to the isolation of stable and widely adapted genotype(s). A few studies that have been conducted on the vital aspect of usefulness of various mating systems and selection procedures have yielded divergent results. The present study was conducted with a view to gain information on the predicted and realized genetic gain under two mating systems and selection procedures for yield improvement in wheat.

Materials and Methods

The materials for the present study comprised two F_2 populations viz. WH 542/Raj 3077 (cross I) and WH 147/HD 2329 (cross II). In each of the F_2 populations, 120 random plants were selfed and crossed in pairs (biparental mating) to obtain 120 F_3 families and 60 BIPF₁'s hybrids, respectively. The parental lines, 120 F_3 families and 60 BIPF₁'s in each of the cross I and cross II were evaluated in three and two replications, respectively. Each entry in a replication was assigned

to a single row plot of 2 m length with a distance of 30 cm and 10 cm between rows and plants, respectively. Data was recorded on all plants except the border plants in each plot on 10 characters (listed in Table 2) in both the crosses.

In both the segregating generations (F_3 , BIPF₁'s) nature selfing was allowed and selection for grain yield was applied in two ways: (i) Phenotypic selection (P); based on individual plant merit, 5% top yielding plants were selected, (ii) geno-phenotypic selection (GP); based on both families and individual plant merit two highest yielding plants from each of the 50% top yielding families were selected maintaining a 5% selection intensity. By following this procedure two parents, BIPF₂ and F_4 progenies were planted in a randomized block design experiment with three replications at research farm, Kisan P.G. College, Simbhaoli (Ghaziabad). Data on the five random plants were recorded on the above 10 characters.

Plot means were used for different statistical analyses. The response to selection was calculated as a difference between the mean relative value of the offspring of selected plants and parental generation before selection. Heritability (broad sense) and predicted response for the directly selected and correlated traits were calculated according to Burton and DeVane (1953) and Johnson *et al.* (1995), respectively. The phenotypic correlation coefficients were estimated according to Al-Jibouri *et al.*, (1958).

Results and Discussion

The parental lines involved in the F_2 populations differed significantly for most of the characters suggesting genetic

diversity among parents. The mean values for grain yield and several other characters of BIPF₁ populations deviated significantly from mean values of their respective F₃ population (Table 1), although the two base populations (F₃ and BIPF₁) received the same input of gametes. The deviation in the mean values may thus be attributed to dominance deviations and epistatic interactions in BIPF₁ populations (Mather and Jinks, 1971).

Table 1. Mean grain yield of various base and selected populations of cross I and cross II

Population	Cross I	Cross II
F ₃	9.45	14.40
BIPF ₁	13.60 ^{aa}	17.65 ^{aa}
F ₄ P	11.35	15.23
BIPF ₂ P	19.56 ^{bb}	18.90 ^{bb}
F ₄ GP	13.38	16.78
BIPF ₂ GP	21.97 ^{cc}	20.90 ^{cc}

P = Phenotypic; GP = Geno-phenotypic; aa = F₃ vs BIPF₁; bb = F₄P vs BIPF₂P; cc = F₄GP vs BIPF₂GP; means significantly higher at P = 0.01 level

Due to first cycle of selection the predicted response (as per cent mean of checks) for grain yield and the

correlated responses for other nine characters, except plant height (cross I and cross II), tiller number and biological yield (cross I) and spikelets/spike (cross II) were relatively high in BIPF₁ populations than in the F₃ populations (Table 2). The predicted response to selection for grain yield and correlated responses for other nine characters were, however, lower than the realized response to selection (Table 2). This discrepancy in the predicted and realized response due to first cycle of selection may be attributed to the biased estimates of genotypic variance and heritability and also some extent to g × e interaction. Further, it was proposed by Robertson (1977) and Nishida and Abe (1974) that positive skewness of genotypic distribution and negative skewness of environmental distribution for a character, the realized response to selection is expected to be high than the predicted response.

The average realized selection response due to first cycle of the selection was greater under biparental mating than under selfing series which may be attributed to increased genetic variability due to recombination that may have taken place following intermating and to relatively high inbreeding depression in selfing series.

Table 2. Predicted and realized response (% mean of checks) for 10 characters in base (F₃ and BIPF₁) and selected (F₄ and BIPF₂) population in cross I and II

Sl.No.	Characters	Base Population		Selected Population			
		F ₃	BIPF ₁	F ₄		BIPF ₂	
				P	GP	P	GP
Cross I							
1.	Grain yield	11.83	28.18	20.11	41.594	43.82	61.54
2.	Days to heading	-0.02	0.69	-1.19	-0.63	2.63	3.12
3.	Days to maturity	-0.08	0.71	-6.09	-5.29	-7.64	-9.55
4.	Plant height	0.67	-0.36	19.46	18.87	15.45	10.36
5.	Tiller number	2.85	1.32	40.98	28.06	14.34	51.71
6.	Spikelets/spike	-0.49	0.56	9.53	11.67	4.13	5.29
7.	Grain/spike	0.05	0.17	-6.47	2.11	12.04	14.74
8.	100-grain weight	0.60	0.89	14.21	9.95	35.28	35.83
9.	Biological yield	2.46	0.77	-16.73	4.75	11.81	27.37
10.	Harvest index	0.00	1.29	44.22	35.17	28.67	26.86
Cross II							
1.	Grain yield	9.88	32.34	5.76	16.53	7.08	18.41
2.	Days to heading	0.02	0.67	-6.15	-8.51	4.38	3.03
3.	Days to maturity	-0.14	0.23	-7.61	-8.62	-10.92	-11.14
4.	Plant height	0.59	0.25	0.28	2.81	0.26	-0.74
5.	Tiller number	0.31	5.01	17.06	21.91	13.40	38.01
6.	Spikelets/spike	-0.78	0.56	2.61	6.75	0.50	4.89
7.	grains/spike	-0.52	1.02	-1.25	-4.39	11.80	4.99
8.	100-grain weight	0.35	0.59	1.17	4.24	13.15	14.21
9.	Biological yield	1.39	4.58	4.37	8.54	4.52	6.68
10.	Harvest index	-0.18	0.85	1.33	7.37	2.47	11.02

P = Phenotypic; GP = Geno-phenotypic

In agreement with the present results several earlier workers Balyan and Verma (1985), Kaushik *et al.*, (1996) and Salvagiotti and Maich (1999) also recommended the use of intermating in early segregating generations in wheat to break undesirable linkages and to retain greater variability for several cycles of selection.

The mean grain yield of the BIPF₂ population was also significantly higher the mean grain yield of respective F₄ populations in both the crosses. Moreover, the frequency distribution pattern of families and plants, on the basis of grain yield per plant, showed that a number of families and plants were grouped in the highest yielding class in BIPF₂ population against one in F₄ population.

The average predicted selection response for grain yield due to second cycle of selection was 49.29% and 45.06% in BIPF₂ populations than in F₄ populations of cross I and cross II, respectively (Table 3). The superiority of predicted response to selection in BIPF₂ over F₄ populations may partly be attributed to reduced variability and higher inbreeding depression in F₄ populations due to two cycles of inbreeding under selfing series as compared to only one cycle of inbreeding under biparental mating system.

The results also showed that owing to the positively correlated response of tiller number, biological yield and harvest index towards increased grain yield selection,

Table 3. Predicted response for second cycle of selection (% mean of checks) for 10 characters in selected (F₄ and BIPF₂) populations of cross I and II

Character	Cross I				Cross II			
	F ₄		BIPF ₂		F ₄		BIPF ₂	
	P	GP	P	GP	P	GP	P	GP
Grain yield	18.23	38.17	77.12	77.80	13.19	3.61	53.85	53.06
Days to heading	-070	0.04	-0.85	-0.89	0.23	0.48	0.78	0.36
Days to maturity	-0.42	-0.17	1.36	0.96	-0.29	-0.19	1.47	-0.46
Plant height	-0.62	-0.37	-0.76	-0.32	0.97	-0.94	0.19	-0.42
Tiller number	1.55	2.82	6.05	5.81	1.71	0.49	1.82	6.39
Spikelets/spike	-0.52	-0.24	-1.63	-1.90	-0.74	0.58	0.73	-0.48
Grains/spike	-0.92	1.12	-1.25	-1.62	-0.10	0.03	1.91	0.58
100-grain weight	-0.37	0.65	3.31	1.27	0.17	-1.64	2.15	1.14
Biological yield	1.63	3.47	6.70	6.77	1.65	0.38	6.72	6.65
Harvest index	-019	0.65	5.15	4.54	0.19	0.31	4.68	4.92

P = phenotypic; GP = Geno-phenotypic

these traits become important yield determining characters in various selected population (Tables 2 and 3). These characters were also significantly and positively associated with grain yield in base and selected populations (Table 4).

In the past also, the improvement of wheat yields were realized primarily because of the high harvest index of semi-dwarf wheats compared to old tall wheats. Biological yield has a high economic value, yet selection for it is not generally made. Sharma (1992) reported that high biomass yielding wheat genotypes are preferred by the farmers in the developing countries because such genotypes produce a high grain yield as well as high yield of non-grain plant parts.

It may be concluded that the efficiency of selection using P and GP procedures under selfing series and

biparental mating system were highly effective in improving grain yield. However, for the second cycle of selection on the basis of predicted response the population derived through biparental mating system was expected to be superior in terms of yield improvement. Further, under biparental mating system GP selection procedure seemed to be more efficient than P selection procedure. The superiority of GP selection procedure emanates from the fact that selection of plants in this procedure is based on their phenotypic values as well as genetic worth of their parental families. In agreement with the present result, it was also argued that the selection of best plants within selected families appears to be effective means of improving yield as compared to selection of best plant (Thakare and Qualset, 1978).

Table 4. Phenotypic correlation coefficients between grain yield and other characters in different populations under selfing and biparental mating system in cross I and cross II

Character Combination	F ₃	BIPF ₁	F ₄		BIPF ₂	
			P	GP	P	GP
CROSS I						
Grain yield vs.						
-Days to heading	-0.007	0.032	-0.559**	0.051	-0.124	-0.127
-Days to maturity	-0.090	0.117	-0.081	-0.062	0.199	0.135
-Plant height	0.125	-0.044	-0.083	-0.047	-0.114	-0.047
-Tiller number	0.904**	0.919**	0.952**	0.799**	0.883**	0.843**
-Spikelets/spike	-0.093	0.056	-0.157	0.007	-0.237	-0.274
-Grains/spike	-0.082	0.019	-0.114	0.179	-0.179	-0.234
-100-grain weight	0.032	-0.192	-0.035	0.085	0.488*	0.188
-Biological yield	0.930**	0.968**	0.974**	0.960**	0.987**	0.987**
-Harvest Index	0.078	0.317*	0.007	0.172	0.748**	0.661**
CROSS II						
Grain yield vs.						
-Days to heading	0.038	0.055	0.068	0.130	0.115	0.054
-Days to maturity	0.001	-0.081	0.056	-0.085	0.216	-0.065
-Plant height	0.137	0.023	0.202	-0.149	0.027	-0.063
-Tiller number	0.033	0.890**	0.951**	0.872**	0.266	0.947**
-Spikelets/spike	0.069	0.009	-0.084	-0.022	0.106	-0.072
-Grains/spike	-0.050	0.174	0.038	-0.008	0.279	0.086
-100-grain weight	-0.226*	0.015	0.066	-0.231	0.312*	0.169
-Biological yield	0.974**	0.848**	0.971**	0.974**	0.978**	0.985**
Harvest Index	0.174*	0.139	0.115	0.202	0.688**	0.735**

P = Phenotypic; GP = Geno-phenotypic; **, * Significant at P = 0.01 levels, respectively.

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