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THE USEFULNESS OF BIPARENTAL MATINGS AND GENO-PHENOTYPIC SELECTION FOR YIELD IMPROVEMENT IN WHEAT (*TRITICUM AESTIVUM* L.)

H. S. BALYAN AND TEJBIR SINGH

Department of Agricultural Botany,
Chaudhary Charan Singh University, Meerut 250 004

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ABSTRACT

Following the geno-phenotypic and phenotypic selection schemes (5% and 10% intensities), the predicted and realized responses to first cycle of selection and the predicted response to second cycle of selection exhibited greater improvement in grain yield under biparental matings than selfing. Further, the geno-phenotypic selection resulted into greater response for yield improvement than phenotypic selection under biparental matings as well as selfing. It clearly suggest that the geno-phenotypic selection following intermating in F_2 may be exercised to obtain enhanced and continuous gains in grain yield in succeeding generations. Further, an increase in grain yield was linked with increase in plant height, tiller number and biological yield. These traits were also significantly and positively associated with grain yield in all populations indicating that an index comprising these traits may be used for selecting high yielding wheat genotypes of suitable height.

Key words : *Triticum aestivum* L., Mating systems, selection schemes, selection response, selection efficiency, correlated response.

The traditional wheat breeding procedure involves crossing of two homozygous lines followed by selection in segregating generations. This procedure suffers from several drawbacks : limited parent participation, rapid fixation of genes, low genetic variability, and poor recombination potential. Intermating in early segregating generations in autogamous crops including wheat has been recommended to (i) generate and retain greater variability for several cycles of selection, (ii) elevate population mean, and (iii) improve chances of occurrence of potentially useful segregants resulting into stable and widely adapted genotype(s) [1-6]. Further, for the isolation of desirable genotype(s) from the segregating populations, it is suggested to make selection of either the best plants (phenotypic selection) or best plants from the superior families (geno-phenotypic selection). Keeping this in view, the present study was designed to find the usefulness of the geno-phenotypic selection scheme over phenotypic selection scheme and biparental matings over selfing for improvement of grain yield in wheat (*Triticum aestivum* L.).

MATERIALS AND METHODS

Eighty biparental ($BIPF_1s$) and 160 selfed (F_3s) families were developed from intermating in pairs and selfing of 160 randomly chosen F_2 plants in each of the two double cross hybrids : Blue Jay/CPAN 1687//Nacozari 76/I 443 (cross I) and Blue Jay/CPAN 1681//HUW 157/HD 2305 (Cross II). The families of ($BIPF_1$) and F_3 base populations alongwith the parents were separately evaluated in randomized block design experiments with two and three replications, respectively. Selection in these populations was exercised following phenotypic (P) (selection of top 5% and 10% plants) and geno-phenotypic (GP) (selection of best 2 plants from each of the top 25% and 50% families allowing 5% and 10% selection intensities, respectively) selection schemes to generate F_4 (F_4P5%, F_4GP5%, F_4P10% and F_4GP10%) and $BIPF_2$ ($BIPF_2$5%, $BIPF_2$GP5%, $BIPF_2$P10% and $BIPF_2$GP10% subpopulations. These subpopulations were evaluated in randomized block design experiments with three replications. In each of the base and subpopulation, the families were evaluated in single row plots of 210 cm length with plot to plot and plant to plant distances of 30 and 15 cm, respectively. Data were recorded on all plants except the border plants in each plot on eight characters : grain yield (g), plant height (cm), spikelets/spike, grains/spike, 100 grain weight (g), tiller number, biological yield (g) and harvest index.

The data on plot means were used for statistical analysis. The means of the base and subpopulations were compared using relative values expressed as % mean of checks (parents). The response to selection was calculated as the difference between the mean relative values of the offspring of selected plants and the base populations before selection. The predicted response for the directly selected (grain yield) and correlated traits was calculated following Johnson *et al* [7]. The mean differences between various populations were tested using t-test. The phenotypic correlation coefficients were estimated following Al-Jibouri *et al* [8].

RESULTS AND DISCUSSION

The parents of each of the two double cross hybrids from which each of the two base populations (F_3 and $BIPF_1$) were derived were genetically diverse [6]. These base populations exhibited considerable variability for grain yield and other traits. However, the variability in $BIPF_1$ populations was greater than in F_3 populations [6].

The results presented here show that the estimates of predicted response for grain yield to first cycle of selection at 5% as well as 10% intensities in the base populations (F_3 and $BIPF_1$) from crosses I and II were positive (Tables 1 and 2). The estimates of predicted correlated response for plant height, spikelets per spike, grains per spike and biological yield (F_3s and BIPF$_1$s) and also tiller number and harvest index (BIPF$_1$s) were positive. However, these estimates for 100 grain weight were negative in all base populations. The predicted correlated responses for the remaining traits were nonisodirectional, possibly due to differences in variances and correlation coefficients [7].

Remarkably, however, the magnitude of predicted selection response for the various traits (except harvest index in cross I) was greater in BIPF$_1$ than in F_3 base populations (Tables 1 and 2). The magnitude of realized response to first cycle of selection in F_4 and BIPF$_2$ subpopulations was still higher than the predicted response in F_3 and BIPF$_1$ base populations. This may arise due to the bias in the estimates of genotypic variance and heritability, presence of G × E-interactions and the positive and negative skewness of genotypic and environmental variances, respectively [9,

Table 1. Estimates of predicted and realized response (as % mean of checks) for eight characters in base (F_3 and BIPF$_1$) and subpopulations (F_4 and BIPF$_2$) obtained due to first cycle of selection in cross I. The values in upper and lower rows are due to 5% and 10% selection intensities, respectively.

Character	Predicted response		Realized response			
	F_3	BIPF$_1$	F_4		BIPF$_2$	
			P[a]	GP[b]	P	GP
Grain yield/plant	3.77	36.88	2.78	5.99	41.14	42.46
	3.21	31.35	8.96	12.74	43.47	52.87
Plant height	0.98	2.92	15.29	15.97	4.08	13.10
	0.83	2.48	14.88	5.46	9.23	9.30
Spikelets/spike	0.74	1.56	4.74	5.10	3.12	3.28
	0.63	1.33	4.32	4.74	3.54	4.06
Grains/spike	0.59	1.86	7.42	7.72	13.39	14.86
	0.50	1.58	7.35	7.50	13.88	14.88
100 grain weight	–0.58	–0.79	–9.98	–10.43	–10.20	–10.43
	–0.49	–0.67	–9.07	–9.07	–12.24	–12.70
Tiller number	–0.24	4.31	2.49	3.41	25.00	26.84
	–0.20	3.66	4.11	7.03	29.64	33.01
Biological yield	0.39	5.45	5.53	7.59	44.71	44.86
	0.33	4.63	9.13	12.83	49.79	58.27
Harvest index	0.42	0.23	0.00	0.00	0.00	0.00
	0.36	0.19	0.00	0.00	–2.86	0.00

Table 2. Estimates of predicted and realized response (as % mean of checks) for eight characters in base (F_3 and BIPF$_1$) and subpopulations (F_4 and BIF$_2$) obtained due to first cycle of selection in cross II. The values in upper and lower rows are due to 5% and 10% selection intensities, respectively.

Character	Predicted response		Realized response			
	F_3	BIPF$_1$	F_4		BIPF$_2$	
			P^a	GP^b	P	GP
Grain yield/plant	4.77	37.32	16.24	17.36	41.52	44.03
	4.05	31.72	18.09	24.03	42.31	46.93
Plant height	1.68	3.06	15.09	15.58	0.94	3.22
	1.43	2.60	16.37	17.26	0.17	0.37
Spikelets/spike	0.28	2.29	–0.10	1.25	2.54	2.64
	0.24	1.95	0.10	–0.30	2.99	2.69
Grains/spike	0.23	1.99	6.24	6.13	15.02	15.76
	0.19	1.69	5.91	5.93	15.63	15.96
100 grain weight	–0.38	–1.58	–6.78	–7.94	–8.64	–8.64
	–0.32	–1.34	–9.35	–9.35	–8.41	–8.88
Tiller number	1.22	4.91	3.82	4.14	15.05	17.78
	1.04	4.17	5.23	7.74	17.23	20.28
Biological yield	0.77	5.84	14.58	15.15	35.09	37.56
	0.65	4.96	17.13	22.10	35.22	39.61
Harvest index	–0.02	1.35	0.00	0.00	2.86	2.86
	–0.02	1.15	–2.86	0.00	2.86	2.86

a = Phenotype; b = Geno-phenotypic

10]. Strikingly, the average realized response of grain yield to first cycle of selection was 9.53 (5% intensity) to 4.43 (10% intensity) and 2.54 (5% intensity) to 2.12 (10% intensity) times greater under biparental mating system than under selfing series in crosses I and II, respectively (Tables 1 and 2). As a result, the mean grain yield of the various BIPF$_2$ subpopulations was also significantly higher than the mean grain yield of the respective F_4 sub-populations (Table 3). Moreover, the frequency distribution pattern of families, on the basis of grain yield per plant, showed that in various BIPF$_2$ subpopulations (cross I and II), 4.35% to 10% families against none in F_4 subpopulations belonged to highest yielding (31-34 g) class (Figs. 1 and 2). Further, the frequency distribution of plants on the basis of grain yield, revealed that more number of plants (3.35% in cross I and 2.44% in cross II) were grouped in the highest yielding class of 40-45 g in various BIPF$_2$ populations against none in F_4 populations (Figs. 3 and 4).

Table 3. Mean grain yield values of subpopulations obtained through first cycle of selection in base populations (F_3 and $BIPF_1$) of cross I and II.

Population	Cross I	Cross II
F_4P5%	16.29	17.61
F_4P10%	17.27	17.89
F_4GP5%	16.80	17.78
F_4GP10%	17.87	18.79
$BIPF_2$P5%	22.37^{aa}	21.44^{aa}
$BIPF_2$P10%	22.74^{cc}	21.56^{cc}
$BIPF_2$GP5%	22.58^{bb}	21.82^{bb}
$BIPF_2$GP10%	24.23^{dd}	22.26^{dd}

P = Phenotypic, GP = Geno-phenotypic; aa = F_4P5% vs $BIPF_2$5%; bb = F_4GP5% vs $BIPF_2$GP5%; cc = F_4P10% vs $BIPF_2$P10%; dd = F_4P10% vs $BIPF_2$GP10%, means singificantly higher at $p < 0.01$.

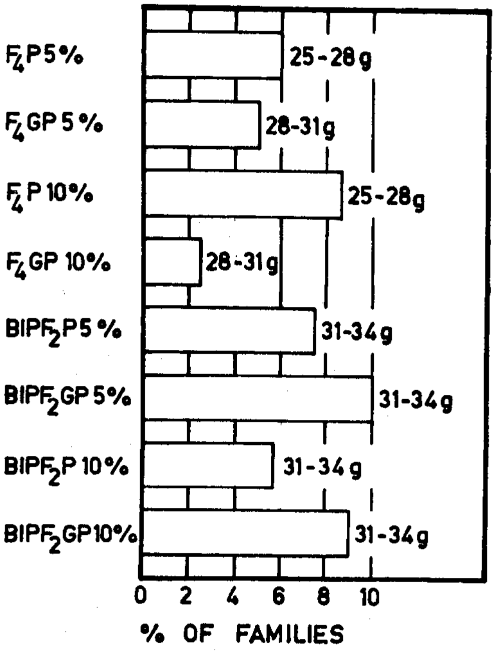

Fig. 1. The frequency distribution of families on basis of grain yield per plant in subpopulations obtained due to selection in F_3 and $BIPF_1$ base populations of cross I.

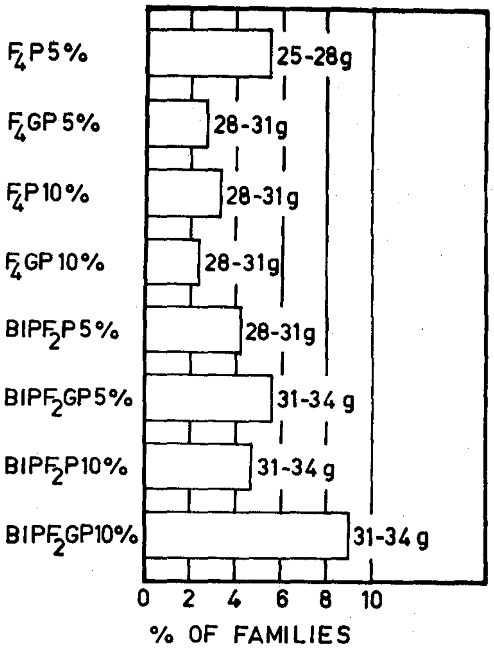

Fig. 2. The frequency distribution of families on the basis of grain yield per plant in subpopulations obtained due to selection in F3 and BIPF1 base populations of cross II.

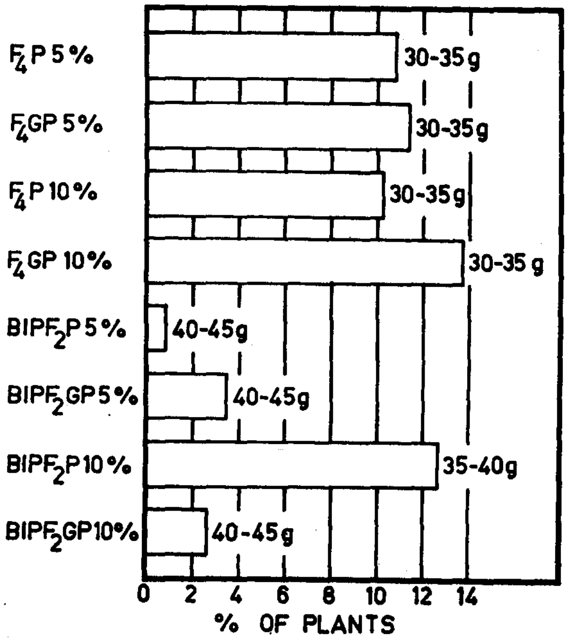

Fig. 3. The frequency distribution of plants on the basis of grain yield per plant in subpopulations obtained due to selection in F3 and BIPF1 base populations of cross I.

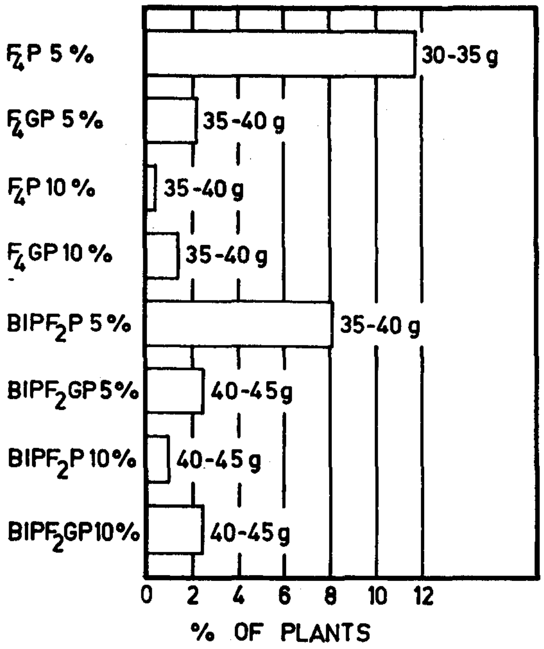

Fig. 4. The frequency distribution of plants on the basis of grain yield per plant in subpopulations obtained due to selection in F_3 and BIPF_1 base populations of cross II.

Due to second cycle of selection, the average predicted selection response (over all populations) for grain yield was greater than the predicted as well as realized responses recorded due to first cycle of selection. Further, the response to second cycle of selection was 7.30% (cross I) and 6.17% (cros II) greater under biparental mating system than under selfing series (Table 4). This may arise due to (i) the release of latent variability as a result of intermatings in F_2, (ii) the difference in the level of inbreeding depression in selected subpopulations under two mating systems, and (iii) presence of non-additive gene effects. Previously, intermatings in F_2 (biparental matings) in self pollinating crops like wheat was recommended to break undesirable linkages and for the acquisition of greater variability for continued response to selection in succeeding generations [1, 5, 6, 11-13].

Both the phenotype (P) and geno-phenotype (GP) selection schemes (at 5% as well as 10% selection intensities) were clearly effective in improving grain yield under both the mating systems (Tables 1 and 2). Remarkably, however, the average (over all populations) realized response for grain yield through first cycle of selection was considerably greater (18.44% in cross I and 12.02% in cross II) following GP scheme than following P scheme.

Table 4. Estimates of predicted response (as % mean of checks) for eight characters due to second cycle of selection in selected subpopulations (F_4 and BIF_2) of cross I and II. The values in upper and lower rows are for populations obtained due to 5% and 10% selection intensities.

Character	Cross I				Cross II			
	F_4		$BIPF_2$		F_4		$BIPF_2$	
	P	GP	P	GP	P	GP	P	GP
Grain/yield/plant	42.40	36.97	49.72	53.50	40.59	43.56	40.46	41.52
	41.58	42.02	36.09	52.87	38.22	41.98	50.29	56.77
Plant height	0.09	0.34	2.45	1.86	0.35	0.90	0.84	2.63
	0.11	0.35	2.23	1.73	0.26	0.64	2.77	2.44
Spikelets/spike	2.12	1.51	0.00	0.00	2.07	2.11	0.00	1.14
	2.35	2.16	0.49	0.00	1.19	1.61	0.99	1.34
Grains/spike	1.59	0.77	0.00	0.00	0.00	0.00	1.32	0.02
	1.79	1.39	0.00	1.82	0.00	0.00	0.00	0.00
100 grain weight	–0.41	–0.59	–4.35	–4.05	–0.43	–0.36	–4.06	-3.14
	–0.99	–0.83	–0.71	-1.59	0.27	–0.44	-3.75	-2.42
Tiller number	5.24	4.28	4.22	6.09	4.67	5.04	5.66	3.92
	4.56	4.81	2.55	4.55	4.24	4.44	6.21	7.08
Biological yield	6.21	5.45	6.94	7.51	5.78	6.20	6.06	5.03
	5.81	5.89	4.72	7.40	5.00	5.62	7.09	7.88
Harvest index	2.59	1.88	2.63	3.70	2.58	2.36	–0.76	2.60
	2.87	2.61	0.97	1.99	1.91	2.38	0.89	1.98

P = Phenotypic: GP = Geno-phenotypic

The estimates of predicted response for grain yield to second cycle of selection. following GP scheme were 23.97% ($BIPF_2$s of cross I), 8.53% (F_4s of cross II) and 8.31% ($BIPF_2$s of cross II) greater than due to P scheme (Table 4). In only F_4s of cross I, greater response was predicted due to P scheme. Further, the frequency distribution of families and plants showed that highest yielding families and plants occurred more frequently in the subpopulations derived due to GP scheme than due to P scheme (Figs. 1-4). Thus, the GP scheme of selection is clearly more efficient than P scheme of selection for improving grain yield under the two mating systems. This superiority of GP scheme emanates from the fact that selection of plants in this scheme is based on their phenotypic values as well as the genetic worth of their parent families.

The results also show that owing to the positive correlated response of plant height, tiller number and biological yield to increased grain yield selection, these traits become most important yield determining characters in the various selected subpopulations (Tables 1, 2 and 4). These characters were also significantly and positively associated with grain yield in base and selected subpopulations (Table 5). Thus, grain yield, tiller number, biological yield and plant height may constitute a selection index to select genotypes of suitable height with high dry matter and grain yield potential.

Table 5. Estimates of phenotypic correlation coefficient between grain yield and seven other traits in base (F_3 and $BIPF_1$) and subpopulations (F_4 and BIF_2) derived due to first cycle of selection. (The values in third and sixth columns are ranges of correlation coefficients. The values in upper and lower rows are for populations obtained due to 5% an 10% selection intensity, respectively).

Character combinations	Cross I			Cross II		
	F_3	BIPF1	Selected Subpopulation	F3	BIPF1	Selected subpopulation
Grain yield						
-plant height	0.37^{aa}	0.42^{aa}	0.04 - 0.19	0.41^{aa}	0.45^{aa}	0.07- 0.04
			0.05 - 0.18			0.08- 0.29^{a}
-Spikelets /spike	0.39^{aa}	0.24^{aa}	0.09 - 0.32^{a}	0.35^{aa}	0.36^{aa}	0.16- 0.32^{a}
			0.12 - 0.35^{aa}			0.13- 0.20^{a}
-Grains/ spike	0.45^{aa}	0.30^{aa}	0.15 - 0.32^{a}	0.43^{aa}	0.31^{a}	0.20- 0.24^{a}
			0.13 - 0.29^{a}			0.14- 0.40^{aa}
-100 grain weight	-0.35^{aa}	-0.16	-0.05 - 0.34^{a}	-0.33^{aa}	-0.19	-0.09- 0.53^{aa}
			0.03 - 0.15			-0.01- 0.49^{aa}
-Tiller number	0.77^{aa}	0.75^{aa}	0.72^{aa} -0.7^{aa}	0.79^{aa}	0.79^{aa}	0.66^{aa}- 0.75^{aa}
			0.64^{aa} -0.75^{aa}			0.72^{aa}- 0.79^{aa}
-Biological yield	0.93^{aa}	0.93^{aa}	0.92^{aa} -0.94^{aa}	0.94aa	0.95aa	0.87aa- 0.92aa
			0.89^{aa} -0.91^{aa}			0.89^{aa}- 0.90^{aa}
-Harvest index	0.07	-0.04	0.17 - 0.38^{aa}	0.15	0.23^{a}	-0.03- 0.44^{aa}
			0.05 - 0.36			0.13- 0.26

a and aa significant at $P \leq 0.05$ and $P \leq 0.01$, respectively.

In conclusion, we feel that in wheat breeding the intermatings in F_2 (biparental matings) followed by geno-phenotypic (GP) selection in succeeding generations may be practiced for obtaining enhanced and continuous gains in grain yield. Secondly, a selection index comprised of grain yield, biological yield, tiller number and plant height may be used for selecting genotypes of suitable height and high grain yield potential.

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