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Relative efficiency of two mating systems and selection procedures for yield improvement in wheat (*Triticum aestivum* L.)

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Summary. The relative efficiences of the biparental mating systems and selfing series in connection with phenotypic and geno-phenotypic selection procedures were evaluated for yield improvement in a cross 'HP1102'×'CPAN 1681' of wheat. Two selection cycles having a 4 per cent selection intensity for grain yield were carried out following both selection procedures under the two mating systems. Following these selection procedures, a greater improvement for grain yield could be achieved with the biparental mating system than with the selfing series. During the first selection cycle, the geno-phenotypic selection procedure had an edge over phenotypic selection procedure. The realized response due to the second cycle of selection and the predicted response for the third selection cycle indicated that the phenotypic selection procedure is more efficient than the geno-phenotypic selection procedure. It is suggested that selection following intermating in early segregating generations is able to overcome several inherent limitations of the simple pedigree method as it is possible to increase genetic variation and to concentrate favourable genes and gene combinations for grain yield. An increase in grain yield was, in general, accompanied by an increase in plant height, peduncle length, 100 grain weight, tiller number and biological yield. Therefore, it is suggested that an index comprised of grain yield, plant height, tiller number, grain weight and biological yield could be used for selecting high yielding genotypes of suitable height.

Key words: Mating systems – Selection procedures – Selection efficiency – Correlated response – *Triticum aestivum* L.

Introduction

The most widely used breeding method in wheat is the hybridization of homozygous diverse genotypes followed by the pedigree method of handling the segregating population in order to isolate genotypes possessing complementary – desirable characteristics of the parents.

The usefulness of this method is limited due to its several drawbacks: limited parent participation, low genetic variability, reduced recombination and rapid fixation of genes. The probability of any individual in the F_2 carrying most of the desirable genes is very low, therefore, selection from early generations is not expected to produce the best balanced genotype(s). Some of these drawbacks/limitations may be overcome by attempting intermating in early segregating generations – biparental mating. This approach is expected to break unfavourable linkages (Moll et al. 1964; Miller and Rawlings 1967; Gill et al. 1973), to retain greater variability for several cycles of selection and to elevate the population mean. It is also expected to improve the chances of assembling the maximum number of potentially important genes leading to the isolation of stable and widely adapted genotype(s).

In addition to mating systems, the selection of a good genotype in any breeding programme depends upon (i) the choice of parents, (ii) the nature of diversity in the base population, (iii) past history of selection, (iv) the magnitude and phase of linkage, (v) the correlated response of one or more traits not directly selected for, (vi) the pattern of genetic variation, and (vii) the breeding methodology followed (Moll et al. 1964; Murty et al. 1967; Bailey and Comstock 1976). With these factors and local variations in selection procedure, selection, in general, is either made for the best individuals i.e. phenotypic selection or for the best individual in the top families i.e. geno-phenotypic selection. A few studies which 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 find out the relative efficiency of the two mating systems, i.e. selfing series and the biparental mating system and two selection procedures i.e. phenotypic and geno-phenotypic, for improvement of yield.

Materials and methods

In the present study, two cultivars 'HP 1102' (red grained triple dwarf) and 'CPAN 1681' (white grained single dwarf) were crossed. The F_1 was raised and selfed during 1978/79. In 1979/80, 160 random F_2 plants were crossed in pairs to obtain 80 biparental progenies (BIPs) = $BIPF_1$s. The selfed seed from 160 F_2 plants was used to raise F_3 progenies.

The F_2 self-progenies (F_3 lines) and biparental crosses ($BIPF_1$s) thus produced were evaluated in randomized block design with three replications and two replications, respectively, in 1980/81. All entries in each replication were raised in a single row plot of 210 cm length with a distance of 30 cm between rows and 15 cm between plants. Data were recorded on all plants except the border plants in each plot on 11 characters: plant height (cm), peduncle length (cm), spike length (cm), spikelets per spike, grains per spike, grains per spikelet, 100-grain weight (g), grain yield (g), tiller number, biological yield (g) and harvest index.

In both segregating generations, F_3 and $BIPF_1$, natural selfing was allowed and the first selection cycle for grain yield was conducted using two selection procedures: (i) phenotypic selection (P); based on individual plant merit 4 per cent top yielding plants were selected; (ii) geno-phenotypic selection (GP); based on both family and individual plant merit the two highest yielding plants from each of the 50% top yielding families were selected, maintaining a 4% selection intensity. Thus, following these selection procedures, four populations, i.e. F_4P, F_4GP, $BIPF_2$P and $BIPF_2$GP, two each from F_3 and $BIPF_1$, were obtained. Suffix P and GP used with filial generations indicate the phenotypic and geno-phenotypic selection procedures used to select respective populations. The above mentioned four populations along with two parents were evaluated in randomized block design with three replications during 1981/82. In these populations natural selfing was allowed and the data were recorded similarly as in preceding generations.

A second cycle of selection was also conducted in these populations in the same way as in the F_3 and $BIPF_1$. The selected progenies i.e. F_5P, F_5GP, $BIPF_3$P and $BIPF_3$GP, along with two parents (checks), were evaluated in a randomized block design with three replications in single row plots during 1982/83. Data were recorded on these populations in the same way as in earlier generations.

In each generation, plot means were used for statistical analyses. The means of selected and parent populations over different years were compared using relative values expressed as per cent mean of checks. The response to selection was calculated as the difference between the mean relative value of the offspring of selected plants and the parental generation before selection. Heritability (broad sense) using family means and predicted response for the directly selected and correlated traits were calculated according to Burton and DeVane (1953) and Johnson et al. (1955), respectively. The difference in mean values of different generations were tested using the t-test. The phenotypic correlation coefficients were estimated according to Al Jibouri et al. (1958).

Results and discussion

The performance of the parental lines (checks) indicated significant differences for most of the traits (Table 1). The parental lines also showed a differential expression of the traits over the years. Their relative ranking did not change, suggesting an absence of genotype-environment interaction. In the base populations, the mean values of several traits in $BIPF_1$ deviated significantly from the means of F_3 (Table 1). This may be attributed to dominance deviations and epistatic interactions in $BIPF_1$s (Mather and Jinks 1971).

The estimates of genetic coefficient of variation (GCV) were relatively smaller than the estimates of the phenotypic coefficient of variation (PCV) in the base populations as well as in selected populations (Tables 2 and 3). This may be attributed to large environmental variance. The estimates of GCV were higher for grain

Table 1. Mean values of different traits in the parents and base populations

Trait	Parents				F_3	$BIPF_1$
	1981–82		1982–83			
	'HP1102'	'CPAN1681'	'HP1102'	'CPAN1681'		
Grain yield/plant	12.75	27.69**	11.91	16.11	18.23	20.84*
Plant height	61.59	97.33**	64.53	91.78**	101.06	104.43
Peduncle length	37.09	52.58**	25.34	32.95**	48.37	49.83
Spike length	12.80	12.94	12.00	12.85**	10.91	10.97
Spikelets/spike	17.20	19.18	19.70	20.95**	19.96*	19.43
Grains/spike	56.48	72.45**	62.51	71.97**	58.10	61.05**
Grains/spikelet	3.31	3.78	3.19	3.43**	2.94	3.15**
100 grain weight	3.43	3.63**	3.45	3.61	3.93	4.29**
Tiller no.	17.35	26.01	7.10	10.81**	12.29	12.47
Biological yield	41.19	87.19**	26.29	45.98**	43.68	48.32**
Harvest index	0.32	0.32	0.55**	0.36	0.42	0.43

** 'HP1102' vs 'CPAN1681' mean significantly higher at $P = 0.01$

*, ** F_3 vs $BIPF_1$ mean significantly higher at $P = 0.05$ and $P = 0.01$, respectively

Table 2. Phenotypic (PCV) and genotypic (GCV) coefficients of variation for different traits in the base populations

Trait	F_3		$BIPF_1$	
	PCV	GCV	PCV	GCV
Grain yield/plant	25.27	12.48	26.47	3.16
Plant height	15.36	13.44	15.36	7.14
Peduncle length	14.01	11.90	14.01	6.79
Spike length	9.96	5.52	10.24	5.41
Spikelets/spike	12.27	5.36	10.14	0.16
Grains/spike	14.21	6.79	14.69	4.02
Grains/spikelet	13.98	6.41	18.27	9.21
100 grain weight	12.26	7.51	10.98	5.60
Tiller no.	20.63	7.65	20.63	7.89
Biological yield	23.61	9.77	26.47	8.48
Harvest index	16.85	7.83	13.66	7.24

Table 4. Predicted response for different traits as % mean of checks in F_5 and $BIPF_3$ for the third cycle of selection

Trait	F_5		$BIPF_3$	
	P	GP	P	GP
Grain yield/plant	1.71	27.12	48.89	32.60
Plant height	−0.61	−4.36	0.82	−0.19
Peduncle length	1.36	−2.74	2.38	3.11
Spike length	0.19	0.07	0.03	−0.26
Spikelets/spike	−0.19	0.05	0.63	−1.00
Grains/spike	−3.27	0.92	6.41	2.20
Grains/spikelet	0.39	0.22	0.19	0.29
100 grain weight	0.05	0.02	0.07	−0.86
Tiller no.	0.94	3.21	2.65	−26.36
Biological yield	−0.40	7.19	16.06	5.39
Harvest index	0.01	0.03	−0.01	0.01

P = Phenotypic; GP = Geno-phenotypic

Table 3. Phenotypic and genotypic coefficients of variation for different traits in the selected populations

Trait	F_4				$BIPF_2$				F_5				$BIPF_3$			
	P		GP		P		GP		P		GP		P		GP	
	PCV	GCV	PCV	GCV	PCV	GCV	PCV	GCV	PCV	GCV	PCV	GCV	PCV	GCV	PCV	GCV
Grain yield/ plant	47.35	9.54	41.03	15.49	41.74	20.66	41.77	20.36	39.91	4.35	37.68	15.92	33.81	16.11	32.65	13.92
Plant height	16.25	12.87	14.94	12.47	15.07	12.29	14.79	11.97	17.53	16.05	13.67	12.39	14.97	13.96	12.87	12.31
Pendunce length	15.12	11.43	13.65	10.76	10.71	7.31	10.29	7.54	24.71	23.20	20.36	18.82	19.31	18.95	12.08	11.26
Spike length	13.08	9.50	10.70	7.98	12.94	8.81	11.26	5.82	11.49	9.02	10.02	7.91	9.21	5.89	6.38	2.62
Spikelets/ spike	10.96	5.71	8.63	5.29	8.92	4.44	10.30	4.41	8.54	5.00	8.08	4.58	8.68	4.49	5.78	4.09
Grains/ spike	18.14	9.25	18.46	9.11	18.19	12.35	17.62	0.05	17.53	13.39	17.77	9.82	16.47	12.13	13.04	8.33
Grains/ spikelet	15.76	7.28	15.21	7.20	14.23	7.28	13.48	2.24	49.64	16.12	15.93	8.83	15.19	10.27	11.60	8.97
100-grain weight	20.09	0.84	9.40	3.49	8.54	1.42	8.31	2.90	11.49	7.43	10.13	5.26	9.55	6.46	42.12	4.81
Tiller no.	39.98	2.33	37.92	11.85	38.93	18.40	41.87	19.64	32.03	14.81	37.80	21.72	32.31	14.72	21.89	0.23
Biological yield	44.57	10.99	41.42	14.59	40.84	20.43	45.41	23.56	39.11	6.60	35.06	12.16	35.88	17.10	26.76	8.22
Harvest	20.27	7.12	19.41	10.20	17.88	4.54	18.02	0.09	16.06	6.87	16.70	8.65	12.43	9.73	11.64	8.97

P = Phenotypic; GP = Geno-phenotypic

yield in populations obtained as a result of first ($BIPF_2$ P, GP) and second ($BIPF_3P$) selection cycles using the biparental mating system. The heritability estimates were also higher in all selected populations compared to their respective parent populations (data not presented in Table). The high estimates of PCV, GCV, and heritability in populations (F_5P, GP and $BIPF_3$ P GP) selected under the second cycle of selection indicated the possibility of further improvement in grain yield through successive selection cycle(s). Such an improvement was expected to be higher under the biparental mating system, since within line variability is considerably diminished in F_5 under the selfing series (Table 4).

The predicted response for grain yield and other traits in all selected populations under both mating systems were lower than the realized response (Tables 5 and 6). This might be attributed to biased estimates of genotypic variance and heritability and also some extent to genotype-environment interaction.

Both procedures of selection, P and GP, were highly effective in improving the grain yield under both mating systems (Table 6). The average realized selection response following P and GP selection procedures due to the first selection cycle was 60.93% and 57.01% under the selfing series and biparental mating system, respectively. The lower average realized selection response in $BIPF_2$ than that of F_4 was not expected. This is due to the relative low response under the P selection procedure. Furthermore, the means of the selected populations obtained due to respective selection procedures under the two mating systems after the first selection cycle did not differ (Table 7). This suggested that the efficiency of the P and GP selection procedures were similar under both mating systems. The average realized response of 17.02% using the selfing series and 28.82% using the biparental mating system as a result of the second selection cycle was, respectively 43.91% and 28.19% less than that of the preceding cycle of selection (Table 6).

The reduced response to selection due to the second cycle of selection in comparison to the first cycle may be explained by reduced variability after one cycle of selection and selfing. The selection response under the biparental mating system

Table 5. Predicted and realized response as % mean of checks for different traits in the base (F_3 and $BIPF_1$) and selected populations (F_4 and $BIPF_2$) obtained as a result of first selection cycle

Trait	Predicted response		Realized response			
	F_3	$BIPF_1$	F_4		$BIPF_2$	
			P	GP	P	GP
Grain yield/plant	10.61	0.74	61.89	59.97	46.38	67.65
Plant height	0.88	−2.53	24.81	24.85	36.72	36.08
Penduncle length	−2.26	−3.07	16.44	16.57	22.02	21.61
Spike length	0.79	1.40	2.01	−0.46	−0.31	0.77
Spikelets/spike	2.45	−2.09	5.75	5.75	0.55	3.48
Grains/spike	1.23	−0.55	1.59	0.48	−5.20	−1.70
Grains/spikelets	−0.25	3.06	6.32	7.99	7.87	4.07
100 grain weight	5.12	3.01	7.10	5.68	7.10	7.10
Tiller no.	0.57	−0.95	36.27	32.90	21.48	35.58
Biological yield	6.20	1.87	50.05	47.08	34.74	60.16
Harvest index	5.37	−1.49	16.66	−22.72	−15.65	27.77

P = Phenotypic; GP = Geno-phenotypic

Table 6. Predicted (F_4 and $BIPF_2$) and realized (F_2 and $BIPF_3$) response as % of mean of checks for second cycle of selection

Trait	Predicted response				Realized response			
	F_4		$BIPF_2$		F_5		$BIPF_3$	
	P	GP	P	GP	P	GP	P	GP
Grain yield/plant	6.67	20.11	32.19	35.75	14.80	27.40	109.75	70.10
Plant height	8.52	2.24	−9.16	14.26	20.82	30.76	27.61	49.33
Peduncle length	4.39	−0.96	−2.62	7.63	27.78	42.56	21.59	33.45
Spike length	2.71	1.55	7.37	5.74	2.01	0.72	4.91	3.38
Spikelets/spike	2.76	5.31	4.76	4.31	1.53	−0.34	1.92	3.89
Grains/spike	−0.01	−0.30	11.76	0.00	−12.98	−19.14	−8.08	−8.88
Grains/spikelet	2.99	3.18	−2.50	0.00	−10.08	−18.43	−9.67	−12.39
100 grain weight	1.13	1.14	−1.99	2.55	2.27	8.78	13.31	26.35
Tiller no.	−0.83	7.72	24.35	27.03	17.15	26.12	72.53	50.90
Biological yield	5.12	14.09	27.28	39.17	27.12	39.65	106.06	76.12
Harvest index	30.30	−4.04	−22.22	−0.74	−0.22	−0.23	0.12	−0.16

P = Phenotypic; GP = Geno-phenotypic

Table 7. Mean values of different traits in the selected populations obtained as a result of first and second selection cycle

Traits	F_4		$BIPF_2$		F_5		$BIPF_3$	
	P	GP	P	GP	P	GP	P	GP
Grain yield/plant	32.27	31.90	29.19	33.43	16.13	17.90	29.47[ccff]	24.18[gg]
Plant height	98.79	98.32	108.22[bb]	107.71	94.42	102.19[dd]	99.78[ff]	116.70[eegg]
Peduncle length	51.98	52.04	54.47[bb]	54.29[cc]	37.17	41.47[ddgg]	35.37	38.82[ee]
Spike length	13.15[a]	12.83	12.93	12.99[cc]	12.68	12.52	13.04	12.85
Spikelets/spike	19.11[bb]	19.11	18.17	18.70	20.63	20.25	20.71	21.11
Grains/spike	64.95[aab]	64.24	60.60	62.84	58.51	54.37[d]	61.37	61.27
Grains/spikelet	3.40	3.36	3.34	3.36	2.95	2.70	2.99	2.90
100 grain weight	3.77	3.72	3.77	3.77	3.61	3.84[dd]	4.00[ff]	4.46[gg]
Tiller no.	29.49	28.76	26.29	29.34	10.45	11.25[dd]	15.37[ff]	13.46[gg]
Biological yield	95.54	93.65	85.79	101.98	45.94	50.47	74.94[ff]	63.65[gg]
Harvest index	0.34	0.35	0.35	0.34	0.36[gg]	0.35	0.40[ff]	0.38

P = Phenotypic; GP = Geno-phenotypic

[a, aa] F_4P vs F_4GP means significantly higher at $P = 0.05$ and $P = 0.01$, respectively

[b, bb] F_4P vs $BIPF_2P$ means significantly higher at $P = 0.05$ and $P = 0.01$, respectively

[cc] F_4GP vs $BIPF_2GP$ means significantly higher at $P = 0.01$

[d, dd] F_5P vs F_5GP means significantly higher at $P = 0.05$ and $P = 0.01$, respectively

[ee] $BIPF_3P$ vs $BIPF_3GP$ means significantly higher at $P = 0.01$

[ff] F_5P vs F_5GP means significantly higher at $P = 0.01$

[gg] F_5GP vs $BIPF_3GP$ means significantly higher at $P = 0.01$

was higher than under the selfing series. This may be attributed to the release of latent variability due to biparental matings, differences in the level of inbreeding of selected populations under two mating systems and the presence of non-additive effects. Palmer (1953); MacKey (1963); Joshi and Dhawan (1966); Jensen (1970); Gill et al. (1973) and Randhawa and Gill (1978) also recommended the use of intercrossing and recurrent selection in early segregating generations in such self-pollinated crops as wheat to break unfavourable linkages and to retain greater variability for several cycles of selection.

In the second selection cycle, the P and GP selection procedures were equally effective under the selfing series. Under the biparental mating system the P selection procedure was more effective for yield (Table 7). The frequency distribution of families, on the basis of grain yield per plant, indicated that under the selfing series only one family could be grouped in F_5GP against none in F_5P in the highest yielding class of 30–40 g (Fig. 1). Whereas under the biparental mating system seven families, including six in $BIPF_3P$ and one in $BIPF_3GP$ (Fig. 3), were grouped in the highest yielding class. Further, the frequency distribution of plants, on the basis of grain yield, revealed that the maximum number of plants in the highest yielding class of 75–80 g were grouped in $BIPF_3P$ (Figs. 2 and 4) suggesting the superiority of the biparental mating system and P selection procedure in yield improvement. Thakare and Qualset (1978) suggested the superiority of a selection procedure involving selection of the best plants from the top families for improving yield in wheat.

In both cycles of selection the realized correlated response for plant height, peduncle length, 100-grain weight, tiller number and biological yield was positive in all populations (Tables 5 and 6). However, for the remainder of the traits, in all populations, the response was not unidirectional. This may be attributed to differences in variance and correlation coefficients (Johnson et al. 1955).

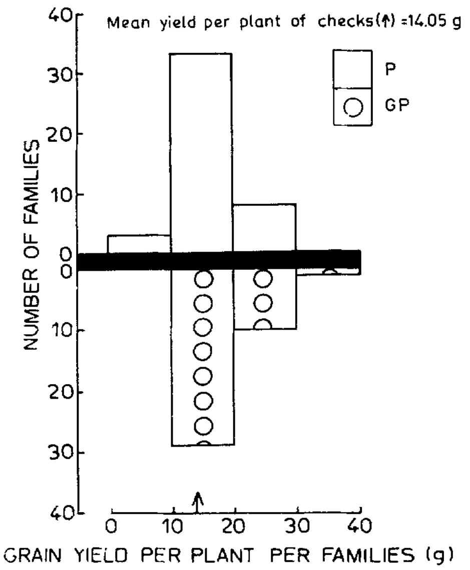

Fig. 1. The frequency distribution of families on the basis of grain yield per plant in F_5 populations selected as a result of phenotypic (P) and geno-phenotypic (GP) selection procedures

It may not be out of place to mention that the phenomenal rise in wheat yield potential during the past few decades is

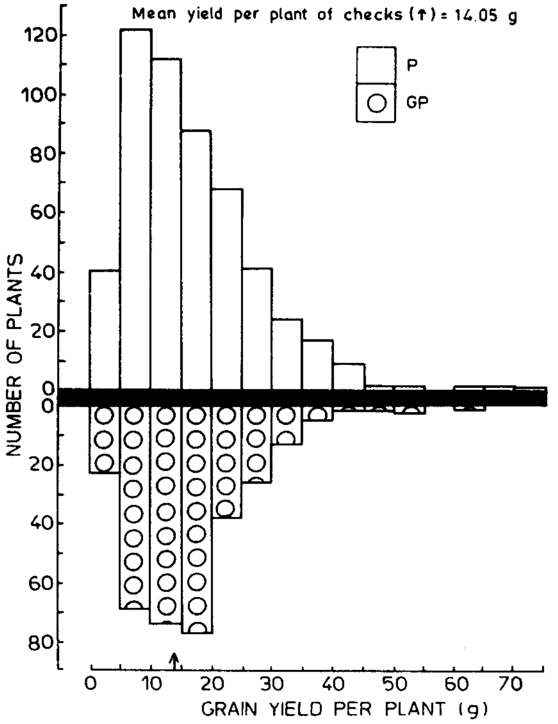

Fig. 2. The frequency distribution of plants on the basis of grain yield per plant in F_5 populations selected as a result of phenotypic (P) and geno-phenotypic (GP) selection procedures

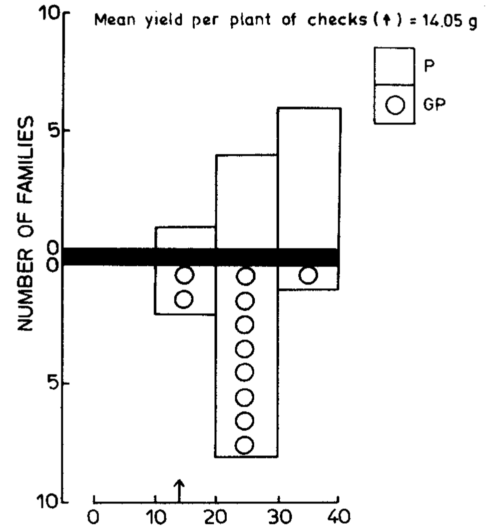

Fig. 3. The frequency distribution of families on the basis of grain yield per plant in $BIPF_3$ populations selected as a result of phenotypic (P) and geno-phenotypic (GP) selection procedures

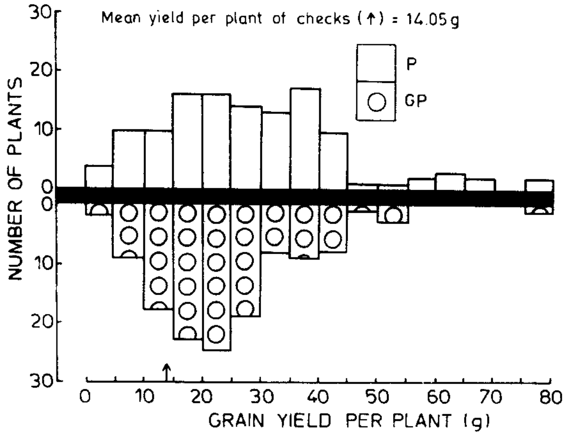

Fig. 4. The frequency distribution of plants on the basis of grain yield per plant in $BIPF_3$ populations selected as a result of phenotypic (P) and geno-phenotypic (GP) selection procedures

Table 8. Phenotypic correlation coefficients between grain yield and other traits in the base populations

Trait combination	F_3	$BIPF_1$
Grain yield/plant		
– Plant height	0.04	0.16
– Peduncle length	0.02	0.10
– Spike length	0.18*	0.39*
– Spikelets/spike	0.23*	0.23*
– Grains/spike	0.34*	0.47**
– Grains/spikelet	0.18*	0.27**
– 100 grain weight	0.25**	0.30**
– Tiller no.	0.40**	0.67**
– Biologicl yield	0.74**	0.88**
– Harvest index	0.42**	0.31**

*, ** Significant at $P = 0.05$ and $P = 0.01$, respectively

attributed to an increased harvest index (Kulshrestha and Jain 1982). However, recent efforts to further increase the yield potential have not been successful (Gill 1979; CIMMYT 1978, 1979), since the maximum limit for the increase of harvest index is believed to have already been achieved. Thus, further improvement in grain yield of wheat may be achieved by increasing the total dry matter, i.e. biological yield (DeWit 1967; Moss and Musgrave 1971; Loomis et al. 1971; Nasyrov 1978).

The results of the present study also support such a conclusion since biological yield in all selected populations has shown a very high and positive correlated response for increased yield selection (Tables 5 and 6). In turn, the maximum contribution to biological yield was made by tiller number which, of course, is accompanied by increased plant height. The tall plants do not suit present day agronomic practices of using high doses of fertilizer and irrigation. The traits related to

Table 9. Phenotypic correlation coefficients between grain yield and other traits in populations derived as a result of first (F_4 and $BIPF_2$) and second (F_5 and $BIPF_3$) selection cycles.

Trait combination	F_4		$BIPF_2$		F_5		$BIPF_3$	
	P	GP	P	GP	P	GP	P	GP
Grain yield/plant								
– Plant height	0.27**	0.22	0.22*	0.37*	0.22	0.00	0.17	0.12
– Penduncle length	0.22*	–0.15	0.11	0.29	0.12	–0.03	0.17	0.14
– Spike length	0.36**	0.32	0.28**	0.45*	0.33*	0.34	0.42	0.39
– Spikelets/spike	0.46**	0.56**	0.43**	0.62**	0.34*	0.34*	0.34	0.16
– Grains/spike	0.36**	0.63**	0.34**	0.46*	0.35*	0.48**	0.51	0.54
– Grains/spikelet	0.18*	0.19	0.17	0.15	0.09	0.42**	0.34	0.56
– 100 grain weight	0.10	0.44*	0.30*	0.09	0.25	0.21	0.15	–0.09
– Tiller no.	0.82**	0.87**	0.84**	0.88**	0.84**	0.81*	0.88**	0.71*
– Biological yield	0.90**	0.92**	0.91**	0.94**	0.90**	0.87**	0.94**	0.89**
– Harvest index	0.12	–0.00	0.07	–0.12	0.16	0.36*	–0.04	0.52

*,** Significant at $P = 0.05$ and $P = 0.01$, respectively

spike, grain weight, tiller number, biological yield and harvest index showed positive association with grain yield in base populations (Table 8). Tiller number and biological yield not only maintained a positive association with grain yield in all selected populations but the magnitude of correlation coefficients was also enhanced (Table 9). An increased dry matter production and grain yield may be realized by use of a selection index including grain yield, tiller number, grain weight, biological yield and plant height.

From the above discussion the following may be concluded. (a) Intermating in early segregating generations is able to overcome the limitation(s) of the pedigree method of breeding, in that it is possible to increase genetic variation so that several cycles of selection are effective. It also help in concentrating favourable genes or gene combinations for grain yield. (b) The efficiency of the phenotypic selection procedure (P), i.e. selection of plants on individual merit, was either the same or better in some cases than by using the geno-phenotypic selection procedure (GP), i.e. selection of best plants in top families. However, before finally establishing the superiority of one selection procedure over the other further studies need to be conducted. (c) A selection index comprised of grain yield, grain weight tiller number, biological yield and plant height may be used as a criteria for selecting genotypes of suitable height with increased dry matter production and grain yield.

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