

Effectiveness of Selection under Different Mating Systems for the* Improvement of Protein Content in Wheat (*Triticum aestivum* L. em Thell.)

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Summary. The effectiveness of selection for the improvement of protein content under random intermating (recurrent selection) and selfing series (pedigree selection) was evaluated in a cross of winter and spring wheats, 'Atlas 66' × 'HD 1977'. Selection of 10 per cent high protein families resulted in an increase of 3.25 per cent and 4.30 per cent of the mean of checks through pedigree and recurrent selection, respectively. The mean protein differences in both methods were not significant. The increase in protein content was accompanied by a decrease in the grains per spike, grain yield and 1000-kernel weight, and the decline was relatively higher in recurrently selected than pedigreed population. Since the pedigree method is simple, less time consuming, economically cheaper, has favourable shifts in association and better correlated responses, it was decided to follow a few cycles of pedigree selection in early segregating generations, after which one or two cycles of recurrent selection in the elite lines could be introduced to increase genetic variation and concentrate favourable genes for grain yield.

Key words: *Triticum aestivum* L. em Thell. – Mating systems-Grain protein content-pedigree Selection – Recurrent selection – Correlated response

Introduction

The usual breeding procedure in wheat (*Triticum aestivum* L. em Thell.) is to cross two homozygous genotypes and then select, in later generations, those plants which combine the desirable features from both parents. This

procedure was very rewarding in the early stages of plant breeding when characters controlled by a few genetic factors were the main targets for selection. However, the improvement of complex quantitative characters such as grain yield and protein content which are the end-products of many plant components, environmental factors and their interactions is a slow and difficult process. To overcome the inherent limitations of reduced recombination and quick fixation in the conventional methods, Palmar (1953), MacKey (1963), Joshi and Dhawan (1966) and Jensen (1970) suggested intercrossing and recurrent selection in early segregating generations. Only a few studies have been reported so far on the usefulness of various intermating procedures for the improvement of wheat (Gill et al. 1973; Redden and Jensen 1974; Byrne and Rasmusson 1974; Singh and Dwivedi 1977).

The importance of winter wheats for the improvement of spring types have been stressed for a long time (Akerman and MacKey 1949). Winter wheats are expected to provide enhanced drought resistance, better resistance to *Septoria tritici* and *S. nodorum* and diverse genes for increased grain yield. Pinthus (1967) found that the number of spikes per unit area, number of kernels per plant and number of spikelets per spike were generally higher in winter wheats than the spring types. Grant and McKenzie (1970), Mani and Rao (1975), Bhullar (1976) and Joshi and Tandon (1977) studied winter-spring crosses of bread wheat and reported that winter wheats have a genuine potential for the improvement of spring types.

A breeding programme to develop improved varieties of wheat with high protein content is in progress at the Punjab Agricultural University, Ludhiana. The parent varieties used include spring types for desirable agronomic traits and a winter wheat, 'Atlas 66', for high protein. The present investigation was undertaken to find the relative effectiveness of different mating systems and selection procedures for the improvement of grain protein content in a cross of winter × spring wheats.

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Materials and Methods

The material was comprised of a wheat cross, 'Atlas 66' × 'HD 1977'. 'Atlas 66' is a high protein winter wheat and is resistant to all the three rusts under the Punjab conditions. Due to very late anthesis, however, the desiccating heat of the Punjab plains burns the green plants at dough stage, resulting in poor grain filling and low yield. 'HD 1977' is a triple-dwarf, low protein, well-adapted, early-maturing and spring wheat but is susceptible to brown rust. For breeding high-protein spring genotypes, 200 random F_2 plants were marked, 100 each as males and females, to make 100 biparental crosses. Two to three heads of each female plant were pollinated to obtain sufficient seed for raising biparental progenies (BIP_1F_1). The remaining heads on each marked plant were selfed to raise 200 F_3 progenies.

The 100 random biparental crosses were divided into four groups each having 25 random progenies. All the 25 biparental crosses of one group, along with their corresponding 50 F_2 selfs (F_3 lines) in each set, were evaluated in three replications but biparental progenies, due to insufficient hybrid seed, could be raised only in two replications. Each entry in a replication of randomized block layout was assigned to a single row plot of 210 cm length with a distance of 40 cm and 15 cm between the rows and plants within a row, respectively. The data on an individual plant basis were recorded on seven characters, viz. tiller number, plant height, ear length, spikelets per spike, grains per spike, grain yield per plant and peduncle length and on a plot basis for three characters, viz. days to anthesis, 1000-kernel weight and protein content.

Based on family performance, 10 per cent high grain protein BIP_1F_1 selfed (BIP_1F_2) and F_3 selfed (F_4) families were selected and one of the highest yielding plants in each replication of the selected families was chosen to raise 20 BIP_1F_2 and 60 F_4 progenies. During 1975-76, 20 BIP_1F_2 and 60 F_4 progenies, along with two parental lines, were evaluated in a randomised complete block design with three replications. Data were recorded on all the ten characters as in the preceding season.

The variance ratio tests were carried in plot means. The heritability (broad-sense) was estimated according to Burton and DeVane (1953), genetic advance for protein content and correlated response for other traits according to Johnson, Robinson and Comstock (1955). The estimates of genotypic and phenotypic variances and covariances were computed and employed to work out genotypic and phenotypic correlations. The significance of phenotypic correlations was tested from the *t*-table of Fisher and Yates (1949) and that of genotypic correlations was not tested due to non-availability of a suitable test. The homogeneity of phenotypic correlations was tested according to Steel and Torrie (1960).

Results and Discussion

The parental lines differed significantly for all the characters except ear length during 1974-75 (Table 1 and 2). The mean values of all characters except days to anthesis were higher in BIP_1F_1 than F_3 , however, the differences were significant only for 1000-kernel weight. Since the BIP_1F_1 and F_3 generations received the same input of gametes, the superiority of the former over the latter

might be attributed to dominance deviations. The mean grain yield and peduncle length in both the BIP_1F_1 and the F_3 generations and that of grains per spike in the BIP_1F_1 generation were significantly higher than the better parent which indicated the presence of transgressive segregation and high potential for genetic improvement of these traits through selection.

The mean performance of the F_4 population obtained after one cycle of pedigree selection was significantly lower for ear length, 1000-kernel weight and days to anthesis than that of recurrent selection (BIP_1F_2) population (Table 2). For grain protein content, the directly selected trait, and for tiller number, plant height, grains per spike, grain yield and peduncle length, the correlated traits, the performance of the BIP_1F_2 generation was higher than the F_4 but the differences were not significant. The performance of the BIP_1F_2 population for grains per spike and peduncle length and of the F_4 for peduncle length was significantly superior to the better parent.

The genetic coefficients of variation for different traits were relatively smaller in magnitude than phenotypic coefficients (Table 3). The phenotypic and genotypic coefficients of variation and broad-sense estimates of heritability for all the traits except grain yield were higher in the F_3 than the BIP_1F_1 which indicated that coupling phase linkages might be predominant for these traits in the parents. For grain yield, however, the estimates of heritability and genotypic coefficients of variation were higher in the BIP_1F_1 than the F_3 population thereby indicating the predominance of repulsion phase linkages for grain yield. Gill et al. (1973), Kochhar (1974), Singh (1975) and Singh and Dwivedi (1977) also reported predominance of repulsion phase linkages for grain yield. The genotypic coefficients of variation and estimates of heritability for plant height, ear length, grains per spike, grain yield, 1000-grain weight and peduncle length were markedly higher in the F_4 than the BIP_1F_2 population. However, for tiller number, spikelets per spike, days to anthesis and protein content these estimates were nearly equal to, or somewhat smaller in the F_4 than the BIP_1F_2 population. The data suggested that both systems of mating were nearly equal in effectiveness for the improvement of protein content but that there seemed to be better associated changes in the correlated traits through pedigree selection rather than recurrent selection.

The genotypic variation for protein content in the F_3 and F_4 populations was nearly equal. However, in the BIP_1F_2 population the variation after one cycle of selection was even more than in the basal BIP_1F_1 population which showed that selection did not reduce the potential for genetic improvement of protein content to be exploited through another cycle of selection. For all correlated traits except peduncle length in the BIP_1F_2 , the selected populations had higher genotypic variations than

Table 1. Mean values of different characters in the base populations during 1974-75

Character	Generation				LSD 5%	
	'Atlas 66'	'HD 1977'	BIP ₁ F ₁	F ₃	BIP ₁ F ₁ vs. others	Rest
Tiller number	11.33	8.25	9.72	9.06	1.59	1.42
Plant height, cm	114.70	76.38	110.96	109.24	5.74	5.13
Ear length, cm	11.80	11.15	11.37	10.98	NS ^a	NS ^a
Spikelets/spike	23.28	20.57	22.18	21.93	1.64	1.46
Grains/spike	34.67	50.33	57.73	54.81	6.54	5.85
Grain yield/plant, g	6.22	12.18	16.77	14.69	2.70	2.42
1000-kernel weight, g	29.08	39.42	39.89	37.72	1.96	1.75
Days to anthesis	125.33	93.42	104.02	104.84	1.69	1.51
Peduncle length, cm	43.48	40.25	49.90	48.93	2.03	1.81
Grain protein, %	17.33	12.48	15.21	14.81	1.26	1.12

^aNS = Non-significant**Table 2.** Mean performance of different characters after one generation of selection (1975-76)

Character	Generation				LSD 5%
	'Atlas 66'	'HD 1977'	BIP ₁ F ₂	F ₄	
Tiller number	14.37	9.23	12.54	11.25	2.74
Plant height, cm	132.43	77.63	124.90	118.61	9.18
Ear length, cm	12.20	11.10	12.00	11.57	0.30
Spikelets/spike	23.93	18.23	21.71	22.34	1.40
Grains/spike	36.63	48.77	52.69	51.02	2.43
Grain yield/plant, g	5.03	13.03	14.93	14.16	4.01
1000-kernel weight, g	22.30	39.43	30.93	29.12	0.88
Days to anthesis	132.60	96.33	109.58	106.52	0.54
Peduncle length, cm	48.30	42.23	55.29	54.10	2.67
Grain protein, %	16.47	11.50	14.87	14.34	1.04

Table 3. Phenotypic (PCV) and genotypic (GCV) coefficients of variation and heritability (broad sense) estimates for different characters in the base and one generation selected populations

Character	PCV				GCV				Heritability			
	Base		Selected		Base		Selected		Base		Selected	
	BIP ₁ F ₁	F ₃	BIP ₁ F ₂	F ₄	BIP ₁ F ₁	F ₃	BIP ₁ F ₂	F ₄	BIP ₁ F ₁	F ₃	BIP ₁ F ₂	F ₄
Tiller number	13.53	18.83	24.41	23.80	2.34	8.85	13.54	9.76	.03	.22	.30	.17
Plant height, cm	7.50	9.10	10.34	11.97	4.95	7.65	6.19	10.71	.44	.71	.36	.80
Ear length, cm	6.52	8.40	10.54	11.10	4.01	5.86	4.84	8.98	.38	.49	.21	.65
Spikelets/spike	5.02	6.23	6.96	34.83	2.22	4.36	3.80	7.51	.20	.49	.30	.05
Grains/spike	9.85	11.57	15.15	14.44	2.06	6.86	4.23	10.17	.04	.35	.08	.50
Grain yield/plant, g	14.98	24.60	37.24	37.60	9.54	5.98	13.55	23.92	.42	.06	.13	.40
1000-kernel weight, g	9.08	10.04	16.53	24.36	7.29	7.92	14.88	23.12	.65	.62	.81	.90
Days to anthesis	2.13	2.63	6.15	4.78	1.55	2.35	5.95	4.67	.53	.80	.94	.96
Peduncle length, cm	7.31	8.67	9.66	10.53	5.31	7.21	4.42	9.13	.53	.69	.21	.75
Grain protein, %	7.11	7.05	8.59	8.88	4.04	5.02	6.85	5.65	.32	.51	.64	.40

Table 4. Phenotypic (r_p) and genotypic (r_g) correlation coefficients in base and selected populations

Character Combination	r_p				r_g			
	Base population		Selected population		Base population		Selected population	
	BIP ₁ F ₁	F ₃	BIP ₁ F ₂	F ₄	BIP ₁ F ₁	F ₃	BIP ₁ F ₂	F ₄
Grain yield								
– Tiller number	.52 ^b	.63 ^b	.45 ^a	.18	.70	.40	.25	-.42
– Plant height	.19	.11	.14	.41 ^b	.29	.02	.16	.55
– Ear length	.21 ^a	.32 ^b	.03	-.10	.18	.31	-1.40	-.45
– Spikelets/spike	.22 ^a	.22 ^b	-.04	-.11	.52	.17	-.66	-.41
– Grains/spike	.26 ^b	.35 ^b	.49 ^a	.43 ^b	.19	.77	.52	.60
– 1000-kernel weight	.19	.15 ^a	.45 ^a	.54 ^b	.47	.55	1.16	.91
– Days to anthesis	-.10	-.10	-.26	-.39 ^b	-.06	-.51	-.59	-.59
– Peduncle length	.21 ^a	.12	.22	.43 ^b	.32	.25	.59	.65
– Protein content	.06	-.01	-.39	-.11	.05	-.38	-.99	-.27
Protein Content								
– Tiller number	-.02	.003	-.08	.20	-.70	-.15	-.29	.53
– Plant height	.02	.11	.15	.06	.24	.12	.15	.13
– Ear length	-.03	.01	.11	.26	.03	-.06	.22	.44
– Spikelets/spike	-.07	.10	.27	.12	.12	.19	.51	.39
– Grains/spike	-.04	-.06	-.02	-.08	-.19	-.11	-.62	-.34
– 1000-kernel weight	.12	.01	-.41	-.23	.06	.05	-.40	-.48
– Days to anthesis	.22 ^a	.19 ^b	.28	.41 ^b	.40	.27	.36	.68
– Peduncle length	-.24 ^a	-.001 ^c	-.01	.04	.10	-.02	.20	.08

^aSignificant at $P = .05$; ^bSignificant at $P = .01$; ^cNonhomogeneity of correlation coefficients between BIP₁F₁ vs F₃ and BIP₁F₂ vs F₄

Table 5. The predicted and actual response (% mean of the checks) for pedigree and recurrent selection systems at 10% selection intensity for protein content

Character	First cycle				Second cycle (Predicted)	
	Pedigree selection		Recurrent selection		Pedigree selection	Recurrent selection
	Predicted	Observed	Predicted	Observed		
Tiller number	-1.49	2.81	-1.63	6.99	5.53	- 5.86
Plant height, cm	1.35	- 1.41	1.39	2.78	1.74	1.53
Ear length, cm	-0.45	3.75	0.13	3.96	4.42	1.52
Spikelets/spike	1.05	5.93	0.27	1.80	3.46	2.79
Grains/spike	-1.22	- 9.48	-0.54	-12.44	- 4.66	- 4.52
Grain yield/plant, g	-4.60	- 2.86	0.82	-16.94	-11.17	-31.23
1000-kernel weight, g	0.50	-15.77	0.51	-16.24	-11.66	- 8.37
Days to anthesis	0.76	- 2.81	0.59	0.63	3.30	2.90
Peduncle length, cm	-0.49	2.67	1.84	2.96	1.04	1.53
Grain protein, %	6.28	3.25	4.09	4.36	4.41	10.29

the basal populations in both systems of mating. High heritability estimates for protein content, days to anthesis, plant height and 1000-grain weight suggested that selection for these traits could be effectively done in early segregating generations. However, when sufficiently high level of protein content is achieved with appropriate plant height, grain size and days to anthesis, it would then be worthwhile to improve the grain yield and other correlated traits.

The estimates of genotypic correlation coefficients for most of the combinations were higher in magnitude than the phenotypic coefficients (Table 4). The estimates of genotypic correlation coefficients of grain yield with ear length and 1000-kernel weight in the BIP₁F₂ population were unrealistic and exceeded unity. The phenotypic correlation coefficients of grain yield with tiller number, ear length, spikelets per spike and grains per spike in both the basal populations (BIP₁F₁ and F₃), with 1000-kernel

weight in the F_3 generation and with peduncle length in the BIP_1F_1 were positive and significant. The association of protein content with days to anthesis in both the BIP_1F_1 and the F_3 populations was positive and significant. A negative significant association of protein content with peduncle length in the BIP_1F_1 population was also observed. As long peduncles are photosynthetically more efficient (Randhawa, Minhas and Singh 1975), this possibly led to plumpy grains with a high yield performance and consequently widened the protein/starch ratio in the grains, thus establishing a negative association with protein content and grain yield. Positive significant phenotypic correlation of protein content with days to anthesis might be attributed to grain shrivelling in late flowering plants (Gill and Brar 1973).

The associations of grain yield and protein content with different traits were generally more favourable in the F_3 than the BIP_1F_1 population. The unfavourable negative correlation of protein content with peduncle length was significantly higher in the BIP_1F_1 than the F_3 population which indicated that improvement in protein content while maintaining a high yield performance was expected to be more appropriate through selfing series than random intermating. The phenotypic correlation coefficients for other pairs of traits under selfing and random intermating series were, however, found to be homogeneous. The presence of a weak correlation between grain yield and protein content in the basal and selected populations showed that improvement in protein content could be affected without appreciable loss in grain yield. However, the decrease in grain yield was expected to be higher through recurrent than through pedigree selection.

The association of grain yield with peduncle length, days to anthesis and 1000-kernel weight and that of protein content with tiller number, plant height, 1000-kernel weight, days to anthesis and peduncle length, were more favourable in the F_4 than the BIP_1F_2 population. This also indicated that the pedigree system of selection was more favourable than recurrent selection. The negative association of protein content with 1000-kernel weight and its positive association with ear length and spikelets per spike indicated that improvement in protein content would result from selection for small seeded types and that the loss in grain yield through reduction in seed weight could be compensated by increasing the number of grains per spike through the increased ear length accommodating more spikelets per spike.

Selection of 10 per cent high protein families resulted in an increase of 3.25 per cent and 4.36 per cent of the mean of the checks through pedigree and recurrent selection, respectively. The predicted and observed response for protein content were in good agreement in recurrent selection, but the actual response in pedigree selection was about half the value predicted. Low realised responses in

pedigree selection might be attributed to an upward bias in the estimation of genetic variation and heritability in the F_3 base population (Table 5). The increase in protein content was accompanied by a decrease in grains per spike, grain yield and 1000-kernel weight in both breeding methods but the decline was relatively higher in the recurrent selected population. Another desirable feature of the pedigree selection was earliness in maturity and reduction in plant height. Although the improvement in grain protein content was nearly equal in both systems of breeding, the favourable associated changes in the pedigreed population indicated the superiority of pedigree selection for the improvement of protein content in early segregating generations. From the estimates of genotypic and phenotypic variation, heritability, genotypic and phenotypic correlations and response to selection it seemed logical to follow a few cycles of pedigree selection in the early segregating generations for increasing protein content while maintaining appropriate levels of seed size, maturity and plant height. In later generations one or two cycles of intermating and recurrent selection could be followed to concentrate the favourable genes for grain yield. Khadr and Frey (1965) have also suggested a similar procedure for the improvement of seed weight in oats.

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