



Effects of selective intermating in bread wheat (*Triticum aestivum*) for crop improvement

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ABSTRACT

The effects of intermating in F_2 generation on mean, genetic variability, heritability and genetic advance in two crosses of wheat (*Triticum aestivum* L.) (WH 542/WH 1080) and (WH 1105/RAJ 3765/WH 283) were studied. The mean and genetic advance of all the seven characters, viz. days to heading, plant height (cm), number of effective tillers, number of grains/ear, 1000 grain weight (g), biological yield/plant (g), grain yield/plant (g) were increased after first cycle of intermating. Second cycle of intermating further showed its positive impact on mean, genetic variability, heritability and genetic advance. In this study the intermated population produced progenies which out yielded the F_2 population indicating the superiority of intermating over the F_2 in generating superior performing progenies. The result indicated that the intermated populations are potential candidates for further selection to improve the grain yield in bread wheat and may prove highly useful in generating promising wheat genotypes having desirable quality traits and stress tolerance.

Key words: Bread wheat, Genetic advance, Genetic variability, Intermating, Segregants

India is one of the major producers of wheat (*Triticum aestivum* L.) and had a harvest of 97.41 million tonnes of wheat in 2017–18, from total production area of about 26.7 million ha (Source: Department of Agriculture Cooperation & Farmers Welfare). One of the principle requirements for development of high yielding cultivars is the genetic variability followed by effective selection or hybridization as per the breeders' requirement. This depends on the continuous supply of new germplasm either from existing variation or creating variability by reshuffling genes governing grain yield, quality or agronomic importance. Apart from relying on new germplasm; creating variability from existing better genotypes depends on hybridization followed by effective handling of subsequent segregants. The success and failure of hybridization is determined by the variability that exists in F_2 generation. Pedigree method has been the most frequently used for selection in segregating generation and has been effective in development of new improved varieties in wheat. However with rapid fixation of alleles in this method it is difficult to obtain rare recombinants and can be overcome by intermating of high performing selected diverse genotypes. Successive selfing after hybridization in self pollinated crops like wheat puts a limit on the appearance of new recombinants and enhances fixation of linkage blocks in early generations. One or

more cycles of selective intermating in between the selfing series are expected to overcome these limitations of the conventional pedigree selection, foster gene recombination, accumulate more desirable genes in populations, ensure the exploitation of hidden genetic variability, shift genetic correlations in the desired direction and ultimately provide better source of material for selection than the original F_2 population and elevate the population mean, degree of heritability and extent of genetic advance under selection along with the mean value, heritability of traits may also be expected to improve in subsequent generations (Panwar *et al.* 2008) which is important for higher genetic gains. Thus, selective intermating can substantially supplement the pedigree breeding method for developing improved wheat genotypes having high yield potential along with other desirable traits via reshuffled alleles in wheat. The potential and effectiveness of this approach has been compared with those of conventional methods by many workers (Yunus and Paroda 1983, Panwar *et al.* 2000 and Panwar *et al.* 2008). Further they have emphasized the use of intermating and recurrent selection in wheat for retaining greater amount of genetic variability in subsequent generations. Keeping in view all these facts, present study was conducted.

MATERIALS AND METHODS

The germplasm material for the present study consisted of F_2 populations of two wheat crosses, Cross I (WH 542/WH 1080) and Cross II (WH 1105/RAJ 3765/WH 283). The characters of each parental line involved in the intervarietal

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Table 1 Origin, pedigree and characteristics of parental varieties for Cross I (WH542/WH1080) and Cross II (WH1105/RAJ3765//WH283)

Genotype	Origin	Pedigree	Characteristics
WH 542	CCSHAU, Hisar	JUPATECO/BLUEJAY/URES	Double dwarf with high yielding potential, suitable for timely sown, high fertility, irrigated conditions, very high tillering. Resistance to all major diseases (Rust, Karnal bunt, etc.), dense square, white spikes with short awns, narrow leaves, compact plant type having IB/IR translocation which carries Lr 26, Yr 9, Sr 31 and Pm 8 genes for disease resistance.
WH 1080	CCSHAU, Hisar	PRL/*2PASTOR	Suitable for rainfed and low input conditions. Excellent quality traits, high sedimentation value. Resistant to lodging drought and all rusts.
WH 1105	CCSHAU, Hisar	MILAN/S87230//BABAX	Semi-dwarf with high yielding potential, suitable for timely sown, high fertility and irrigated conditions, dark green foliage, high degree of resistance to all major diseases (Rust, Karnal bunt etc.), semi-erect early growth, semi erect plant type.
Raj 3765	RAU, Durgapura	HD2402/VL639	Early maturing variety, very good for chapatti making, bread making, biscuit making and high protein content.
WH 283	CCSHAU, Hisar	HD1981/RAJ821	High yielding potential, suitable for timely sown, high fertility, irrigated conditions. Bold shining amber grains and excellent for chapatti making. Resistant to rusts and Karnal bunt.

crosses is presented in Table 1.

The 100 phenotypically superior plants from F_2 population were intermated within the cross and between the cross during 2014–2015. The seeds from first cycle of intermated plants in each of F_2 populations were harvested in bulk as selected intermated population I (SIM-I) for cross I and selected intermated population II (SIM-II) for cross II. Further selective intermating was also done between these two F_2 populations. The seeds harvested from such intermated plants in bulk were constituted as selective intermated population III (SIM-III). Half of the seeds of first cycle of intermating of each cross were saved separately and remaining half were space planted during 2015–2016 and further second cycle selective intermating within and between population was done among 100 phenotypically superior plants. The hybrid seeds representing two cycle of selective intermating were harvested in bulk as SIM-I (2 cycles) for cross 1 and SIM-II (2 cycles) for cross 2 and SIM-III (2 cycles). Final evaluation of variability in seven populations was done by raising population of F_2 's (from saved half seed of F_1 's), first cycle of selective intermating (from saved half seed) and second cycle of selective intermating in randomized complete block design with three replications in 3 m length plot of 12 paired rows each with row to row distance of 20 cm and plant to plant distance of 10 cm during 2016–2017. Observations were recorded on five randomly selected plants from each population for seven traits namely: days to heading, plant height (cm), number of effective tillers, number of grains per ear, 1000 grain weight (g), biological yield/plant (g) and grain yield/plant (g).

Statistical analysis of data for experiment

The investigation involved the study of 7 populations {Intermated progenies of F_2 populations of two wheat

crosses namely WH542/WH1080 (cross I) and WH1105/RAJ3765//WH283 (cross II) over first Cycle and second Cycle of selective intermating and F_2 of two crosses}. The parents involved for every cross varied for agronomic and quality traits.

The analysis of data was carried out following standard statistical procedure following the method as described by Panse and Sukhatme (1978). The results for variability parameters estimates, viz. mean, phenotypic coefficient of variation, heritability and genetic advance as percent of mean across characters and crosses have been presented in Table 2 and Table 3.

RESULTS AND DISCUSSION

Genetic variability

The analysis of variance for mean of seven characters studied in intermated and F_2 populations revealed significant variation for almost all the traits studied in each population. This shows that the populations generated sufficient variation in two crosses which can be used for genetic improvement. Thus intermating provides chances of finding superior recombinants in later generations from the release of variability due to fostered recombination because of change of genetic background. This method has been found effective for increasing the mean values of grain yield and its components in wheat crop (Yunus and Paroda 1983, Panwar *et al.* 1990, 2008; Singh and Panwar 2006).

Mean performance of various traits in different populations

A wide range of variation was observed for all the 7 characters in different populations. The means of all the three intermated populations (SIM-I, SIM-II and SIM-III) for first and second cycles of selective intermating were higher in comparison to the mean of F_2 population of two crosses for

Table 2 Mean values and phenotypic coefficients of variation (PCV) in F_2 and different selectively intermated populations of Cross I (WH542/ WH1080) and Cross II (WH1105/RAJ3765//WH283) for first cycle and second cycle of intermating

Character	Parameter	F_2 Cross I	F_2 Cross II	Selected Intermated populations for year (Firstcycle)			Selected Intermated populations for year (Secondcycle)			LSD (5%)
				SIM- I	SIM -II	SIM -III	SIM -I	SIM -II	SIM- III	
Days to heading	Mean	85.07	87.37	83.11	85.1	81.67	81.86	83.32	80.4	5.1
	PCV	3.78	2.78	2.14	2.60	3.00	1.70	2.06	2.05	
Plant height (cm)	Mean	88.46	89.53	86.84	87.31	84.94	86.14	86.42	82.85	3.7
	PCV	5.75	5.37	4.33	5.01	4.99	3.21	4.05	3.43	
Number of effective tillers	Mean	9.72	10.45	10.71	11.9	12.48	11.82	12.35	12.95	2.3
	PCV	16.46	13.91	14.48	12.73	11.33	11.16	11.59	11.19	
Number of grains per ear	Mean	49.45	50.97	50.59	52.16	52.46	52.53	53.66	54.24	4.6
	PCV	7.73	5.48	7.03	3.97	5.48	5.44	3.53	3.70	
1000 grain weight (g)	Mean	43.36	42.83	44.01	43.56	44.50	44.22	44.15	45.6	2.1
	PCV	3.41	3.93	2.97	3.37	2.48	2.35	2.21	4.3	
Biological yield/ plant (g)	Mean	44.98	46.77	47.20	49.11	51.49	49.14	50.66	52.3	7.9
	PCV	11.83	11.35	11.03	10.96	7.08	10.3	9.97	9.8	
Grain yield/plant (g)	Mean	20.19	20.87	21.11	22.05	23.00	22.38	22.93	24.4	3.1
	PCV	13.19	11.37	12.91	10.04	7.45	8.47	7.96	7.32	

Table 3 Heritability broad sense (%) and Genetic Advance (% of mean) for seven characters in F_2 and different Selected Intermated wheat populations of Cross I (WH542/WH1080) and Cross II (WH1105/RAJ3765//WH283) for First and Second cycles of intermating

Character	Parameter	F_2 Cross I	F_2 Cross II	Selected intermated populations (First cycle)			Selected intermated populations (Second cycle)		
				SIM -I	SIM -II	SIM-III	SIM- I	SIM- II	SIM- III
Days to heading	h ²	76.18	73.3	84.41	87.4	85.5	89.06	93.2	90.3
	GA	5.94	4.1	3.72	4.69	5.29	3.13	3.96	3.82
Plant height (cm)	h ²	69.60	80.16	86.40	90.9	79.20	92.05	92.50	85.9
	GA	8.24	4.62	7.72	9.38	8.15	6.09	7.72	6.07
Number of effective tillers	h ²	74.25	84.6	77.11	90.2	73.00	83.46	94.2	87.3
	GA	25.17	24.25	23.00	23.64	7.04	19.19	22.50	20.58
Number of grains/ear	h ²	66.97	85.2	71.38	88.5	89.60	86.84	90.7	93.5
	GA	10.67	9.63	10.35	7.25	10.12	9.74	6.60	5.07
1000 grain weight (g)	h ²	84.35	87.00	87.30	87.9	86.60	89.76	90.20	91.2
	GA	5.93	7.05	5.35	6.11	4.43	4.35	4.12	4.01
Biological yield/plant(g)	h ²	76.58	80.1	90.99	87.5	76.1	92.82	92.9	93.4
	GA	18.67	18.37	20.68	19.75	11.09	19.94	19.09	13.36
Grain yield/plant(g)	h ²	82.81	82.10	89.72	84.4	80.00	90.25	89.9	91.5
	GA	22.50	19.23	23.83	17.46	12.28	15.75	14.74	12.02

all the characters, except days to heading and plant height. These intermated populations were significantly better than F_2 population for all the traits, eg days to heading, plant height, number of effective tillers, number of grains per ear, 1000 grain weight (g), biological yield/plant (g) and grain yield/plant (g). The days to heading mean values varied from 87.37 (F_2 Cross II) to 80.4 (SIM-III second cycle) whereas plant height (cm) mean varied from 89.53 (F_2 Cross II) to 82.85 (SIM-III second cycle). Number of effective tillers mean had range of variation from 9.72 (F_2 Cross I) to 12.95

(SIM-III second cycle) and the mean value for number of grains/ear varied from 49.45 (F_2 Cross I) to 54.24 (SIM-III second cycle). 1000-grain weight (g) mean values ranged from 42.83 (F_2 Cross II) to 45.6 (SIM-III second cycle). The mean range of biological yield/plant (g) was from 44.98 (F_2 Cross I) to 52.3 (SIM-III second cycle) whereas grain yield/plant (g) mean ranged from 20.19 (F_2 Cross I) to 24.4 (SIM-III second cycle).

Increased mean values in intermated populations for almost all the characters in two crosses might be due to

pooling of favourable alleles because of recombination resulting from intermating. In both the crosses, intermating considerably improved the mean performance of grain yield/plant compared to the F_2 progenies mean. Similar results were reported in wheat by Nematulla and Jha (1993). Number of effective tillers, as a yield contributing trait, showed higher performance in intermated populations for two crosses of wheat which was in agreement with the research reported by Mahalingam *et al.* (2011a) and Mahalingam *et al.* (2011b) in rice. Other yield contributing traits, viz. number of grains/ear, 1000-grain weight, biological yield/plant showed improved mean performance in intermated populations compared to F_2 's which is in agreement with previous research findings (Nematulla and Jha 1993, Amudha *et al.* 2006, Prakash and Verma 2006, Mahalingam *et al.* 2011a, Mahalingam *et al.* 2011b). In this study reduced plant height accompanied by increased grain yield/plant in selective intermated populations (SIM-I, SIM-II and SIM-III) in Cross-I and Cross-II compared to mean of F_2 population of two crosses indicates the chances of selecting shorter transgressive segregants wheat lines with high yielding ability. Similar results for short plant height and higher grain yield were reported in bread wheat (Nematulla and Jha 1993) and rice (Amudha *et al.* 2006). Further, comparison of mean values between three intermated populations revealed that mean performance of SIM-III for first and second cycles of selective intermating was significantly superior to SIM-I and SIM-II (for first and second cycles of selective intermating) for days to heading, plant height, number of effective tillers, number of grains/ear, 1000-grain weight (g), biological yield/plant (g) and grain yield/plant (g). The superiority of selective intermating between F_2 as compared to intermating within F_2 appeared to be due to additional variability released due to fostered recombination by accumulating favourable genes (Nematulla and Jha 1993, Prakash and Verma 2006) and another possible reason could be release of latent genetic variability by breaking undesirable linkages. Thus, selective intermating method can be applied for achieving an appreciable increase in the mean of the subsequent population presumably due to accumulation of desirable genes (Jensen 1978).

Phenotypic coefficient of variation analysis

The phenotypic coefficient of variation measures the magnitude of variability present within the population. A low value of coefficient of variation (CV) generally depicts low variability among the samples of population (Prakash and Verma 2006) demonstrated moderate to high phenotypic coefficient of variations in biparental and selfed wheat and barley populations, respectively. The F_2 population had higher phenotypic coefficient of variation for all the traits than intermated populations for first cycle and second cycle of selective intermating except for 1000 grain weight (g) for SIM-III populations (for second cycle of selective intermating) and higher PCV for four days to heading in SIM-II (for First cycle). Similar results were reported earlier

by Panwar *et al.* (2008) and Manickavelu *et al.* (2006) in rice for higher or comparable PCV in F_2 population observing that intermating within single cross populations resulted in less recombination and reduced genetic variance. Further greater genetic variation was observed in SIM-III population for most of the traits in comparison to SIM-I and SIM-II (for first cycle and second cycle of selective intermating) this may be due to intermating between two crosses F_2 which released more variability than mere selfing (Manickavelu *et al.* 2006) in rice. The days to heading had range of phenotypic coefficient of variation from 3.78 (F_2 Cross I) to 1.70 (SIM-I second cycle), whereas the plant height (cm) phenotypic coefficient of variation varied from 5.75 (F_2 Cross I) to 3.21 (SIM-I second cycle). Number of effective tillers had wide range of phenotypic coefficient of variation from 16.46 (F_2 Cross I) to 11.16 (SIM-I second cycle). The phenotypic coefficient of variation for number of grains/ear varied from 7.73 (F_2 Cross I) to 3.53 (SIM-II second cycle), whereas the phenotypic coefficient of variation for 1000-grain weight (g) ranged from 4.3 (SIM-III second cycle) to 2.21 (SIM-II second cycle). The range of phenotypic coefficient of variation for biological yield/plant (g) was from 11.83 (F_2 Cross I) to 7.08 (SIM-III first cycle). For grain yield/plant (g) phenotypic coefficient of variation ranged from 13.19 (F_2 Cross I) to 7.32 (SIM-III second cycle). Similar results were reported by Chander *et al.* (1993), Pawar *et al.* (2000) and Pawar *et al.* (2008).

Number of effective tillers, biological yield/plant (g) and grain yield/plant (g) showed moderate PCV over all populations. Days to heading, plant height (cm), number of grains/ear and 1000-grain weight (g) showed low PCV over all the populations. Further greater genetic variation was observed in SIM-III population for all the traits in comparison to SIM-I and SIM-II (for First and Second cycles of selective intermating). Manickavelu *et al.* (2006) in rice and Naik *et al.* (2009) in safflower reported similar increase for genetic variation in intermated populations.

Heritability broad sense (%) analysis

The comparison of estimates of broad sense heritability between the means of selective intermated populations and mean of F_2 populations revealed that heritability estimate improved for days to heading, number of effective tillers, number of grains/ear, 1000 grain weight (g), biological yield/plant (g), grain yield/plant (g) in selected intermated populations (SIM-I, SIM-II and SIM-III for First and Second cycles of selective intermating). Higher heritability estimates in SIM-III for days to heading, 1000 grain weight (g), biological yield/plant (g), grain yield/plant (g) as compared to SIM-I and SIM-II (for First and Second cycles of selective intermating) were reported which could be effectively used for crop improvement.

All the traits under study were found to be moderate to highly heritable in intermated populations. Days to heading in SIM-III Second cycle (93.2), plant height in SIM-II Second cycle (92.50), number of effective tillers in SIM-II Second cycle (94.2), number of grains per ear in SIM-III

Table 4 t test values for comparison of different populations

Trait	Parameter	Difference between the means of the two populations F ₂ (Cross I) and SIM I cycle I	Difference between the means of the two populations F ₂ (Cross II) and SIM II cycle I	Difference between the means of the two populations SIM- I and SIM III (cycle I)	Difference between the means of the two populations SIM- II and SIM III (cycle I)	Difference between the means of the two populations SIM- I and SIM III (cycle II)	Difference between the means of the two populations SIM- II and SIM III (cycle II)	Difference between the means of the two populations SIM- I and SIM III (cycle II)	Difference between the means of the two populations SIM- II and SIM III (cycle II)	Difference between the means of the two populations SIM- III (cycle I) and SIM III I) and SIM III (cycle II)
Days to heading	t value	7.13	8.98	6.39	13.55	9.19	16.63	7.48	8.26	5.82
	P value< Significance at P<0.05	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001	0.00001
Plant height (cm)	t value	3.44	4.56	4.51	5.21	11.8	10.68	2.01	2.12	5.52
	P value< Significance at P<0.05	0.000638	0.00001	0.00001	0.00001	0.00001	0.00001	0.044202	0.034609	0.00001
Number of effective tillers	t value	6.01	9.36	11.37	3.74	7.7	3.69	7.32	2.64	3.06
	P value< Significance at P<0.05	0.00001	0.00001	0.00001	0.000207	0.00001	0.000257	0.00001	0.008544	0.002306
Number of grains/ear	t value	2.91	4.58	5.51	1.160	6.95	4.00	5.72	6.22	7.18
	P value< Significance at P<0.05	0.003337	0.00001	0.00001	0.2465	0.00001	0.000075	0.00001	0.00001	0.00001
1000 grain weight (g)	t value	4.42	4.49	3.86	7.16	9.82	10.92	1.67	4.64	6.81
	P value< Significance at P<0.05	0.000013	0.00001	0.000133	0.00001	0.00001	0.00001	0.094526	0.00001	0.00001
Biological yield/plant (g)	t value	4.03	4.18	9.09	4.97	7.18	3.96	3.58	2.90	2.45
	P value< Significance at P<0.05	0.000068	0.000035	0.00001	0.00001	0.00001	0.00089	0.000383	0.003941	0.014482
Grain yield/plant (g)	t value	3.23	4.91	7.93	4.55	12.36	9.52	5.16	4.14	9.25
	P value< Significance at P<0.05	0.000134	0.00001	0.0001	0.00001	0.00001	0.00001	0.00001	0.000042	0.00001
		Significant	Significant	Significant	Significant	Significant	Significant	Significant	Significant	Significant

Second cycle (93.5), 1000-grain weight (g) in SIM-III Second cycle (91.2), biological yield/plant (g) in SIM-III Second cycle (93.4) and grain yield/plant (g) in SIM-III Second cycle (91.5) showed high heritability. Heritability for days to heading was minimum in F_2 Cross II (73.30) and maximum (93.2) in SIM-III Second cycle, whereas heritability for plant height (cm) was minimum in F_2 Cross II (69.60) and maximum (92.50) in SIM-II Second cycle. Heritability for number of effective tillers was minimum (73.00) in SIM-III first cycle and maximum (94.2) in SIM-II second cycle. Heritability for number of grains/ear was minimum (66.97) in F_2 Cross I and maximum (93.5) in SIM-III Second cycle. Heritability for 1000-grain weight (g) was minimum in F_2 Cross I (84.35) and maximum (91.2) in SIM-III second cycle. Heritability for biological yield/plant (g) was minimum (76.10) in F_2 Cross I and maximum (93.4) in SIM-III second cycle. Heritability for grain yield/plant (g) was minimum (80.0) in SIM-III first cycle and maximum (91.5) in SIM-III second cycle.

The improved value of heritability for yield and its components is of interest to breeders as it improves selection response for characters (Yunus and Paroda 1983). Bekele *et al.* (2014) also reported the estimates of broad sense heritability between the BIPs and the F_3 and revealed that heritability estimates improved in BIPs for heading days in cross I, grain yield/plant and days to heading in cross II, and biomass yield/plant, grain yield/plant, harvest index and 1000-grain weight in cross III. Higher heritability estimates for different traits in BIPs as compared to selfed progenies were also reported in bread wheat (Yunus and Paroda 1983), in barley (Prakash and Verma 2006).

Genetic advance (% of mean) analysis

Genetic advance being the product of heritability, phenotypic standard deviation and selection differential, it potentially indicates the selection intensity. Genetic advance (% of mean) was highest for number of effective tillers 25.17 (F_2 Cross I), grain yield/plant (g) 23.83 (SIM-I first cycle) and biological yield/plant (g) 20.68 (SIM-I first cycle). Genetic advance (% of mean) for days to heading was maximum in F_2 Cross I (5.94) and minimum (3.13) in SIM-III second cycle. Genetic advance (% of mean) for plant height (cm) was maximum in (9.38) in SIM-II first cycle and minimum in F_2 Cross II (4.62). Genetic advance (% of mean) for number of effective tillers was maximum (25.17) in F_2 Cross I (73.00) and minimum (7.04) in SIM-III first cycle. Genetic advance (% of mean) for number of grains/ear was maximum (10.67) in F_2 Cross I and minimum (5.07) in SIM-III second cycle. Genetic advance (% of mean) for 1000-grain weight (g) was maximum in F_2 Cross I (7.05) and minimum (4.01) in SIM-III Second cycle. Genetic advance (% of mean) for biological yield/plant (g) was maximum (20.68) in SIM-III First Cycle in F_2 Cross I and minimum (11.09) in SIM-III First cycle. The genetic advance (% of mean) for grain yield/plant (g) was maximum (23.83) in SIM-I First cycle and minimum (12.02) in SIM-III Second cycle. The estimates of GA (% of mean)

of mean) in selective intermated populations SIM-I and SIM-II (for First and Second cycles of selective intermating) were lower for traits days to heading and plant height but higher in SIM-III (for First and Second cycles of selective intermating) compared to F_2 population mean; however, it was higher in selective intermated population SIM-II and SIM-III for Second cycle for number of effective tillers, and biological yield/plant (g) for SIM-I and SIM-II for Second cycle and grain yield/plant (g) in SIM-I First cycle. Expected genetic advance (% of mean) was highest for grain yield/plant (g) 23.83 (SIM-First Cycle) and biological yield/plant (g) 20.68 (SIM-I first Cycle). Manickavelu *et al.* (2006) demonstrated higher % GA in F_3 as compared to BIPs for most of the measured traits in rice.

The high or moderate heritability estimate were coupled with high or moderate % GA in intermated populations for traits number of effective tillers, biological yield/plant (g) and grain yield/plant (g). Therefore, these characters offer more opportunity for improvement through selection among the intermated populations in the desired direction. The intermated populations were significantly better than F_2 population for number of effective tillers, number of grains/ear, 1000 grain weight (g), biological yield/plant (g) and grain yield/plant (g). Thus selective intermating method seems to be an effective method for achieving an appreciable increase in the mean of the subsequent population.

In the present study the intermated population produced progenies which out yielded the F_2 population and indicated the superiority of intermating over the F_2 in generating superior performing progenies. The result indicated that the intermated population are potential candidates for selection to improve the grain yield in wheat and use in different breeding programmes.

The traits number of effective tillers, biological yield/plant (g) and grain yield/plant (g) with high to moderate heritability estimate coupled with high genetic advance as percent of mean also showed high estimates of PCV values. Therefore, these characters offer more opportunity for improvement through selection among the intermated population in the desired direction. However, for other traits like plant height, days to heading, number of grains/ear and 1000 grain weight (g) the estimates of PCV and %GA were relatively low even though the estimates of heritability were moderate to high in most cases, hence gives less chance for selection. This showed that the intermating of segregants in F_2 had only very little effect on recombination in those traits with low % GA but high to moderate heritability. This is in agreement with Yunus and Paroda (1983) in bread wheat. Therefore, more cycles of intermating of selected segregants could be suggested to release more variability for the improvement in such cases (Manickavelu *et al.* 2006).

In this study analysis of variance for mean of 7 characters studied in intermated and F_2 populations revealed significant variation for almost all the traits in each population indicating that populations generated sufficient variation in two crosses which can be used for subsequent genetic improvement. Thus intermating provides chances

of finding superior recombinants in later generations from the release of variability due to fostered recombination due to change of genetic background.

Increased mean values in intermated populations for almost all the characters in two crosses asserts pooling of favourable alleles because of recombination resulting from intermating. In both crosses intermating considerably improved the mean performance of grain yield/plant compared to the F_2 progenies mean. Number of effective tillers, as a yield contributing trait, showed higher performance in intermated populations for two crosses. Traits, viz. number of grains/ear, 1000 grain weight, biological yield/plant showed improved mean performance in intermated populations compared to F_2 's. Reduced plant height accompanied by increased grain yield/plant in selective intermated populations (SIM-I, SIM-II and SIM-III) in cross I and cross II compared to mean of F_2 population of two crosses indicated the chances of selecting shorter transgressive segregant wheat lines with high yielding ability. Further, comparison of mean values between three intermated populations revealed that mean performance of SIM-III for First and Second cycles of selective intermating was significantly superior to SIM-I and SIM-II (for First and Second cycles of selective intermating) for days to heading, plant height, tillers/plant, number of grains/ear, 1000-grain weight (g), biological yield/plant (g) and grain yield/plant (g). The superiority of selective intermating between F_2 as compared to intermating within F_2 appeared to be due to additional variability released due to γ accumulation of favourable genes between diverse parents. The improved values of heritability for yield and its components is of importance as it improves selection response for the characters.

The estimates of GA (% of mean) in selective intermated populations SIM-I and SIM-II (for First and Second cycles of selective intermating) were lower for trait's days to heading and plant height but higher in SIM-III (for First and Second cycles of selective intermating) compared to F_2 population mean; however, it was higher in selective intermated population SIM-II and SIM-III for Second cycle for number of effective tillers, and biological yield/plant (g) for SIM-I and SIM-II for Second cycle and grain yield/plant (g) in SIM-I First cycle. The traits number of effective tillers, biological yield/plant (g) and grain yield/plant (g) with high to moderate heritability estimate coupled with high genetic advance as percent of means showed also high estimates of PCV values. Therefore, these characters offer more opportunity for improvement through selection among the intermated populations in the desired direction. For other traits 1000 grain weight, plant height, days to heading and days to maturity, the estimates of PCV and % GA were relatively low even though the estimates of heritability were moderate to high in most cases, hence it gives less chance for selection. This showed that the intermating of segregants in F_2 had only very little effect on recombination in those traits with low %GA but high to moderate heritability. The

high or moderate heritability estimate was coupled with high or moderate % GA in intermated populations for number of effective tillers, biological yield/plant (g), grain yield/plant (g). Therefore, these characters offer more opportunity for improvement through selection among the intermated populations in the desired direction. Thus selective intermating method seemed to be an effective method for achieving an appreciable increase in the mean of the subsequent population presumably due to accumulation of desirable genes. On the basis of the results obtained from the selective intermated populations and F_2 populations of two crosses it may be concluded that the higher mean values in all selected intermated populations (SIM-I, SIM-II and SIM-III for First and Second cycles of selective intermating) and wider range values for genetic variability in SIM-III compared to F_2 populations of two crosses for most of the characters studied in two crosses asserts release of additional variability due to selective intermating accumulating favourable genes. The efficiency of intermating over F_2 was witnessed in this investigation in terms of days to heading, number of tillers/plant, number of grains/ear, 1000-grain weight (g), biological yield/plant (g), grain yield/plant (g) and other yield related traits. The wider range accompanied by a higher values of mean, phenotypic coefficient of variation, heritability and genetic advance as percentage of mean for biological yield/plant and grain yield/plant in selective intermated populations provides opportunity for further selection in intermated populations.

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