A COMPARATIVE STUDY OF FIRST AND SECOND CYCLES OF INTERMATING WITH BASIC POPULATION IN WHEAT

BY

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Thesis submitted to the Haryana Agricultural University in partial fulfilment of the requirements for the degree of :

MASTER OF SCIENCE

IN

PLANT BREEDING

College of Agriculture
Haryana Agricultural University
H I S A R



To

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Singer

Hemant Kumar

CERTIFICATE - I

This is to certify that this thesis entitled "A comparative study of first and second cycles of intermating with basic population in wheat" submitted for the degree of Master of Science, in the subject of Plant Breeding, of the Haryana Agricultural University, is a bonafide research work carried out by Shri Subhash Chander under my supervision and that no part of this thesis has been submitted for any other degree.

The assistance and help received during the course of investigation have been fully acknowledged.

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CERTIFICATE - 11

This is to certify that the Chesis entitled,

"A comparative study of first and second cycles of intermating
with basic population in wheat" submitted by Shri Subhash Chander
to the Haryana Agricultural University in partial fulfilment
of the requirements for the degree of Master of Science in
the subject of Plant Breeding, has been approved by the
Student's Advisory Committee after an oral examination on the
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IN TRODUCTION

Wheat is the cheapest source of carbohydrates and proteins which provides almost 20% of the total food calories for the people and is staple food for about 35% of the world population. Wheat is too, often passed off as merely a starchy food crop; it contains other valuable nutritive materials, notably proteins, minerals and vitamins. In fact the amino acid yield per acre from wheat far exceeds that of animal products for every one of the essential amino acid. Wheat is thus an important food grain of the world. presently, wheat is harvested from about 226.10 million hactares with a total production of 540.23 million tonnes In this, wheat is only next every year (Anonymous, 1990). to rice in acreage and production and is grown over 24.09 million hactares with an annual production of 53,99 million tonnes (Anonymous, 1990). Further increase in production can only be met by the development of varieties of high yield potential in future as their is absolutely no scope of increasing area under wheat cultivation.

The conventional pedigree selection, though significant and productive in its own right, imposes restrictions on the chances of recombination rates and thereby limits the accumulation of desirable alleles spread over various loci. The probability that any one individual in F_2 generation of a cross would carry most of the potentially adaptive genes is very remote. Hence, chances of producing best balanced genotype through selection in F_2 and onwards are limited.

Further this method utilizes the only fixable gene effects (additive and additive x additive) and thus, the method seems to be inadequate to explore the range of genetic variability for complex characters like yield in wheat (Joshi and Dhawan, 1966 and Jensen, 1970).

The hidden variability can be exploited by intermating in early segregating generation. This approach has been reported to break undesirable linkage, enhance variability, elevate the population mean and improve the chances of assembling the maximum number of potentially useful genes leading to the isolation of stable and widely adapted genotypes (Verma et al.1979; Yunus and Paroda, 1982 and Balyan and Verma, 1995). Further, this approach would not only elevate the population mean but also retain useful variability to be effective for several cycles of selection (Kumar, 1973; Singh and Dwivedi, 1978; Verma et al., 1979; Singh et al., 1986; Yunus and Paroda, 1983 and Srivastava et al.1989). Though encouraging results were reported on one hand, contradictory results were also often obtained (Pederson, 1974; Bos, 1977; Snape, 1978; Radden and Jensen, 1974; Stam, 1977; Yonezawa, 1983).

In view of the above it is imperative to make comparisons of F₂ variability with that of early generation intermating so that a breeder can choose the most efficient breeding approach for genetic improvement of the population in wheat. It is, therefore, proposed to undertake the present investigation with the following objectives.

 To study the extent of genetic variability generated through first and second cycles of intermating for yield and yield components. 2. Impact of intermating on correlation coefficients for different traits.

REVIEW OF LITERATURE

The literature on wheat has been reviewed, partly on the basis of results, pertaining to intermating in segregating generations, recurrent selection, role of intergenotypic competition in selection and selection in segregating generations etc. The intermating in segregating generations and recurrent selection have been found to be more efficient for improvement of several traits of economic importance than the most commonly followed pedigree method of breeding.

Intermating in segregating generations or recurrent selection is expected (i) to break undesirable linkages (ii) to retain greater variability for several cycles of selection (iii) to elevate population mean and (iv) to assemble genes to give rise, widely adapted and stable genotypes.

Improvement through conventional breeding methods has been relatively difficult task because yield showed complex inheritance (Paroda and Joshi, 1970a; Virk and Aulakh, 1975; Sharma and Singh, 1982; Gill et al.1983; Verma and Luthra, 1983) and its components are negatively correlated (Smocek, 1969; Chaudhry et al.1970; Knott and Kumar, 1971; Knott and Talukdar, 1971; Jatasra and Paroda, 1978). To generate useful variability, various mating systems like biparental mating, double cross, three way cross etc. have been suggested (Jensen, 1970; Gill et al.1973 and Verma et al. 1978; Singh and Sharma, 1976 and Kar et al. 1978).

The conventional pedigree method though offers opportunities for using breeder's skill and obtaining genetic

information but has been reported to be less effective for improving seed yield in wheat (De Pauw and Shebeski, 1973) and the method has the several other drawbacks, namely (1) limited parent participation (ii) rapid fixation of genes (iii) low genetic variability (iv) poor recombination potential (Andrus, 1963; Jensen, 1970). To maximize heterozygosity, crossing over the recombination among alleles at the linked loci, mass or visual selection followed by intercrossing of the selected plants can be done in every generation or in early second generation. In the presence of linkages and correlated response, the large recombination potential otherwise expected owing to the independent action of the genes was not realized (Clegg et al. 1972). If cross involves representatives of population and the trait being improved is controlled by a number of genes, a wide segregation may occur which will require large population to be grown (Langham, 1949). Mac Key (1953) also optioned to have sufficient F, population because a very minute part of potential of cross is realized in small populations.

sibmating in early generation can create maximum gene recombination and maximum fitness. Therefore, Hanson (1959) and Andrus (1963) proposed atleast one or more cycles of intermating in early generations. Hensel (1964) supported the idea of intermating in early segregating generation and recognized the possibilities of getting better segregants after each cycle of intermating due to accumulation of desirable genes. For full utilization of variability arising through an initial hybridication, Bliss and Gates (1968) suggested

recurrent cycles of crossing and selection for the improvement of traits being governed by large number of genes. Jensen (1970) also favoured the intermating at F1 and F2 levels for the improvement in creals. The method was suggested for the wider use of germplasm, simultaneous inputs of parents creation of persistent gene pools, breaking of linkage blocks, release of hidden variability and general fastering of genetic recombination. Jensen (1978) demonstrated that diallel selective mating system can be integrated into breeding programme for strengthening the conventional breeding procedures. Khadr and Frey (1965) have used recurrent selection successfully to increase seed weights in oats. Joshi and Dhawan (1966), Compton, (1968), Gill et al. (1973), Verma and Kumar (1974) have recommended recurrent selection in wheat. Miller and Rawlings (1967) and E1-Adl and Miller (1971) in cotton; Hanson et al. (1967) in case of soyabean; Redden and Jensen (1974) in case of wheat and barley; Matzinger and Wernsman (1968) in case of tobacco demonstrated that recurrent selection helped to break undesirable linkage blocks and resulted in shifts in the genetic correlation.

The studies reported from India showed the recurrent selection could be integrated with the conventional breeding programme in order to maintain genetic variability for continued genetic improvement and breaking the existing yield barriers in self pollinated crops. Comparative studies to understand the effectiveness of mating system were also made in wheat. Mean of biparental progenies were found to be superior than selfed generation for almost all the characters in wheat by Gill et al.(1973). They reported high heritability

estimates in biparental progenies and some shift in correlation between yield component traits. Similar results were also reported by Lal (1975) in wheat. He found that the intensity of few unfavourable genes was reduced and favourable correlations appeared in intermated populations. Means of the biparental progenies was found to be excelled over selfed progenies and notable shift in genetic correlations was established in many studies (Singh and Dwivedi, 1978; Verma et al. 1978, 1979; Yunus and Paroda, 1982, 1983; Balyan and Verma, 1985; Singh et al. 1986 and Srivastava, 1988). Singh, Bhullar and Gill (1986) compared biparental approach with conventional selfing approach for various characters. In the case of grains/spike, grain weight and grain yield the biparental progenies depicted higher mean, wider range, greater phenotypic and genotypic variance, high genotypic coefficient of variability as well as heritability and genetic advance as per cent of mean than Fis and Fis.

The theoretical evaluation of the usefulness of intermating in general, have dependent on different linkage considerations and the assessment criteria followed. Baker (1968) assumed that the advantage of intermating will be the greatest with tight inkages (when value of 'P' is small). In two locus model, he objective of intermating was an attempt to increase the robability of recovering AB/AB genotypes from a repulsion cass for different linkage intensities and sample size is igner under intermating than under selfing. Miller and Rawling 1967) and Meredith and Bridge (1971) found that intermated upulation could provide better source of material for selection an original F2 population in cotton due to breaking of ikage blocks. They found that the negative correlation

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between yield and fibre strength was weakened in intermated populations. Similar results were observed in cotton by Bains (1971) cited by Joshi (1979).

For intermating, sufficiently large number of plants should be used in a segregating generation because estimates of genetic correlations (and selection based on them) have such a high sampling error in smaller samples that selection is practically ineffective. Thus the expected effects of random intermating on genetic variance in self pollinated crops will depend upon the linkage relationship involved. Assuming recombination of linked genes with predominantly additive genetic effects, the genetic variance has been predicted either to increase or to decrease with regulation and coupling phase linkage (Miller and Rawling, 1967; Baker, 1968 and Yunus and Paroda, 1982) with preponderance of repulsion phase linkages, the random intermating would result in increased range of genotypic values and hence the increased genetic variance of the population. With coupling phase linkage a decrease in genetic variance would be anticipated due to lowering of the frequencies of extreme types,

Tyagi (1987) recommended intercrossing in early generation with selection for desirable segregates in cotton. He found that some correlations were significant and negative in the selfed families but were non-significant and negative or positive in the biparental intermated progenies. The reduction or disappearance of negative association in biparental intermated progenies is thought to be due to breakage of linkages predominantly in a repulsion phase. He further proposed that

several cycles of intercrossing would further increase variability and produce a greater number of desirable segregants for selection.

Many controversial reports are also available about the feasibility and usefulness of intermating approach of breeding for generating variability. Pederson (1974) questioned the usefulness of intermating in F, generation to release desirable segregants. It was argued that the frequency of desirable homozygotes can also be increased following directional selection in F₃ generation. Bos (1977) and Snape (1978) emphasized that intermating of Fo plants cannot always be considered a possibility of increasing desired segregants in the population because it depends upon the distribution of genes on chromosomes. This conclusion confirms the results of Pederson (1974). Redden and Jensen (1974) worked out the effect of intermating both in presence or absence of selection in segregating populations of wheat and barley. They concluded that there is a reason to believe the positive results of intermating in breeding programme of inbreeding crops, provided the additive component of genetic variance is important. Stam (1977). however, reported that the short term effects of intermating is negligible but in long run, it is superior to selfing specially when many loci are involved. Limitation in release of more variability through biparental mating approach was also observed by Harlan et al. (1940) and Frey (1975) due to low initial variation. Therefore, they suggested recurrent breeding and multiple cross approaches which provide more

scope of generating genetic variability through new gene recombination resulting from breakage of tight linkages and accumulation of genes from number of diverse parents involved increases. Randhawa and Gill (1978, 1980) and Nanda et al. (1981) reported that recurrent selection approach is of little value for improvement in wheat. Sneep (1977) made a valuable observations that the frequency of favourable genotypes in double cross is considerably lower than conventional Fa generation of 2 parents differing for all the alleles. If the parents are differing for 21 alleles, about 2.1 million population is needed to get one desired type. It questioned the feasibility of multiple cross approach. Rana and Sheshagiri (1983) also supported these observations about multiple cross approach. Yonezawa (1983) made computations to assess the value of intermating before selection in self pollinated crops. It was shown that selfed or partially intermated populations often have greater genetic variance than intermated populations. However, these studies are based on intercrossing the plants at random before selection whereas in the breeding programme only selected plants are intermated.

The foregoing review, reveals that intermating approach despite some contraversies, can prove useful to elevate the population mean. Thus it seems to be realistic to work out the relative efficiency of different mating systems.

MATERIALS AND METHODS

The present investigations were carried out during the year 1990-91 at the experimental farm of Department of Plant Breeding, Haryana Agricultural University, Hisar.

The experimental material consisted of three populations viz. F₂, BIPs I cycle, BIPs II cycle developed in each of the two intervarietal wheat crosses, namely WH 416 x HD 2160 (Cross 1) and WH 416 x HD 2329 (Cross II). Among the parental varieties two namely, WH 416 and HD 2329 are the high yielding semi-dwarf varieties adapted to north western and northern plain zones, respectively. The third variety, i.e. HD 2160 is the triple dwarf line possessing excellent resistance to the rusts. General characteristics of parental varieties are presented in Table 1.

Development of experimental material

Large F₂ populations (5000 plants) of the two crosses were raised during the crop season 1988-89. One hundred thirty plants were randomly selected in each F₂ population and 65 paired crosses were attempted to produce BIPs I cycle, half seed of BIPs I cycle was reserved and remaining half seed of each 65 BIPs I cycle was space planted, during 1989-90. One hundred thirty single plants were randomly selected and 65 paired crosses were attempted in each cross to produce BIPs II cycle. F₁s of two crosses were also raised to get F₂ seed of the two original crosses.

Table 1: Characteristics of parent varieties used in crossing programme.

Variety	Par <i>e</i> ntage	Main characteristics
WH 416	WH 147 - UP 368	A semi-dwarf with high yield potential, good tillering; long ear, slow rusting to leaf rust but susceptible to yellow rust; Amber and soft grains.
HD 2160	Masoc 3-yt-54- NIOB-Calidad/ Tobofn/HD 1949	Triple dwarf, highly resistant to rusts, stout straw. Amber, fairly bold grains and resistant to lodging.
HD 2329	HD 1962-8-4870- K65/HD 1553 x UP 262	A double dwarf variety of medium maturity and high yield potential. Fairly good resista to lodging but susceptible to rusts grains are amber, hard and bold.

All the three populations viz. F₂, BIPs I cycle and BIPs II cycle of each cross were evaluated in randomized block design with three replications. Each population was space planted in 25 rows of 3.5 m length in each replication. The plant to plant distance was kept 15 cm and the row to row distance was 25 cm. One hundred twenty five plants from each population were randomly selected to record observations on different characters.

Data Recording

The data was recorded on 125 randomly selected plants per plot in each replication. The terminal plants of each plot were excluded to minimize the border effect. The observations for following traits were recorded.

- Tillers per plant: Total number of tillers per plant were counted at the time of harvesting.
- Grains per ear: Total number of grains were counted in the main ear at maturity.
- 3. Grain weight per ear (g): The weight of grains of the ear of main tiller was recorded in grams.
- 4. <u>Biological yield per plant (q)</u>: The mature plant was harvested from the base and weight of whole plant was recorded in grams.
- 5. Grain yield per plant (q): The weight of grains per plant was recorded in grams.

Statistical Analysis

The experimental data recorded on different characters were subjected to following statistical analysis.

1. Analysis of variance and covariance: The analysis of variance and covariance was done for partitioning the variance and covariance as shown below:

Source		d.f.	M,S.S Observed	Expected	M.S. Observe	s. d Expected
Replic	ations	(r-	1			
Popula	tions	(p-	1) MS ₂	$r\sigma_{g}^{2} + \sigma_{e}^{2}$	MP ij	ro 2 ij Foe ij
Error		(r-1)		σ _e ²	™ _e	σ _e ij
To tal		(rp-	-1)		·	
Where,						
	r	=	number of rep	lications		
	P	=	number of pro	genies in e	ech popul	ation
	σ ² g	=	genotypic var	i anc e		
	σ ²	쿅	error variano	e		
	σ _g jj	=	genotypic cov	griance of	character	x _i an i x _j

The genotypic and phenotypic variances were calculated as follows:

= error covariance of character X_i and X_j

$$\sigma_{g}^{2} = \frac{Ms_{2} - Ms_{3}}{r}$$

$$\sigma_{p}^{2} = \sigma_{g}^{2} + \frac{Ms_{3}}{r}$$

The genotypic and phenotypic coveriances were calculated using the following formula:

$$\sigma_{g_{\underline{i}\underline{j}}} = \frac{MP_{\underline{i}\underline{j}} - Me_{\underline{i}\underline{j}}}{r}$$

$$\sigma_{p_{ij}} = \sigma_{g_{ij}} + \frac{\sigma_{e_{ij}}}{r}$$

Parameters of Variability: They were computed as follows: 2.

(i) Mean
$$(\overline{X}) = \frac{X_{ij}}{N}$$

where,

 $X_{ij} = Any observation in the ith progeny and$ j th replication.

N = Total number of observati

(11) Standard error = S.E.(m) = $\frac{MS_3}{r}$

(iii) Heritability in broad sense (h2b)

$$= \frac{\sigma_{\mathbf{q}}^2}{\sigma_{\mathbf{p}}^2}$$

(iv) Genetic advance (GA) = $\sigma_D h^2 b$

Genetic advance percent of mean = $\frac{i \sigma h^2 b}{x}$ x 100

Where 'i' is the coefficient of selection for selection intensity (5% in present case)

Significance of difference of means of the (v) different populations was tested with student's t-test as under:

$$t = \frac{\overline{x}_1 - \overline{x}_j}{\frac{(MS_3)_1}{n_i} + \frac{(MS_3)_1}{n_j}}$$

Where, $(MS_3)_1$ and $(MS_3)_1$ are the error variances of the two populations of size n; and n; respectively.

Analysis of correlation: The nature and extent of association between yield and its component traits was calculated with simple correlations as follows:

Genotypic correlation coefficient (r Gij) =

$$= \frac{\sigma_{g_{1}}}{\sqrt{\sigma_{g_{1}}^{2} \times \sigma_{g_{1}}^{2}}}$$

Phenotypic correlation coefficient (r P it) =

$$=\frac{\sigma_{p_{ij}}}{\sigma_{p_{i}}^{2} * \sigma_{p_{i}}^{2}}$$

Path Coefficient Analysis:

3.

The genotypic correlation coefficients were subjected to this analysis. Path coefficients were obtained according to Dewey and Lu (1959). A set of simultaneous equations in the following form were solved

 $r_{ny} = p_{ny} + r_{n2}p_{2y} + r_{n3}p_{3y} + \cdots + r_{n}p_{xy}$ Where,

Pny = path coefficient between the character and yield

r_{n2}, r_{n3} · · · · r_{nx} = Correlation coefficients

between that character and each of other

yield component in turn.

The following correlation materices were formed:

$$\begin{bmatrix} \mathbf{r}_{1y} \\ \mathbf{r}_{2y} \\ \mathbf{r}_{ny} \end{bmatrix} = \begin{bmatrix} 1 & \mathbf{r}_{12} & \mathbf{r}_{13} & \dots & \mathbf{r}_{1n} \\ \mathbf{r}_{21} & 1 & \mathbf{r}_{23} & \dots & \mathbf{r}_{1n} \\ \mathbf{r}_{n1} & \mathbf{r}_{n2} & \mathbf{r}_{n3} & \dots & 1 \end{bmatrix}$$

Where,

r₁₂, r₂₁ and So on, and r_{1y} = Correlation between one component characters and yield.

The B matrix was inverted (B-1) and path coefficient (P_{ij}) were obtained as follows:

$$(P_{1j}) = (A) \times (B^{-1})$$

The indirect effects for a particular character through other characters were obtained by multiplication of direct path and particular correlation coefficient between those two characters, respectively.

Indirect effect = rii x Pii

Where,

and Pij = Ply P2y · · · · Pny

The residual factors, i.e. the variation in yield unaccounted for these associated was calculated from the following formulae. Residual factors $(\overline{X}) = 1-R^2$

Where,

EXPERIMENTAL RESULTS

Three populations, viz. F₂, BIPs I cycle and BIPs II cycle generated from each of the two bread wheat crosses, viz., wh 416 x HD 2160 (Cross I) and WH 416 x HD 2329 (Cross II) were studied to compare the variability generated through first and second cycles of intermatings for yield and its components. Also the impact of intermating was worked out on intermelationship of different traits. The results obtained are presented below:

- Analysis of variance: All the three populations, viz.,

 F₂, BIPs I cycle and BIPs II cycle were subjected to
 analysis of variance. The populations had significant
 differences with eachother. BIPs I cycle differed
 significantly from F₂ population for all the traits
 studied in each cross. The comparison of BIPs II cycle
 with BIPs I cycle showed that the former differed
 significantly from later for all other traits except
 grain weight per ear in each cross.
- (ii) Mean performance for various characters in different populations:

The data pertaining to mean for five characters namely, tillers per plant, grains per ear, grain weight per ear, biological yield per plant and grain yield per plant in three populations, viz., F₂, BIPs I cycle and BIPs II cycle are presented in Table 2 and 3 for cross I and cross II, respectively. BIPs I cycle and BIPs II cycles were significantly superior to the F₂ population

rable 2: Mean values of various characters studied in different populations in Cross-I

Characters	Populations					
	F ₂	BIPs I cycle	BIps II cycle			
Tillers per plant	10.71 <u>+</u> 1.16 ^a	11.79 <u>+</u> 1.07 ^b	13.33 <u>+</u> 0.89 ^C			
Grains per ear	43.27 <u>+</u> 2.06ª	53.06 <u>+</u> 1.96 ^b	58.95 <u>+</u> 1.86°			
Grain weight per ear (g)	1.62+0.22	2.60 <u>+</u> 0.22 ^b	2.81 <u>+</u> 0.21 ^b			
Biological yield per plant (g)	54.46 <u>+</u> 4.18 ^a	59.02 <u>+</u> 2.73 ^b	64.63 <u>+</u> 2.13 ^C			
Grain yield per plant (g)	16.09 <u>+</u> 1.86 ^a	20 .9 8 <u>+</u> 1.77 ^b	23 .47<u>+</u>1.52^C			

a-c : Mean of different populations followed by same letter are not significantly different at the 0.05 probability level following student's t-test.

Table 3: Mean values of various characters studied in different populations in Cross-II

Characters	Populations				
	F ₂	BIPs I cycle	BIPs II cycle		
Tillers per plant	9,41+1,22	11.67 <u>+</u> 1.18 ^b	15.24+1.33°		
Grains per ear	48.04 <u>+</u> 1.73 ^a	55.96 <u>+</u> 1.63 ^b	60.68 <u>+</u> 1.37 ^C		
Grain weight per ear (g)	1.78 <u>+</u> 0.24 ^a	2.85 <u>+</u> 0.25 ^b	2.92 <u>+</u> 0.24 ^b		
Biological yield per plant (g)	58.24±3.80 ^a	61.03 <u>+</u> 3.31 ^b	66,65 <u>+</u> 3,14 ^C		
Grain yield per plant (g)	15.29 <u>+</u> 2.33 ^a	20.97 <u>+</u> 2.09 ^b	23.95 <u>+</u> 2.11 ^C		

a-c: Mean of different populations followed by same letter are not significantly different at the 0.05 probability level following student's t-test.

in respect of mean performance for all the five characters namely, tillers per plant, grains per ear, grain weight per ear, biological yield per plant and grain yield per plant in both the crosses. BIPs II cycle had significantly higher mean than BIPs I cycle for all the five characters except grain weight per ear in both the crosses.

11) Estimates of genotypic and phenotypic variances: Results pertaining to variances for different populations are summarized in Table 4 and 5 for cross I and II, respectively. Phenotypic variances (σ_p^2) were higher in magnitude than their respective genotypic variances (σ_g^2) for all the five characters studied in both the crosses.

In cross I, the σ_p^2 were more in BIPs I cycle than F_2 for all the characters except biological yield per plant. The σ_p^2 were also more in BIPs II cycle as compared to BIPs I cycle for grains per ear, grain weight per ear and grain yield per plant in cross I. In cross II, BIPs I cycle revealed higher σ_p^2 than F_2 for grains per ear and grain weight per ear. However, BIPs II cycle exhibited less σ_p^2 than BIPs I cycle for grains per ear and grain weight per ear.

In cross I, the σ_g^2 was more in BIPs I cycle than F_2 for all other characters except biological yield per plant. Similarly, BIPs II cycle showed higher σ_g^2 than BIPs I cycle for all other characters except biological yield per plant. However, in cross II, the σ_g^2 was more in BIPs I cycle than F_2 for all the five characters studied. BIPs II cycle showed higher σ_g^2 than BIPs I cycle except grain weight per ear in which same values were observed in both the populations in cross II.

Table 4: Genotypic variance $(\sigma_{\mathbf{g}}^2)$ and phenotypic variance $(\sigma_{\mathbf{p}}^2)$, in different populations of cross-I

Characters	_	<u></u>	lations	
		F ₂	BIPs I cycle	BIPs II cycle
Tillers per plant	σ ² g	9,13	10.05	10,31
	σ ²	11.15	11.77	11.49
Grains per ear	σ- ² g	26.95	28,75	33.04
	σ ²	33.31	34.50	38,23
Grain weight per ear (g)	σ ²	0.28	0.29	0.31
	σ ² p	0.35	0.36	0.37
Biological yield per plant (g)	σ- <mark>2</mark>	101.62	94.88	92.97
	σ²	127.87	106.02	99.77
Grain yield per plant (g)	σ ²	20.96	23.69	26.16
• = ==	σ ² p	26.15	28.39	29.61

Table 5: Genotypic variance (σ_{g}^{2}) and phenotypic variance (σ_{p}^{2}), in different populations in cross II.

Ch aracters			Popul at	
		F ₂	glba I	BIPs II cycle
Tillers per plant	5 g	8,58	8.66	12.01
	σ <mark>2</mark>	10.83	10.76	14.63
Grains per ear	or 2 €	19,10	20,68	21.73
	σ ² p	23.61	24.65	24.53
Grain weight per	σ_{g}^{2}	0,32	0.37	0.37
	σ-2 p	0.41	0 .4 6	0.45
Biological yield per plant (g)	or 2 g	88.46	91.03	97.76
hor hr 131	σ- <mark>2</mark>	110.08	107.51	112,55
Grain yield per plant (g)	o−2/9	31.02	32.34	38.95
b (a)	o-2	39.18	38.87	45,65

iv) Estimates of heritability and genetic advance as percentage of mean:

The results pertaining to the estimates of heritability in broad sense (h²) and genetic advance as percentage of mean (G.A.% x) are presented in Table 6 and 7 for cross I and cross II, respectively. Almost all the characters expressed moderate to high heritability estimates (broad sense) in all the population of both the crosses.

In cross I, highest heritability was recorded for tillers per plant (82%) followed by grains per ear (81%), grain yield per plant (80%) and grain weight per ear and biological yield per plant (79%) in F₂ population.

In cross II, highest heritability was observed for grains per ear (81%) followed by biological yield per plant (80%), tillers per plant and grain yield per plant (79%) and grain weight per ear (74%) in F_2 population.

An improvement in heritability estimates was recorded in both BIPs I and II cycles for almost all the characters in the two crosses.

F₂ population exhibited highest percentage of genetic advance than BIPs for almost all the characters. In cross I, grain weight per ear showed highest percent of genetic advance (59.26%) followed by tillers per plant (52.36), grain yield per plant (52.2), biological yield per plant (33.82) and grains per ear (22.12) in F₂ population. The genetic advance reduced in BIPs I and II cycles.

Table 6: Heritability in broad sense (h2) and genetic advance as percentage of mean (GA % X) in different populations in cross 1

Characters			Popul ations	
		F ₂	BIPs I cycle	BIPs II cycle
Tillers per plant	h ²	0,82	0.85	0.90
	GA % x	52.36	50.91	46.74
Grains per ear	h^2	0.81	0.93	0.86
	ga % 🕏	22,12	18.91	18.58
Grain weight per	h ²	0.79	0.79	0.92
ear (g)	GA % x	59.26	37.59	36.70
Biological yield	h ²	0.79	0.89	0.93
per plant (g)	GA % x	33.82	32.01	29.52
Grain yield per	h^2	0.80	0.83	0.88
plant (g)	GA ≯ x	52.20	43.44	41.99

Table 7: Heritability in broad sense (h^2) and genetic advance as percentage of mean $(GA \% \times)$ in different populations in cross II.

Characters	Populations Populations			
		F ₂	BIÞs I cycle	BIPs II cycle
Tillers per plant	h ²	0.79	0.80	0.82
	ga 🗴 🗓	56.86	46,35	42.17
Grains per ear	h ²	0.81	0.84	0.89
	GA% x	16.78	15.26	14,82
Grain weight per	h ²	0.74	0.79	0.81
ear (g)	GA% X	58,42	38.94	38.26
Biological yield	h ²	0.80	0.85	0.87
per plant (g)	G#% x	29.53	29.49	28.34
Grain yield per	h^2	0.79	0.83	0.85
plant (g)	GA% R	66.46	50.95	49.35

In cross II, grain yield per plant (66.46) exhibited highest percentage of genetic advance followed by grain weight per ear (58.42), tillers per plant (56.86), biological yield per plant (29.53) and grains per ear (16.78) in F₂ population. A reduction in genetic advances in the intermated population was recorded.

Association among traits: The genotypic and phenotypic correlation coefficients between various combinations of all the five characters for the three different generations, namely, F₂, BIPs I cycle and BIPs II cycle were worked out and are presented in Table 8 and 9 for cross I and cross II, respectively.

observed between grains per ear and biological yield per plant and between biological yield per plant and grain yield per plant in F₂. BIPs I cycle and new positive and significant correlation appeared between tillers per plant and grain yield per plant. However, the correlation between grains per ear and biological yield per plant disappeared in this population. In BIPs II cycle two new positive and significant correlations between tillers per plant and grain yield per plant and grains per ear and between grains per ear and grain yield per plant were established.

In cross II, F₂ showed only two positive and significant correlations between tillers per plant and grain yield per plant and between grains per ear and biological yield per plant. In case of BIPs I cycle and BIPs II cycle the close relationship between tillers per plant and grain yield per plant not only maintained but also improved. However, the relationships between grains per ear and

Table 8: Genotypic (below diagonal) and phenotypic correlation coefficients for various traits in different populations in cross I.

Characters	Popula-		Characte	rs		
	tions	Tillers per plant	Grains per e∋r	Grain weight per ear	yield	Grain yield per plant (g)
Tillers per	F ₂		-0.236	-0.317	0.389	0.395
plant	BIPs I cycle		0.312	0.145	0,287	0.576
	BIPs II		0.494	0.239	0.276	0.594
Grains per ear	F ₂	-0.316		-0.352	0.510	0.327
	BIPs I cycle	0.286		0.193	0.154	0.391
	BIPs II cycle	0.582		0.286	0.223	0.486
Grain weight	F ₂	-0.342	-0.362		-0.346	0.098
per ear (g)	BIPs I cycle	0.167	0,205		0,129	0.27
	BIPs II cycle	0.246	0.299		0.138	
Biological	F ₂	0,396	0.543	0.385		0.54
yield per plant (g)	BIPs I	0.312	0.211	0.182		0.69
	cycle BIPs II cycle	0,293	0.256	0.159		0.69
Grain yield per plant (g)	F ₂	0.542	0.397	0.103	0.75	4
	BIPs I cycle	0,619	0.466	0.283		
	BIPs II	0,648	0.493	0.416	0.79	4

^{*} Significant at 5% level.

Table 9: Genotypic (below diagonal) and phenotypic correlation coefficients for various traits in different populations in cross II.

Characters	Popula-	-	Chara	cters		
	tions	Tillers per plant	Grains per ear	Grain weight per ear (g)	Biolo- gical yield per plant	Grain yield per plant (g)
Tillers per plant	F ₂		-0.318	-0.201	0,312	0.402
	Blps I cycle		0.214	0.388	0.294	0.427
	Blba II		0.458	0.542	0,235	0.568
Grains per ear	F ₂	0,306		-0.189	0.562	0.302
	BIPs I cycle	0,289		0.165	-0.180	0.376
	BIPs II	0.467		0.217	0,314	0.482
Grain weight	F ₂	-0.243	-0.201		-0,286	-0.098
per ear (g)	Blps I cycle	0.394	0.183		-0.101	0.247
	BIPs II	0.561	0.231		0.205	0.409
Biological	F ₂	0.322	-0.462	-0.297		0.327
yield per plant (g)	Blps I cycle	0.319	-0.196	-0.098		0.399
	BIPs II	0.249	0.342	0.219		0.414
<pre>Grain yield per plant(g)</pre>	F ₂	0.508	0.386	-0.106	0.387	1
	BIPs I cycle	0.520	0.479	0.268	0.448	3
	Blps II	0.668	0,508	0.498	0,49	·

^{*} Significant at 5% level.

biological yield per plant reduced to non-significant value in BIPs I cycle. On the other hand, five new positive and significant correlations viz., tillers per plant and grains per ear; tillers per plant and grain weight per ear; grains per ear and grain yield per plant grain weight per ear and grain yield per plant and biological yield per plant and grain yield per plant were established in BIPs II cycle.

vi) Path coefficient analysis: Path coefficient analysis was carried out to find out the direct and indirect effects of various characters on yield per plant at the genotypic level in three populations, viz., F₂, BIPs I cycle and BIPs II cycle of both the crosses. The phenotypic and genotypic correlation coefficients alongwith direct and indirect effects of various characters on yield per plant in F₂, BIPs I cycle and BIPs II cycle populations are presented in Table 10 and 11 and are diagramatically represented in Fig.I and 2 for cross I and cross II, respectively.

The results pertaining to F₂, BIPs I cycle and BIPs II cycle of each cross showed that the direct effects were, in general, of higher magnitude than those of indirect effects for most of the characters.

In F₂ population of cross I, the partitioning of genotypic correlation between yield per plant and its component characters indicated that tillers per plant had the highest positive direct effect on yield per plant (.624) followed by grains per ear (.436) and biological yield per plant (.425). Although, grain weight per ear had negative direct effect (-0.022), its indirect effects on yield per plant via

Table 10: Correlation coefficients and direct (diagonal) and indirect effects of various characters on grain yield in different populations of Cross I

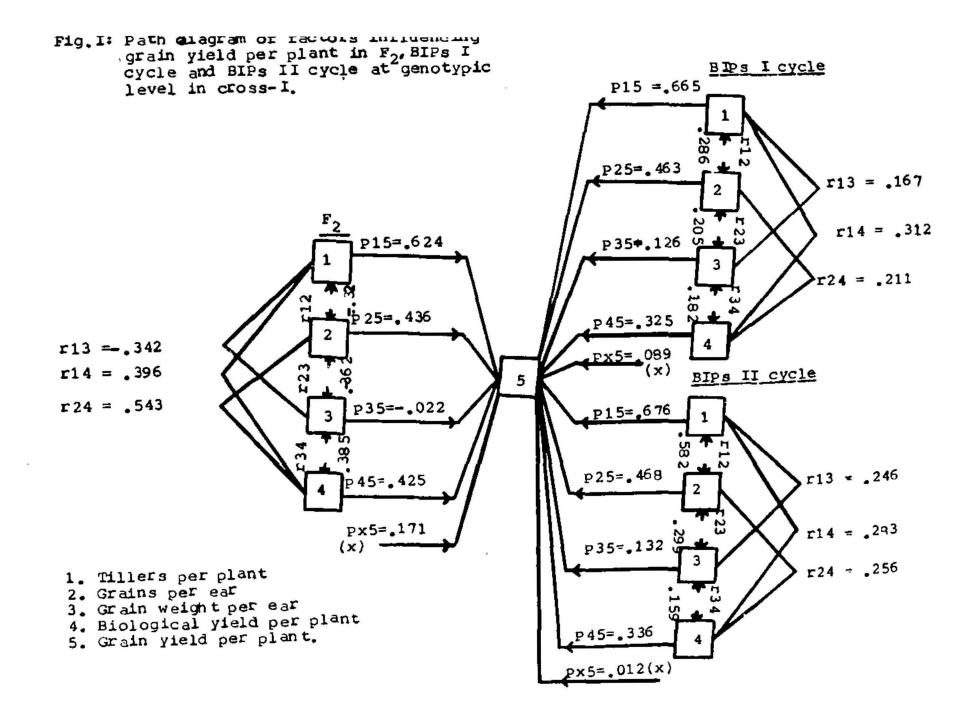
Characters F ₂			Effects via				Genotypic Phenotypic	
		1	2	3	4	correlation correla coefficients coeffic		
1.	Tillers per plant	0.624	0.033	-0.026	-0.089	0.542	.395	
2.	Grains per ear	-0.013	0.436	-0.006	-0.020	0.397	.327	
3.	Grain weight per ear	-0.024	0.013	-0.022	0.136	0.103	.098	
4.	Biological yield per	0.189	0.156	-0.016	0.425	0.754	.6 41*	
	plant (g)					Residual = 0.	170516	
BIPs	Icycle							
1.	Tillers per plant	0.665	0.038	-0.009	-0.075	0,618	.576*	
2.	Grains per ear	-0.003	0.463	-0.002	0.008	0.466	.391	
3.	Grain weight per ear	.0.112	0.045	0.126	0.124	9,283	.272	
4.	Biological yield per	0.199	0.185	0.053	0.325	0.762	. 686 *	
•	plant (g)					Residual = 0,089113		
BIPS	II cycle						**	
1.	Tillers per plant	0.676	0.121	-0.005	-0.143	0,649	. 59 4*	
-	Grains per ear Grain weight per ear Biological yield per plan	0.004	0.468 0.067 0.188	0.002 0.132 0.063	0.019 0.128 0.336	0.493	. 486*	
						0.416	. 396	
						0.784	.691*	
						Residual = 0.	012439	

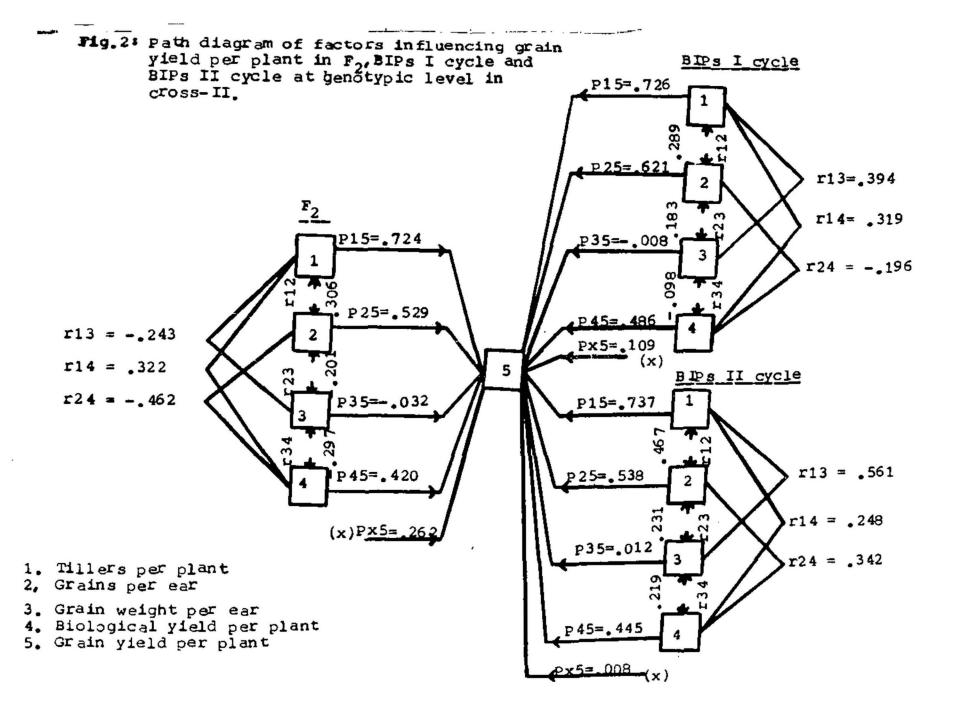
^{*} significant at 5% level.

Table 11:Correlation coefficients and direct (diagonal) and indirect effects of various characters on grain yield in different populations of Cross II

Char	acters		<u>Eff</u>	Genotypic Phenotypic					
		1	2	3	4		ion correlation		
						<u>coefficier</u>	ts coefficient		
2									
L.	Tillers per plant	0.724	0.076	-0.126	-0.166	0.508	• 40 2*		
2.	Grains per ear	-0.166	0.529	0.003	0.020	0.386	.302		
3.	Grain weight per ear	-0.124	0.014	-0.032	0.036	-0.106	-0.098		
4.	Biological yield per	0.021	0.012	-0.066	0.420	0.387	.327		
	Plant (g)					Residual = 0,262039			
BIP s	I cycle								
1.	Tillers per plant	0.726	0.126	-0.146	-0.186	0.520	₂ 427*		
2.	Grains per ear	-0.174	0.621	0.004	0.028	0.479	.376		
3.	Grain weight per ear	0.198	0.042	<u>-0.008</u>	0.036	0.268	.247		
4.	Biological yield per plant (g)	0.026	0.015	-0.079	0.486	0.448	.398		
						Residual = 0.109491			
BIPS	: II cycle					- 450	.568*		
1.	Tillers per plant	0.737	0.128	-0.198	0.001	0.668	.482*		
2.	Grains per ear	-0.170	0.538	0.008	0,132	0.509	.409*		
3.	Grain weight per ear	0.205	0.145	0.012	0.136	0.498			
4.	Biological yield per	0.036	0.022	-0.009	0.445	0.494	. 41 4*		
-•	plant (g)			Residual = 0.008352					

^{*} Significant at 5% level.





biological yield per plant (.136) and via grains per ear (.013) were responsible for positive correlation with grain yield.

The direct effects of tillers per plant, grains per ear and grain weight per ear increased in BIPs I cycle of cross I. The direct effect of grain weight per ear was positive as against negative value of this effect in F_2 population. The direct effect of biological yield per plant was positive but less than F_2 population whereas its indirect effects via other characters were strong and positive as against low/negative value in F_2 population.

The direct effects of tillers per plant, grains per ear, biological yield per plant and grains weight per ear increased to some extent in BIPs II cycle of cross I. In addition, most of the indirect effects were towards higher side in BIPs II cycle as compared to P2 and BIPs I cycle.

The estimates of direct and indirect effects of various characters on yield per plant in the F₂ population of cross II revealed that the direct effects of tillers per plant was highest, positive (.724), followed by grains per ear (.529) and biological yield per plant (.420) on grain yield per plant in F₂ population. The grain weight per ear showed negative direct effect (-0.032)on grain yield per plant. In BIPs I cycle of this cross the direct effect of tillers per plant on yield per plant remained unchanged and the direct effect of grains per ear and biological yield per plant were improved considerably in BIPs I cycle of cross II. The negative direct effect of grain weight per ear was reduced considerably in BIPs I cycle.

The direct effects of almost all the characters on grain yield per plant improved considerably in BIPs II cycle as compared to F_2 of cross II. In addition, indirect effects of grains per ear via biological yield per plant, grain weight per ear and tillers per plant improved in BIPs II cycle. Similarly, indirect effects of biological yield per plant via tillers per plant and grains per ear also exhibited improvement in BIPs II cycle. The grain weight per ear showed direct positive effects and high positive indirect effects via other characters in BIPs II cycle as against negative direct effect in F_2 and BIPs II cycle populations.

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DISCUSSION

In wheat, considerable progress has been made on production front during the last two decades but much of this progress has largely been due to the incorporation and manipulation of major genes which led not only to increase in production but also to stablize the production. It may be noted, however, that the improvement in yield per se has been slow due to the fact that yield is governed by complex polygenic systems. Further, Allard and Hansche (1964) attributed the slow progress to either inadequate initial variability or the existing use of single plant selection in early generation that was inadequate to exploit the range of useful variability available.

Thus, the conventional pedigree methods, no doubt, offers opportunities for using breeder's skill and obtaining genetic information but failed to provide enough opportunity to isolate the desired genotypes and, therefore, proved less effective for improving complex characters like grain yield in wheat (De Pauw and Shebeski, 1973) because with this method recombination is not only restricted to F₂ population but is further curtailed by linkage which is the probable cause of association among traits (Clegg et al., 1972). Moreover, the complex genetic mechanism for transmission of yield contributing traits did not allow the required progress in the

improvement of yield and its components. Nevertheless, the possibility of getting transgression always exists (Hansel, 1971 and Joshi, 1979). The chances of such transgression can be enhanced through encouraging the process of recombination in which the co-ordinated genetic influence on yield components is established (Joshi and Dhawan, 1966), Hanson (1959) and Andrus (1963) proposed atleast one cycle of sibmating in early generation which would provide maximum gene recombination and maximum fitness. The probabilities of getting better segregants due to accumulation of desired genes are also increased in intermated population (Hanse, 1964). A number of studied on the effectiveness of intermating to generate variability and increased mean performance are available (Jensen, 1970; Gill et al. 1973; Lal, 1975; Singh and Dwivedi, 1978; Verma et al. 1978; Yunus and Paroda, 1982, 1983; Stivastava et al. 1989 and Verma, 1989).

Most of the studies on intermating have suggested the usefulness of this method in segregating generations to break underirable linkages enhancing the variability and elevating population mean. In majority of the cases, however, the comparison of Blps with corresponding selfing population have been reported in case of only one cycle of intermating. In the present investigation the comparison of Blps I and Blps II cycles have been made with the corresponding F₂ population in two wheat crosses and the results are discussed below.

Significant statistical differences between different populations, namely, F₂, Blps I cycle and Blps II cycle of two crosses were found for tillers per plant, grains per ear,

biological yield per plant and grain yield per plant. BIPs also differed significantly from F₂ for grain weight per ear in both the crosses. The results of analysis of variance clearly showed that the material had sufficient variability to give valid comparisons of the different populations for the characters studied. As such the populations were compared from the mean differences, variances heritability estimated and genetic advance from the different characters.

A comparison of mean values of different characters in the BIPs and F2 populations of two wheat crosses suggested that the mean values for all the characters in the BIPs (I and II cycle) were significantly higher than F2 population. addition, BIPs II cycle had significantly higher mean performance for all the characters except grain weight per ear than Blos I cycle in both the crosses. The significant deviations in mean performance might be attributed to the dominance deviation and epistatic interaction in BIPs (Mather and Jinks, 1971). Higher mean performance of BIPs than F2 population is also expected mean major portion of genetic variation is additive and additive x additive type. The results of the present investigation are in conformation to those studies which favoured one or two cycles of selective intermating for achieving an appreciable increase in the mean in resultant populations because of the accumulation of desirable genes Gill et al., 1973; Singh and Dwivedi, 1978, Yunus and Paroda, 1982; Balyan and Verma, 1985; singh et al. 1986 and Srivastava, 1988 In addition, the release of concealed variability by breaking undesirable linkages and the dominance components could play

at least some role towards increase in mean performance of the BIPs. Gill et al. 1973; Lal. 1975; Yunus and Paroda, 1982 and 1983; Balyan and Verma, 1985; Singh et al. 1986 and Srivastava 1988 also demonstrated the usefulness of biparental approach in elevating population mean in different wheat crosses.

Considerable improvement in the mean values for various quantitative characters of economic importance was also reported in other, often and self-pollinated, crops like cotton (Miller and Rawlings, 1967; Meadows, 1968; Bains, 1971; William et al. 1971) and tobacco (Matzinger, et al. 1972). Singh and Murty (1973) also found considerable improvement for various characters in pearl millet through the use of biparental matings.

The BIPs I and BIPs II cycles maintained high genotypic variance for most of the characters in the two crosses. The high genotypic variance with the high mean of the BIPs would be desirable for making suitable selection in the material generated through intermatings. High and genetic variance of BIPs may be due to breakage of undesirable linkages Perkins and Jinks, 1970 . Gill et al., 1973, Massy, 1962, and Matzinger and Wernsman, 1968.

The estimates of h^2 in broad sense and genetic advance as percentage of mean for all the characters in both the crosses revealed that BIPs II cycle had highest h^2 and lowest G.A.% followed by BIPs I cycle and F_2 , respectively. High heritability estimates in case of BIPs as compared to selfed

progenies were also reported by Gill et al. (1973). Similars results were obtained by Rændhowa and Gill (1978) and Balyan and Singh (1983) for certain characters in the populations generated through intermating in segregating generations. Improvement in h² following intermating is most desirable in the sense that it would help in selection for the traits easily in these populations (Weibel, 1965; Mc Neal, 1960; Sharma and Knoot, 1964; Johnson et al 1966; Paroda and Joshi, 1970; Rana et al. 1973; and Sharma et al. 1978). Genetic advanve expressed as percentage of mean was found less in BIPs as compared to F_2 population, consequently high h^2 is not accompaniest by high genetic advance. This inconsistency may be attributed to low and high magnitude of phenotypic standard deviation which is an important component of genetic advance. Moreover the mean of the trait is also an important factor in the estimate of genetic advance expressed as percentage of The result of the present investigation are in agreement with Ketata et al. (1976), Islam (1976), Ahmed et al. (1977) and Pawar et al. (1985).

Changes in the interrelationship of traits demonstrated the significance of intermating approach in the present study. New significant and positive correlation appeared in BIPs I cycle as compared to F₂ between tillers per plant and grain yield per plant in cross I. Two new positive correlations between tillers per plant and grains per ear and grain yield per plant and grains per ear and grain yield per plant and grains per ear were observed in BIPs II cycle. Similarly in cross II, five new positive correlations between tillers per

plant and grains per ear, tillers per plant and grain weight per ear, grains per ear and grain yield per plant and biological yield per plant and grain yield per plant appeared in BIPs II cycle as compared to F2 and BIPs I cycle populations. On the other hand, correlations between grains per ear and biological yield per plant disappeared in BIPs as compared to F₂ in both the crosses. The shifts in correlations due to bip arental matings in early segregating generations have also been reported by Gill et al. 1973; Redden and Jensen, 1974; Lal, 1975; Randhawa and Gill, 1978, 1980; Verma et al. 1979; Yunus and Paroda, 1982, Balyan and Verma, 1985; Balyan and Singh, 1987 and Srivastava, 1988. The decrease or increase in the magnitude of correlation coefficients may be attributed to possible breakage of coupling and repulsion phase linkages, respectively, due to intermating in F, generation (Miller and Rawlings, 1967). Thus, the intermating in segregating generate ion may be particularly useful in situations where repulsion phase linkages are prevalent. Also, in situations where changes in correlation coefficients particularly from undesirable to desirable ones could provide greater scope for increasing the frequency of rare recombinants in segregating generation. The result of the present investigation indicated that the two cycles of intermating have helped in the change of correlations between different traits.

Path coefficient analysis further provided an insight into the inter-relationship of various characters with grain yield. In the two crosses, the characters viz, tillers per

plant, grains per ear and biological yield per plant showed highest direct effect on grain yield in that order in the three populations viz., F₂, BIPs I cycle and BIPs II cycle in both the crosses. Highest direct effect of tillers per plant on grain yield was also reported by Fonsece and Patterson, 1968; Barrige, 1974; Jaimini et al. 1974; Lal. 1975; Quick, 1978, Yunus, 1980 and Yunus and Paroda, 1982. Thus, the direct effects of these characters were responsible for their high positive genotypic correlations with grain yield per plant.

In general, the direct effects were highest in BIPs II cycle as against to BIPs I cycle or F_2 . However, the direct effect of biological yield per plant decreased in BIPs I cycle than F_2 in cross I. Similarly, the direct effect of grain weight per ear and biological yield per plant were less in BIPs II cycle than BIPs I cycle in cross II. But these associations, were still high enough to contribute high positive correlation with grain yield per plant. It is evident that with few exceptions, all the indirect effects were higher in magnitude in BIPs II cycle in comparison to F_2 and BIPs I cycle in both the crosses. On the contrary, Lal (1975) reported that the direct effects of some characters were inconsistent in different populations.

From the aforesaid discussion it was observed that:

1. Biparental progenies exhibited significantly higher mean performance for all the characters as compared to F2 populations in both the crosses. Most of the characters also maintained sufficient high genetic variance in BIPs cycles.

- 2. Some new positive and significant correlations got established in BIPs. In BIPs, correlation of grain yield was established with tillers per plant, grains per ear and grains per ear, grain weight per ear biological yield per plant in cross I and II, respectively.
- 3. Improvement in heritability and direct effects for almost all the characters in BIPs was observed in the two crosses.

SUMM ARY

The present investigation was carried out in three populations each of the two inter-varietal crosses of wheat (Triticum aestivum L.em.Thell) viz., WH 416 x HD 2160 (cross I) and WH 416 x HD 2329 (cross II) to study the extent of genetic variability generated through first and second cycles of intermating for yield and its components and to see the impact of intermating on correlation coefficients for different traits.

To achieve the aforesaid objectives, all the three populations, viz., F₂, BIPs I and BIPs II cycle were laid in randomized block design with three replications. Each population was space planted in 25 rows of 3.5 m length in each replication. The plant to plant distance was kept 15 cm and row to row distance was 25 cm. One hundred twenty five plants from each population were randomly selected to record observations on five characters viz., tillers per plant, grains per ear, grain weight per ear, biological yield per plant and grain yield per plant and were subjected to statistical analysis.

The analysis of variance revealed that the $\rm F_2$ population differed significantly than BIPs for all the traits. This indicated that the material was suitable for further analysis.

Both BIPs were significantly superior to the F₂ population in respect of mean performance for all the five characters in both the crosses. BIPs II cycle also exhibited significantly

higher mean performance than BIPs I cycle for all the characters except grain yield per ear in both the crosses.

and II cycles for all the characters except biological yield per plant in crosses I. Thus, BIPs had high mean performance alongwith sufficient high genotypic variance for most of the traits in the two crosses. Improvement in heritability was observed in BIPs as compared to F₂. However, a reduction in genetic advance as percentage of mean in the recorded in the BIPs of the two crosses for most of the traits.

Correlation studies demonstrated a shift in association between yield component traits in intermated populations. Three correlations viz., tillers per plant with grains per ear, tillers per plant with grains per ear with grain yield per plant and grains per ear with grain yield per plant in cross I and five correlations viz., tillers per plant with grains per ear, tillers per plant with grain weight per ear, grains per ear with grainyield per plant, grain weight per ear with grain yield per plant and biological yield per plant with grain yield per plant in cross II, were established in BIPs as compared to F₂. However, the correlation between grains per ear and biological yield per plant disappeared in BIPs as against to F₂ in both the crosses.

path coefficient analysis revealed that the tillers per plant had the highest direct effect followed by grains per ear and biologicalyield per plant, respectively in all the three populations in both the crosses. The direct and indirect effects showed improvement for most of the traits in BIPs as compared to F2s in both the crosses.

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^{*} Original not seen