

POPULATION IMPROVEMENT IN WHEAT

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THE basic procedure in understanding the nature of variation present in a given population is to partition it into components attributable to different causes, i.e. genetic and environmental. The genetic effects can further be partitioned into additive, dominance and epistatic effects. In most of the genetical studies, the relative estimates of components of genetic variation in self-pollinated crops, are based on the information derived from diallel analysis and the estimates are likely to be biased due to the presence of correlated gene distribution and epistatic interaction. North Carolina Mating Designs (Comstock and Robinson, 1952; in the present case NCD II has been used) give unbiased estimate of the components of genetic variance, but have not been commonly used in self pollinated crops.

Induced polygenic variations are expected to have similar pattern as the natural (normal) populations. However, genetic variability of mutagen treated populations, due to breakage of linkage, change in modifier complexes and pleiotropic effects, is expected to show different variability pattern when compared with the normal untreated populations.

Keeping in view the above points, this paper reports the estimates of components of genetic variance of biparental progenies in untreated and mutagen treated populations of bread wheat (*Triticum aestivum* em. Thell.) for yield and certain yield attributes. The efficacy and efficiency of cyclic intermating coupled with selection (population improvement) as compared to the standard selection procedures (pedigree method) in self-pollinated crops have been evaluated.

MATERIALS AND METHODS

Four F_2 populations, 'Norteno M 67 \times S 331', 'Norteno M 67 \times NP 876' and the same two crosses produced by crossing EMS (0.4% aqueous solution) treated parents, were used for producing biparental (NCD II; Comstock and Robinson, 1952) progenies. In the cross 'Norteno M 67 \times S 331', 100 random F_2 plants were grouped in 25 sets of four plants each, within each set using two plants as males and two as females, four fullsib crosses were made thus yielding 100 fullsib families. However, in the F_2 s (untreated as well as treated) of the cross 'Norteno M 67 \times NP 876', due to poor seed setting adequate seeds of fullsib families (80) of only 20 sets could be obtained. The progenies were grown in randomized block design with three replications. Each plot was a row of 15 plants spaced 6 cm apart within rows and 30 cm between the rows. Eliminating border plants, individual plant data were recorded on ten competitive plants per plot for days to heading, plant height, tillers/plant, spike length, grains/spike, test weight, and yield/plant. Plot means were used for statistical analysis. The estimates of variances were obtained according to the method given by Comstock and Robinson (1952).

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RESULTS

The analysis of variance of biparental progenies (D II) of the four populations (Norteno M 67 × S 331, untreated; Norteno M 67 × S 331, treated; Norteno M 67 × NP 876, untreated; Norteno M 67 × NP 876, treated; hereafter the populations would be referred to as populations I, II, III and IV, respectively) for seven characters, namely, days to heading, plant height, tillers/plant spike length, grains/spike, test weight and yield/plant, are presented in Table 1. The biparental progenies differed significantly for most of the characters among all the four populations.

The estimates of components of additive and dominance genetic variance (σ^2_A and σ^2_D) for the four populations are presented in Table 2. The estimates of additive component of genetic variance were significant for days to heading, plant height, spike length and test weight in population I, whereas in the treated population (population II) it was significant for days to heading, plant height, spike length and yield/plant. In population III, significant estimates of additive genetic variance were obtained for days to heading, plant height, grains/spike and test weight, whereas in the corresponding EMS treated population (population IV) for all the characters, except tillers/plant and yield/plant, the estimates of additive component were significant. The estimates obtained from the treated populations were larger than those from the untreated populations in both the crosses for all the characters, except test weight in populations II and IV where the additive genetic variance decreased in the treated populations as compared to the untreated.

The estimates of dominance components of genetic variance were non-significant for all the characters in populations I and II, except for test weight in population II. Tillers/plant, spike length, test weight and yield/plant in population III, and plant height, tillers/plant, test weight and yield/plant in population IV showed significant estimates of dominance components. The relative estimates of σ^2_D for plant height, spike length, test weight and yield/plant in population II and plant height in population IV (the two treated populations) were larger than those in the untreated populations (populations I and III). For the remaining characters the trend was opposite.

DISCUSSION

The validity and applicability of the various parameters to be estimated from the North Carolina Mating Design II would depend on the fulfilment of certain assumptions as laid down by Comstock and Robinson (1952). The assumptions involved in deriving the genetic interpretation of variance components are (a) regular diploid behaviour at meiosis, (b) population gene frequency should be half at all loci, (c) random choice of the individuals taken for producing experimental material, (d) no multiple allelism, (e) no correlation of genotype at separate loci, i.e., no linkage or if linkage exists it should not be in

TABLE 1
Analysis of variance of normal and treated biparental progenies (MCD II) for seven characters in bread wheat

Sources	d.f.	Days to heading		Plant height		Tillers/plant		Spike length		Grains/spike		Test weight		Yield/plant	
		N	T	N	T	N	T	N	T	N	T	N	T	N	T
Sets	24	14.17	107.70	64.41	271.75	2.54	5.00	1.57	3.81	51.86	91.38	26.88	26.49	13.91	30.23
Replications in sets	50	25.57	13.76	156.69	116.33	6.19	8.25	1.38	1.57	60.84	85.74	35.04	20.24	20.12	28.68
BIP's in sets	75	**	**	**	**	*	*	**	**	**	**	**	**	**	**
(a) Males in sets	25	6.00	9.17	48.37	53.52	2.09	2.27	0.58	1.09	55.88	55.86	17.38	15.27	9.35	14.33
(b) Females in sets	25	6.85	6.94	89.47	58.62	1.49	1.85	0.68	1.05	69.96	59.74	15.40	20.79	9.97	14.72
(c) M × F in sets	25	3.31	17.79	31.93	80.96	1.94	2.54	0.59	1.49	50.98	70.14	26.79	13.57	8.65	17.24
Error	150	1.93	2.29	33.73	13.79	1.90	1.71	0.39	0.56	45.69	69.03	12.20	5.83	9.53	7.98
Sets	19	205.09	209.58	233.85	570.30	4.35	7.40	3.10	5.24	101.59	105.81	133.61	92.57	28.70	29.38
Replications in sets	40	30.54	68.08	122.16	490.18	13.84	8.23	3.37	2.43	76.72	85.97	20.17	35.31	74.12	26.69
BIP's in sets	60	19.21	31.55	74.20	103.30	2.76	3.02	0.87	1.29	69.43	51.75	31.10	33.02	16.65	12.09
(a) Males in sets	20	35.69	43.05	99.59	80.80	1.68	2.96	0.56	1.19	94.45	89.16	29.42	44.35	11.58	14.03
(b) Females in sets	20	14.46	36.95	75.03	163.59	2.09	2.58	0.98	1.83	48.18	32.00	55.17	30.18	11.47	11.06
(c) M × F in sets	20	7.48	16.65	47.99	65.52	4.51	3.53	1.09	0.54	65.66	34.10	23.73	24.55	26.92	11.18
Error	120	5.67	13.45	31.68	24.74	2.28	1.70	0.47	0.68	53.49	56.97	11.18	17.40	13.44	6.61

*, **Significant at P=0.05 and 0.01, respectively; N=Untreated population; T=Treated population.

TABLE 2
Estimates of additive (σ_A^2) and dominance (σ_D^2) components of genetic variance of biparental progenies (MCD II) for seven characters in bread wheat

Characters	Norteno M 67 × S 331				Norteno M 67 × NP 876			
	Normal		Treated		Normal		Treated	
	σ_A^2	σ_D^2	σ_A^2	σ_D^2	σ_A^2	σ_D^2	σ_A^2	σ_D^2
Days to heading	3.14**	1.22	7.38**	0.66	11.72**	2.41	16.90**	1.60
Plant height	24.64**	-13.32	32.54	9.58	26.21**	21.73	37.78**	54.37**
Tillers/plant	-0.76	1.26	0.02	0.58	-1.84	2.97**	-0.50	2.44*
Spike length	0.101*	0.14	0.36	0.21	-0.21	0.82**	0.64**	-0.18
Grains/spike	9.17	1.36	18.16	-28.44	3.76**	16.22	17.65*	-30.48
Test weight	7.42*	-2.98	3.82	7.49*	12.37**	16.73**	8.47**	9.53
Yield/plant	-0.08	-0.13	3.29*	4.08	-10.26	17.97*	0.24	6.09*

disequilibrium with respect to the coupling and repulsion phases, (f) no epistatic interaction.

Bread wheat is a diploidized hexaploid, no multivalents are formed at meiosis and there is regular separation of chromosomes ($n = 3x = 21$) to the opposite poles. The assumption of $p = q = 0.5$ is fulfilled as the population used was an F_2 generation of a cross of homozygous lines. A good stand of usable F_2 plants population avoids any risk of sampling effects and constitutes an assurance that this assumption is fully satisfied. Since the F_2 plants were taken at random from a large population, the assumption of taking random plants is well satisfied i.e., there was no bias in the selection of individual parent plants for developing the experimental material. The fulfilment of the assumption of no multiple allelism is assured by the fact that multiple alleles in an F_2 of homozygous lines can occur only from mutations. The spontaneous mutations are rare. There is, therefore, little possibility of the origin of new alleles. On the other hand, the assumptions of absence of linkage and epistasis are rather unrealistic and these always cause an upward bias in the estimates, particularly σ^2_D (Comstock and Robinson, 1948).

Most of the earlier workers, employing Design II, had recommended the use of eight random plants in a set from the base population, using four of them as males and four as females, producing 16 biparental progenies per set (Matzinger, Wernsman and Cockerham, 1972). Because of the difficulty in producing abundant crossed seeds in wheat and the limited number of heads per plant for crossing in a nested fashion, a set consisted of four plants, $m = n = 2$ (m and n being males and females, respectively) and $m \times n = 2 \times 2 = 4$ biparental progenies per set were produced. No doubt, number of progenies per set was half of that studied in maize and multiflowered self-pollinated crops, viz., tobacco, but the variability was adequately sampled by having large numbers (20 to 25) of sets per cross.

The additive components of genetic variance constituted the major source of genetic variation for most of the component characters among the D II progenies of the four populations. For yield, nonadditive component was substantial and significant. Nonadditive component was also significant for some of the components of yield, particularly, tillers/plant, spike length and test weight. Results of the present study and those reported earlier suggest that in wheat, in general, additive component is predominant for most of the components of yield. The differences in the relative importance of additive and nonadditive components as reported by various workers may be attributed to the diversity of the parents chosen for generating the experimental populations, the genetic design employed, the specific crosses studied and sampling effects. Genetic diversity of the parents was related with the magnitudes of the estimates; diverser the parents, greater was the variability. For almost all the characters σ^2_A and σ^2_D were larger in the cross Norteno M 67 \times NP 876 as compared to those in Norteno M 67 \times S 331. The cultivars Norteno M 67 and S 331 are of Mexican

origin and carry the same dwarfing gene (Norin 10), whereas NP 876 is an Indian tall variety and differs markedly from the Mexican varieties.

The parental lines were treated with EMS (0.4%) to examine the effects of the mutagen on the nature and magnitude of the genetic variance. A considerable increase in the magnitude of additive component of genetic variance was noted in treated D II progenies as compared to the progenies derived from untreated parents for all the characters, except test weight in both the crosses. However, no definite pattern was obtained for the estimates of nonadditive component; it increased for plant height, spike length, test weight and yield/plant in 'Norteno M 67 × S 331' progenies and for plant height in 'Norteno M 67 × NP 876' progenies, whereas for rest of the characters an opposite trend was observed. Studying the effects of mutagen on genetic variances, Burton and Powell (1969) and Micke (1969) reported an increase in the proportion of nonadditive genetic variance for forage yield in pearl millet and for green matter production and glucoside content in *Melilotus albus*, respectively. A substantial increase in the magnitude of additive genetic variance was observed by Gardner (1969) in irradiated population of corn for grain yield. Sharma *et al.* (1976), based on diallel analysis of EMS treated and untreated progenies of spring wheat reported a considerable increase in the magnitude of additive genetic variance in EMS treated population for days to heading, plant height, spike length, test weight and yield/plant.

The increase in the estimates of genetic variance of the EMS treated populations may be due to the breakage of linkages resulting in release of concealed genetic variability. Further, the mutagens must have caused micro-mutations (polygenic) and thus increased genetic variance. Relatively larger increase in σ^2_A as compared to that in σ^2_D may be ascribed to creation of new variability. Any change (mutation) of the modifier complexes would alter the expression of neutral alleles and the homeologous loci which have been silenced during the course of evolution of the allohexaploid bread wheat (Brewer, Sing and Sears, 1969) and is thus likely to increase the genetic variance, particularly additive variance. Inter-allelic interactions resulting in dominant variation are an outcome of the evolutionary processes and thus any change in the genetic milieu is likely to disrupt the intra-allelic interaction. However, the epistatic effects (confounded with σ^2_D in the present case) are expected to show random variation in the mutagen treated populations and the traits which are under greater influence of intra-allelic interactions are expected to exhibit more fluctuation among the treated progenies and such a trend was observed in the present study.

In self-pollinated crops, pedigree method of breeding is the most commonly used method for handling hybrid populations. Under this approach, only part of the potential genetic variability is carried through generations. For polygenic characters, in order to recover all possible segregants and recombinants, large size of segregating populations are to be grown. If the two parents involved in hybridization differed for 'n' number of allelic pairs, kinds of genotype possible

in $F_2=3^n$ and the smallest perfect population in F_2 to recover all the possible genotypes $=4^n$. This calculation assumes independent assortment of genes. Linkage (repulsion phase) would further complicate the picture and still larger populations would be required for recovering every possible genotype. Though it is not always possible to have precise information about the number of genes segregating and effects of selection, the conclusion is inescapable that the number of possible combinations from most hybrids is so large that only a small proportion can be dealt with at any one time. Further, in the subsequent generations due to increase of homozygosity and selection among and within lines, variability decreases rapidly. A particular genotype missed in F_2 generation has very little chance to be picked up in later generations. Individual plants selected in F_2 generations set the limit of ultimate performance (barring environmental interactions) of a line derived from that particular plant. The effectiveness of selection in F_2 generation is likely to be adversely affected by undesirable genetic linkages, polygenic and complex inheritance of quantitative traits and genic and genotype \times environment interactions.

The alternative to the standard breeding method is population improvement method. The basic difference between the two approaches lies in the fact that in the latter generations, the population itself is improved generation by generation, thus, steadily increasing the chances of finding individuals with excellent combinations of characters. Intercrossing gives maximum opportunity for the re-arrangement of genes in the linkage groups, and provides a wide range of genetic background against which the gene arrangements may be expressed. Selection followed by intermating would not only raise the mean of the population but would also maintain variability for selection to be effective till later generations. It has been reported that intermating in F_2 , even of random plants, results in accumulation of favourable alleles (Gill *et al.*, 1973 and Singh and Dwivedi, 1979).

Reviewing the breeding methodology in autogamous crops Joshi and Dhawan (1966) emphasised that segregating populations should be handled in such a way as to bring about the accumulation of favourable gene constellations through intermating between superior individuals or lines. In wheat, additive genetic variance has been found to be predominant for most of the yield characters as revealed in the present study, thus intermating of the segregants is bound to mop up the additive effects and raise the mean. Populations developed from intercrossing of selected plants in segregating generations are expected to have still higher means. It has, therefore, been suggested that mass selection with concurrent random or selective mating in early segregating generations could be a useful breeding strategy in wheat and other self pollinated crops.

SUMMARY

Biparental progenies (North Carolina Design II) derived from F_2 s produced separately from normal parents and the same parents treated with

EMS (0.4%) were analysed for estimating components of genetic variances for yield and certain yield components in bread wheat. Additive genetic variance constituted the major source of variation for all the component characters except tillers/plant which along with yield showed greater importance of dominance component. Diversity of parents influenced the estimates; genetic variances were higher in the cross which involve diverse parents. Mutagen treatment increased the additive genetic variance for all the characters except test weight whereas nonadditive genetic variance varied in a random fashion. In self pollinated cross, such as wheat, it is encouraging that additive genetic variance were predominant and thus could be exploited most effectively by resorting to population improvement approach.

REFERENCES

- Brewer, G. J., C. F. Sing and E. R. Sears., (1969). Studies of isozyme patterns in Nullisomic-Tetrasomic combinations of hexaploid wheat. *Proc. nat. Acad. Sci.* **64**: 1224-1229.
- Burton, G. W. and J. P. Powell. (1969). Effect of recurrent thermal neutron and EMS seed treatments on general and specific combining ability for pearl millet for forage yield. *Proc. Symp. on Induced Mutations in Plants*, 1969, pp. 433-443.
- Comstock, R. E. and H. F. Robinson., (1952). Estimation of average dominance of genes. Heterosis (ed. J. W. Gowen), Iowa State College Press, Ames., IOWA., pp. 494-516.
- Gardner, C. O. (1969). Genetic variation in irradiated and control populations of corn after ten cycles of mass selection for high grain yield. *Proc. Symp. Induced Mutations in Plants IAEA, Vienna*. PP. 469-76
- Gill, K. S., S. S. Bains, Gursharan Singh and K. S. Bains. (1973). Partial diallel test crossing for yield and its components in *Triticum aestivum*. *Proc. IV int. Wheat Genet. Symp. Missouri, Columbia* (1973), pp. 29-33.
- Joshi, A. B. and N. L. Dhawan. (1966). Genetic improvement in yield with special reference to self fertilizing crop. *Indian J. Genet.* **26A**: 101-113.
- Matzinger, D. F., E. A. Wernsman and C. C. Cockerham. (1972). Recurrent family selection and correlated response in *N. tabacum* I. Dixie Bright 244 × Cocker 139. *Crop Sci.*, **12**: 40-43.
- Micke, A. (1969). Improvement of low yielding sweet clover mutants by heterosis breeding. *Proc. Symp. on Induced Mutations in Plants* (1969), pp. 541-550.
- Sharma, G. S., R. B. Singh, B. D. Singh and R. M. Singh. (1976). EMS induced polygenic mutation for yield and yield components in spring bread wheat (*Triticum aestivum* L.). *Cereal Research Communication*, **4**(3): 321-333.
- Singh, R. B. and S. L. Dwivedi. (1979). Effects of biparental mating in a naturally self-fertilizing species, *Triticum aestivum* em. Thill. *Proc. V int. Wheat Genet. Symp.* (1978), New Delhi.