

ANALYSIS OF GENETIC PARAMETERS IN A SELF-POLLINATED CROP BREAD WHEAT

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SUMMARY

Biparental progenies produced following North Carolina Mating Design III in F_2 population of two distinct bread wheat crosses (Sonalika \times Norteno and Pusa Lerma \times Shera) and the corresponding F_3 s were analysed to characterise nature and magnitude of genetic variances governing yields traits. Design III analysis revealed highly significant estimates of additive components of genetic variance for all the characters under study whereas dominance components were significant only for two characters in one of the two crosses. Design III progenies had higher means than F_2 selfs (F_3). On the other hand, additive genetic variance (σ^2A) estimated from variance component from D III analysis was considerably higher than that estimated from the analysis of F_2 selfed progenies. Since, the estimates of additive variance were predominant, intermating of F_2 segregants would result in accumulation of favourable genes, resulting in higher means.

Population breeding, intermating in segregating generations coupled with selection, is gaining importance in self-pollinated crops (Matzinger and Wernsman, 1968; Reden and Jensen, 1974; Singh and Dwivedi, 1968). North Carolina Mating Designs (Comstock and Robinson, 1948, 1952) have commonly been used in characterizing genetic parameters in improvement of crosspollinated crops. However, with extra efforts these designs could also be used in self-pollinated crops. The present study aims to compare the useful and efficiency of North Carolina Design III progenies and the corresponding selfs with regard to the estimates of different components of genetic variance and progeny means for grain yield and its attributes.

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MATERIALS AND METHODS

Two wheat crosses, Sonalika \times Norteno (S \times N) and Pusa Lerma \times Shera (PL \times Sh) were selected for the study. Forty random F_2 plants of each cross were backcrossed, using as males, to each of the two parental lines (females) of the cross, to produce forty pairs of backcross progenies (N.C. Design III). Simultaneously, all the 40 F_2 plants used for backcrossing were selfed to produce F_3 progenies. The forty pairs of F_2 backcross progenies and the corresponding F_2 selfed progenies of each cross were grown in a compact family block design with two replications. The F_2 backcrosses and the F_3 progenies constituted two family blocks. The 80 F_2 backcross progenies and the 40 F_3 progenies were randomized within each family block. The plot size was a simple row of 15 plants, which were spaced 15 cm apart within a row and 23 cm between rows. Observations were recorded on ten competitive random plants per plot for six characters. The statistical analysis of 80 F_2 backcross progenies was done following D III of Comstock and Robinson (1948, 1952) and of F_3 progenies following the randomized complete block design, using plot means.

RESULTS

Analysis of variance

Mean squares from ANOVA of F_2 backcross and selfed progenies of the two crosses for six characters are presented in Table 1. The mean squares due to females were significant for grains per spike, grain yield of 3 spikes and test weight in the cross Sonalika \times Norteno (S \times N) and for plant height, grains/spike and test weight in the cross Pusa Lerma \times Shera (PL \times Sh). The variances due to males were significant for all the characters in the cross S \times N and four characters, viz, plant height, spike length, grain yield of 3 spikes and test weight in the cross PL \times Sh. Variances due to males \times females were significant only for two characters, plant height and grains/spike in the cross S \times N. The F_3 progenies differed significantly for all the characters in both the crosses except for yield/plant in the cross S \times N.

Means of D III and F_3 progenies

The over-all means of the F_2 backcross progenies and the F_2 selfed progenies for six characters are given in Table 2. The means of D III were higher than those of F_3 progenies for grain yield/plant and grain yield/3 spikes in both the crosses and for spike length and grain number per spike in the cross Sonalika \times Norteno.

TABLE 1

Analysis of variance of F_2 backcross progenies (DIII) and the corresponding F_3 families for six characters in wheat

Source	D.F.	Mean squares					
		Plant height	Spike length	Grains/spike	Grain yield of 3 spike	Test weight	Grain yield/plant
<i>Cross : Sonalika × Norteno (S × N)</i>							
<i>N.C. Design II</i>							
Replications	1	78.80	7.14**	44.22	4.00**	201.54**	89.74*
Females (Parent lines)	1	20.10	1.22	1465.72**	5.72**	200.21**	41.14
Males (F_2 's)	39	332.04**	1.49**	37.39**	1.49**	62.48**	41.86**
Males × Females	39	63.41*	0.95	32.97*	0.90	19.59	24.57
Error	79	32.59	0.59	17.16	0.48	12.46	19.50
<i>F₃ progenies</i>							
Replications	1	826.89	3.52	6.27	0.21	7.50	13.67
Progenies	39	269.16**	1.09**	41.13*	1.07*	47.58**	15.57
Error	39	63.84	0.34	21.64	0.53	11.01	14.62
<i>Cross : Pusa Lerma × Shera (PL × Sh)</i>							
<i>N.C. Design III</i>							
Replications	1	353.26*	14.61**	185.74**	18.18**	116.10*	1398.77**
Females (Parent lines)	1	551.00**	1.00	185.28	0.67	90.65**	76.83
Males (F_2 's)	39	314.45	1.41**	38.51	1.52**	41.63**	43.04
Males × Females	39	43.54	0.36	27.57	0.66	10.32	28.05
Error		55.95	0.57	20.36	0.39	7.96	26.59
<i>F₃ progenies</i>							
Replications	1	267.37*	5.62**	46.21	0.01	0.05	20.72
Progenies	39	272.93**	1.80**	54.17*	1.14	44.34**	20.59
Error	39	66.08	0.39	31.55	0.43	11.49	11.67

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

Components of genetic variance

The estimates of σ^2_m , σ^2_{mf} from D III and σ^2_G (F_3) are given in Table 2. The estimates of additive (σ^2_A) and non-additive (σ^2_D) components of genetic variance from D III and a joint estimate of $\sigma^2_A + \frac{1}{4} \sigma^2_D$ from F_3 progenies are given in Table 3. The estimates of σ^2_A were significant for six characters in the cross S×N and for four characters, plant height, spike length, grain yield of 3 spikes and test weight in the cross PL×Sh. The estimates of σ^2_{mf} were significant only for plant height and grains/spike, in the cross S×N. The average degrees of dominance ranged from zero to 0.45 (for grains/spike) in the cross PL×Sh and from 0.23 (plant height) to 0.63 (grains per spike) in the cross S×N.

The estimates of σ^2_G (F_3) were significant for all the characters in both the crosses except for yield/plant in the cross S×N.

DISCUSSION

The estimates of genetic components of variance using D III revealed the predominance of additive genetic variance and non-significance of non-additive genetic variance for all the characters in both the crosses, except plant height and spike length in one cross only. The average degree of dominance in these cases, however, was partial. Thus breeding procedures designed to exploit additive genetic variance were most effective for the improvement of several plant characters. Among the two crosses studied, the cross Sonalika × Norteno was relatively better for both higher mean performance and the magnitude of genetic variability among the populations. Simple recurrent selection would be most effective in not only accumulating favourable genes for increased yield and other characters but also in the breakage of undesirable linkage and help in the exploitation of fixable epistatic effects, if present.

Assuming simple genetic model, gene effect (g) = mean (μ) + additive effect (d_a) + dominance effect (h_a) and ignoring linkages and epistatic effects, following are the expectations for means and components of genetic variance from the analysis of F_2 backcross progenies and the corresponding F_3 progenies.

Mean		Genetic variance components		
D III	N_3		D III	F_3
		σ^2_m	σ^2_{mf}	σ^2_G
Σha	$\frac{1}{4} \Sigma ha$	$\frac{1}{4} \sigma^2_A$	σ^2_D	$\sigma^2_A + \frac{1}{4} \sigma^2_D$

TABLE 2
Means and genetic variance components for six characters estimated from F_2 backcross progenies
and F_3 progenies of two wheat crosses

	Mean				Genetic variance components					
	Cross $S \times N$		Cross $PL \times Sh$		Cross $S \times N$			Cross $PL \times Sh$		
	$DIII$	F_3	$DIII$	F_3	σ^2_m	σ^2_{mf}	$\sigma^2_{gF_3}$	σ^2_m	σ^2_{mf}	$\sigma^2_{gF_3}$
Plant height (cm)	102.88	101.70	99.27	101.12	74.860	15.41*	102.66	64.625	-6.20	153.43**
Spike length (cm)	12.09*	11.73	10.66	10.34	0.225	0.18	0.38**	0.210	-0.10	0.71**
Grains/spike	52.66*	50.35	52.75	52.34	5.058	7.90*	9.72*	4.539	3.60	11.31*
Grain yield/3 spikes (gm)	6.39*	6.03	5.53*	5.21	0.252	0.21	0.27*	0.282	0.14	0.36**
Test weight (gm)	39.99	40.17	34.28	34.03	12.504	3.56	18.28**	8.418	1.18	16.42**
Grain yield/plant (gm)	20.67**	17.87	19.20**	16.77	5.590	2.53	6.47	4.112	0.73	4.46*

From Design III $\sigma^2_m = \text{Males MS} - \text{Error MS}/2r$, $\sigma^2_{mf} = \text{Male} \times \text{Female MS} - \text{Error MS}/r$ —From RBD : $\sigma^2_g = \text{Progenies} - \text{Error MS}/r$,
where r = number of replications.

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

TABLE 3

Estimates of additive (σ^2_A) and non-additive (σ^2_D) components of genetic variance and average degree of dominance (\bar{a}) in wheat.

Character	Cross <i>S</i> × <i>N</i>				Cross <i>PL</i> × <i>Sh</i>			
	<i>DIII</i>			<i>F</i> ₃	<i>DIII</i>			<i>F</i> ₃
	σ^2_A	σ^2_D	\bar{a}	$\sigma^2_A + \frac{1}{4}\sigma^2_D$	σ^2_A	σ^2_D	\bar{a}	$\sigma^2_A + \frac{1}{4}\sigma^2_D$
Plant height	299.45**	15.41*	0.23	102.66**	258.50**	-6.20	0.00	153.43**
Spike length	0.90**	0.18*	0.45	0.38**	0.84**	-0.10	0.00	0.71**
Grains/spike	20.23**	7.90*	0.63	9.72*	18.15	3.60	0.45	11.31*
Grain yield/ ₉ spikes	1.01**	0.26	0.46	0.27*	1.13**	0.14	0.35	0.36**
Test weight	50.02**	3.56	0.27	18.28**	33.67**	1.18	0.19	16.42*
Grain yield/plant	22.36**	2.53	0.34	6.47	16.45	0.73	0.21	4.46*

In absence of dominance, average of all D III crosses and average of all F_3 progenies will be equal. D III mean will be higher or lower than that of F_3 's, if the estimate of Σha is (+) or (-). In the present study, there was evidence of inbreeding depression in F_3 performance for grain yield/plant and grain yields/3 spikes in both the crosses, indicating the operation of dominant genes in the expression of these characters. However, the dominance variance component (σ^2_D) for both the characters was not significant. Thus dominance effects, as observed from the analysis of means, do not appear to be very strong except plant height and grains/spike in the cross $S \times N$.

As regards genetic variance, $\sigma^2_G (F_3)$ should be equal to $4 \sigma^2_m$ in case dominance is absent and less than $4\sigma^2_m$ in presence of dominance.

The findings of the present study are not in complete agreement with this theoretical expectation. The estimate of σ^2_A was considerably higher than that of $\sigma^2_A + \frac{1}{4} \sigma^2_D$ estimated from F_3 progenies for all the characters in both the crosses except spike length in the cross $PL \times Sh$. It, therefore, appears that the assumptions underlying these models do not hold for the data under consideration. Environmental variances, and sampling errors would also cause bias in the results. It will, therefore, be of interest to extend this study to include several populations with large size.

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