Indian J. Genet., **55** (3): 266–272 (1995)

COMPARISON OF THE OBSERVED AND PREDICTED FREQUENCIES OF TRANSGRESSIVE SEGREGATES FOR YIELD AND RELATED TRAITS IN TWO BREADWHEAT POPULATIONS

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(Received: August 16, 1990; accepted: June 11, 1995)

ABSTRACT

The genetic parameters estimated in seven basic sets of generation mean analysis and F_2 triple test-cross progenies were used to predict the frequency of recombinant inbred lines derivable from F_2 breadwheat populations of Harrier x S 308 and Redpoll x HD 2204 crosses grown over two environments. The validity of predictions was tested by comparing the expected frequency with the observed frequency of transgressive segregates scored on family means of 183 F_6 lines. These lines were randomly derived through SSD in each of the F_2 populations. In majority of cases, a close goodness of fit was achieved between the predicted and observed frequency of recombinant inbred lines. Recombinant inbred lines were obtained exceeding the parental limits for plant height, peduncle length, 100-grain weight and days to heading. The skewed distribution observed for predicted frequency of recombinant inbreds was due to the presence of additive x additive type epistatic interaction. The results of the experiments clearly demonstrated that genetic analysis of a character in early generation of a cross of breadwheat can provide the necessary information to predict accurately the likely outcome of inbreeding in F_2. The breeding strategies for recovery of recombinant inbred lines having desired level of performance has been suggested.

Key words: Breadwheat, transgressive segregation, cross performance, recombinant lines.

In self-pollinated crops like wheat, the ultimate goal of a plant breeder is to have high yielding pure lines that usually arise as recombinant inbred lines. A large F_2 population is required in order to have a higher probability of recovering one or more "desirable" pure lines from a cross and the breeder is faced with examining a large number of single plants in the F_2 generation, the majority will be discarded [1, 2]. Sometimes a cross is rejected later in the advanced generations. Therefore, it is useful to have early generation assessment of cross which would eventually produce the largest number of "desirable" recombinant inbred lines in order to save time and resources. Based on the estimation of gene effects and genetic components of variance, it is possible to predict the range of inbred lines which can be derived from a cross [3]. The present study has been planned to predict the range of inbred lines and test the predictions by evaluating 183 F_6 inbred lines derived randomly from two breadwheat crosses.

MATERIALS AND METHODS

From two divergent wheat crosses (Harrier x S 308 and Redpoll x HD 2204), a random sample of 183 F_6 inbred lines derived through single seed descent (SSD) techniques from each F_2 population was grown. The material was advanced by raising the off-season crop at the IARI Regional Station, Wellington (Nilgiris). For estimation of gene effects and genetic components of variance, back-crossed and selfed generations (both parents, F_1, F_2, F_3, BC_1, BC_2) and triple test-cross progenies (TTC) were developed in each cross. For TTC progenies, 30 F_2 plants were randomly selected and back-crossed to the parents and the F_1 resulting into 90 TTC progenies in each cross.

Each experimental material was sown in adjacent blocks in completely randomized block design in two environments simulated by two dates of sowing (November 24, 1984 and December 27, 1984). Each of the TTC progenies were grown in a single-row plot with two repeats. For generation mean analysis, single-row plots of the parents, F_1, BC_1 and BC_2 and 40 F_3 plant progenies each, and 15-row plot of F_2 generation were grown in three repeats. To evaluate and compare with the predicted frequency of transgressive segregates, a set of 183 F_6 randomly derived recombinant inbred lines in each of the two populations were raised in a single-row plot along with their parents and F_1 generation with two repeats. Each row was spaced at 30 cm and accommodated 20 seeds at 7.5 cm spacing. Ten competitive plants were taken randomly from each plot to record observations. Data were recorded on the days to heading, plant height, tillers per plant, spike length, peduncle length, spikelets per spike, grains per spike, 100-grain weight, and grain yield per plant.

Based on estimates of gene effects [4] and components of variance [5], the potential of a cross of descending the superior inbred lines was predicted according to the method described by Jinks and Pooni [3] and Jinks [6]. The accuracy of predictions were assessed by comparing the expected frequency of lines with the observed frequency in populations of F_6 randomly derived inbred lines [7].

RESULTS AND DISCUSSION

The probability of obtaining inbreds that fall outside the parental range or exceeding the F_1 is predicted using the estimates of parameters d (additive effect), i (additive x additive epistatic effect), h (dominance effect), and D′ (additive variance and also additive x additive variance, if present). These estimates were obtained from triple test-cross analysis combined with generation mean analysis [8]. The additive effect was significant for all the characters except tillers per plant, grain yield per plant and grains per spike, whereas dominance effect was significant for peduncle length, spikelets per spike and days to heading in the cross Harrier x S 308 in the 24 November sowing (Table 1). The estimates of additive variance made possible to predict transgressive segregation over the parents for plant height, peduncle length, spikelets per spike, 100-grain weight, and days to heading in the first sowing and for plant height and days to heading in late sowing. On the contrary, the prediction in F_1 was possible only for peduncle length, spikelets per spike and days to heading in the early sowing. Although, both additive and dominance effects were significant for all the characters except grains per spike in late sowing, prediction was possible only for plant height and days to heading as additive variance was significant for only these two characters.

Table 1. Estimates of genetic parameters involved in calculating the frequency of transgressive segregates for nine characters in the breadwheat cross Harrier x S 308

Parameter	Plant height	Spike length	Peduncle length	Spikelets per spike	Tillers per plant	Grain yield per plant	100-grain weight	Days to heading	Grains per spike
				I Sowing : 24 November					
$[\hat{d}]$	- 11.29	- 0.81	- 4.14	1.51	NS	NS	- 0.76	4.05	NS
$[\hat{h}]$	NS	NS	- 15.23	3.68	NS	NS	NS	- 7.52	NS
$[\hat{i}]$	- 12.70	NS	- 4.97	NS	NS	NS	0.28	- 2.55	NS
$\hat{D}$	484.75	NS	71.20	1.54	NS	NS	0.11	0.98	63.22
				II Sowing : 27 December					
$[\hat{d}]$	- 11.83	- 0.76	- 4.71	0.90	- 1.08	- 4.06	- 0.72	5.17	2.56
$[\hat{h}]$	32.67	- 1.67	- 5.68	2.95	8.11	16.07	- 0.54	- 16.66	NS
$[\hat{i}]$	- 10.57	- 0.58	- 3.11	NS	1.56	3.71	NS	- 2.28	NS
$\hat{D}$	159.70	NS	NS	NS	NS	NS	NS	4.89	NS

NS—nonsignificant estimates of genetic parameters.

For the cross Redpoll x HD 2204, the significant gene effects and additive variance in both the environments are depicted in Table 2. In this cross, the prediction over parents was possible for plant height, peduncle length, 100-grain weight and days to heading in both the environments (i.e. sowing dates) and for spike length and grains per spike in early and late sowings, respectively. The prediction of recombinant inbred lines over the F_1 was possible for peduncle length, 100-grain weight and days to heading in both sowing dates, and for

Table 2. Estimates of genetic parameters involved in calculating the frequency of transgressive segregates for nine characters in the breadwheat cross Redpoll x HD 2204

Parameter	Plant height	Spike length	Peduncle length	Spikelets per spike	Tillers per plant	Grain yield per plant	100-grain weight	Days to heading	Grains per spike
I Sowing : 24 November									
$[\hat{d}]$	15.84	0.42	6.49	NS	NS	NS	0.36	2.16	- 2.19
$[\hat{h}]$	- 23.68	NS	- 10.77	NS	NS	7.53	- 0.41	- 3.64	15.04
$[\hat{i}]$	- 14.27	0.46	- 5.22	- 0.59	NS	NS	- 0.35	1.72	6.35
$\hat{D}$	118.14	0.32	17.10	NS	NS	NS	0.17	6.37	NS
II Sowing : 27 December									
$[\hat{d}]$	11.79	NS	6.59	NS	NS	NS	0.27	1.68	- 5.77
$[\hat{h}]$	NS	NS	- 19.49	NS	3.46	NS	- 1.11	3.19	NS
$[\hat{i}]$	- 7.35	NS	- 4.08	NS	NS	NS	- 0.27	- 2.25	NS
$\hat{D}$	164.10	1.52	29.53	1.16	NS	NS	0.20	3.24	62.38

NS—nonsignificant estimates of genetic parameters.

plant height in early sowing. This discrepancy in prediction may be due to genotype x environment interaction.

A perusal of Tables 3 and 4 indicates a good agreement between the predicted and observed frequencies of transgressive segregates for all the characters where prediction was possible except for days to heading and plant height in the cross Redpoll x HD 2204 in early sowing. These crosses had been studied for their detailed genetic architecture [8]. In this context, it is worth mention that significant difference between the observed and expected number of transgressive segregates occurred for those characters where none of the genetic models could explain the genetic variance, and the inheritance of the characters was proved to be more complex either due to operation of linked digenic epistatic genes or higher order interactions [8]. Therefore, the discrepancy in the predicted frequency of recombinant inbred lines may be a result of genotype x environment interaction or linked repulsion linkage.

It was further seen (Tables 3, 4) that symmetrical distribution was observed for predicted frequency of recombinant inbred lines for spikelets per spike in the cross Harrier x S 308 in November sowing and for 100-grain weight and grains per spike in the cross Redpoll x HD 2204 in December sowing. However, for majority of characters, the distribution was skewed. The skewness might have resulted due to the presence of additive x additive type epistasis that was accommodated in the prediction equation wherever required. These

Table 3. Goodness of fit (χ^2) of expected (E) and observed (O) numbers falling into three phenotypic classes from a sample of 183 in F_6 generation randomly derived inbred lines of the breadwheat cross Harrier x S 308 grown in two environments

Phenotypic class of transgressants		Plant height	Spike length	Peduncle length	Spikelets per spike	Tillers per plant	Grain yield per plant (g)	100-grain weight (g)	Days to heading	Grains per spike
					I sowing : 24 November					
$> P_1$	O	67	—	85	17	—	—	3	18	—
	E	87	—	84	20	—	—	0	12	—
	χ^2	2.60	—	0.01	0.24	—	—	3.00	1.20	—
$< P_2$	O	19	—	21	25	—	—	15	1	—
	E	25	—	26	20	—	—	14	0	—
	χ^2	0.82	—	0.53	0.56	—	—	0.14	1.00	—
$> F_1$	O	—	—	—	0	—	—	—	—	—
	E	—	—	—	0	—	—	—	—	—
	χ^2	—	—	—	0.00	—	—	—	—	—
					II sowing : 27 December					
$> P_1$	O	75	—	—	—	—	—	—	14	—
	E	84	—	—	—	—	—	—	17	—
	χ^2	0.51	—	—	—	—	—	—	0.29	—
$< P_2$	O	14	—	—	—	—	—	—	1	—
	E	7	—	—	—	—	—	—	0	—
	χ^2	2.33	—	—	—	—	—	—	1.00	—
$> F_1$	O	—	—	—	—	—	—	—	0	—
	E	—	—	—	—	—	—	—	0	—
	χ^2	—	—	—	—	—	—	—	0.00	—

P_1 and P_2 are the higher and lower scoring parents, respectively.

— represents the cases where due to nonsignificant genetic parameters predictions not done.

0 indicates very low predicted frequencies.

results revealed that for majority of characters, namely, plant height, peduncle length, 100-grain weight, and days to heading, there were fair chances of selecting recombinant inbred lines surpassing the limits of the parents from a small number of inbred lines derivable from these crosses. This implied high degree of dispersion of increasing number of alleles for these characters. High frequency of recombinant inbred lines surpassing the parental limits has been reported in wheat [7] and barley [9]. The low frequency of recombinant inbred lines exceeding the F_1 value for days to heading in the cross Harrier x S 308 and for 100-grain weight in Redpoll x HD 2204; and those exceeding the parental limits for spikelets per spike, 100-grain weight and days to heading in the cross Harrier x S 308 implied that a very large number of inbred lines should be raised so as to select superior recombinant inbred lines for these characters. Incidentally, the prediction of recombinant

Table 4. Goodness of fit (χ^2) of expected (E) and observed (O) numbers falling into three phenotypic classes from a sample of 183 F_6 randomly derived inbred lines of breadwheat cross Redpoll x HD 2204 grown in two environments

Phenotypic class of transgressants		Plant height	Spike length	Peduncle length	Spike-lets per spike	Tillers per plant	Grain yield per plant	100-grain weight	Days to heading	Grains per spike
				I sowing : 24 November						
$> P_1$	O	1	15	62	—	—	—	81	10	—
	E	1	11	69	—	—	—	90	11	—
	χ^2	0.00	0.62	0.37	—	—	—	0.47	0.05	—
$< P_2$	O	70	71	3	—	—	—	5	35	—
	E	81	86	0	—	—	—	8	79	—
	χ^2	0.80	1.43	3.00	—	—	—	0.69	16.98**	—
$> F_1$	O	51	—	—	—	—	—	—	22	—
	E	3	—	—	—	—	—	—	14	—
	χ^2	42.67**	—	—	—	—	—	—	1.78	—
				II sowing : 27 December						
$> P_1$	O	10	—	55	—	—	—	29	63	59
	E	13	—	59	—	—	—	21	69	43
	χ^2	0.39	—	0.14	—	—	—	1.28	0.27	2.51
$< P_2$	O	56	—	4	—	—	—	24	6	30
	E	67	—	5	—	—	—	21	3	43
	χ^2	0.98	—	0.11	—	—	—	0.20	1.00	2.32
$> F_1$	O	—	—	—	—	—	—	2	—	—
	E	—	—	—	—	—	—	1	—	—
	χ^2	—	—	—	—	—	—	0.33	—	—

P_1 and P_2 are the higher and lower scoring parents, respectively.

— represents the cases where due to nonsignificant genetic parameters predictions not done.

0 indicates very low predicted frequencies.

**Significant at 1% level.

inbred lines for yield and some of its components could not be performed due to nonsignificant genetic parameters. However, the results of this investigation clearly established the possibility of predicting the performance of recombinant inbred lines based on genetic parameters estimated in early generations for several characters. This could considerably reduce the load on resources for continuation of low yielding lines up to later generations [10] and reduce the possibility of discarding lines with good yield potential in early generations [11]. Based on this technique, a plant breeder could practice judicious selection among the crosses and thus concentrate the efforts and resources on the more desirable crosses.

ACKNOWLEDGEMENT

The first author thanks the Indian Council of Agricultural Research, New Delhi, for the award of a Senior Research Fellowship.

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