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ESTIMATION OF GENETIC PARAMETERS THROUGH GENERATION MEAN ANALYSIS IN BREADWHEAT

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ABSTRACT

Estimates of gene effects based on analysis of generation means were obtained for four yield traits, namely, grains/spike, grain weight of 3 spikes, yield/plant and 100-grain weight in several crosses of breadwheat (*Triticum aestivum* L. em Thell). The contribution of additive gene effects (d) were important in the inheritance of number of grains/spike and 100-grain weight, whereas the dominance gene effects (h) contributed significantly for grain weight of 3 spikes and yield/plant. Among the epistatic effects, additive x additive interactions was of considerable importance for all the characters.

Key words: Breadwheat, generation mean analysis, components of variance.

In self-pollinated crops the genetic parameters have essentially been obtained employing diallel analysis (graphic and combining ability) and generation mean analysis. Generation mean analysis, a first degree statistics, is a simple but useful technique for characterising gene effects for a polygenic character [1–3]. The greatest merit of generation mean analysis lies in the estimate of epistatic gene effects, viz., additive x additive (i), additive x dominance (j) and dominance x dominance (l), which the most commonly used design, i.e. the diallel analysis, fails to detect. If this design is used in conjunction with another design, a greater reliance could be put on genetic estimates thus obtained. The inheritance of yield and three important yield traits was therefore, studied using generation mean analysis and diallel mating design involving eight elite pure lines of wheat.

MATERIALS AND METHODS

Eight diverse cultivars of wheat, viz. Kalyan Sona, Sonalika, Moti, Janak, Arjun, HD 2021, Raj 821 and S 331, were crossed in a diallel fashion excluding the reciprocals. A trial

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consisting of 28 F_1s, 28 F_2s, 28 BC_1s and 28 BC_2s and the eight parents were grown in compact family block design with three replications at the Banaras Hindu University Research Farm. Each plot of the parents and F_1s had a single row, while those of F_2s and back-crosses had ten and two rows, respectively. The spacing was 30 x 10 cm. Data were recorded on 10 plants per plot of the parents and F_1s, 20 plants from each BC_1 and BC_2, and 100 plants from each F_2 in each replication for four quantitative characters: grains/spike, grain weight of 3 spikes, yield/plant, and 100-grain weight.

Mather's scaling test was used to identify the interacting crosses [4]. The gene effects in the interacting crosses were estimated using the six-parameter model of Hayman [1]. The graphic analysis of the F_1 diallel progenies was also carried out in accordance with [5, 6] and component analysis using the models of [7, 8].

RESULTS AND DISCUSSION

GRAINS PER SPIKE

The scaling test indicated 18 out of 28 crosses to be interacting. Among these significant estimates of epistasis were obtained in 14 crosses (Table 1). One cross showed complementary epistasis, while the remaining 17 crosses indicated duplicate type of interaction. The estimates of $\hat{d}$ were significant in most of the crosses, while $\hat{i}$ was the most important type of epistasis. Clearly, the contribution of additive gene effects to the mean was much higher as compared to those of dominance and epistatic gene effects. In general, crosses involving var. Kalyan Sona showed a higher contribution of additive gene effects to the mean.

Graphical analysis indicated partial dominance, nonallelic interactions (significant deviation of b from unity), and asymmetrical distribution of genes among the parents. In the component analysis, $\hat{D}$ was significant, while $\hat{H}_1$ and $\hat{H}_2$ and other estimates were nonsignificant (Table 2).

GRAIN WEIGHT OF THREE SPIKES

Scaling test indicated epistasis in 14 crosses, of which 6 crosses exhibited significant estimates of epistatic gene effects. Five of the interacting crosses exhibited complementary type of epistasis, while the remaining nine crosses displayed duplicate epistasis. The contributions of $\hat{h}$ and $\hat{i}$ to the mean effects, $\hat{m}$, were more pronounced than those of other gene effects. All the significant estimates of $\hat{j}$ and $\hat{i}$ were negative, whereas those of $\hat{i}$ were positive. Further, all the significant estimates of $\hat{h}$ were positive.

Table 1. Estimates of gene effects based on analysis of generation means for four characters in breadwheat

Cross			$\hat{m}$	$\hat{d}$	$\hat{h}$	$\hat{j}$	$\hat{i}$	$\hat{l}$	Type of epistasis
			Number of grains/spike						
Kalyan Sona	X	Sonalika	54.5	19.2**	20.1*	20.7*	19.3*	–23.7	D
	X	Moti	49.9	10.7**	16.8**	17.9**	–4.4	–14.4	D
	X	Janak	54.2	8.8**	11.2	13.1	3.0	0.8	D
	X	Arjun	58.3	8.9**	9.3	12.3	3.0	–18.2	D
	X	HD 2021	61.8	5.4**	2.7	–9.1	–5.1	24.9	D
	X	Raj 821	52.6	15.0**	24.5**	28.4**	9.7	–40.4**	D
	X	S 331	55.4	10.4**	22.7**	19.4**	4.6	–10.7	D
Sonalika	X	Moti	41.9	2.4**	22.0**	23.7**	–2.1	–33.2**	D
	X	Janak	48.7	–8.2**	4.3	6.0	–12.0**	–2.7	D
	X	HD 2021	51.2	–9.3**	–14.0**	–13.7**	–15.6**	27.2**	D
	X	Raj 821	46.7	–2.8**	–9.8**	–5.7	–6.8*	12.8*	D
Moti	X	HD 2021	49.5	–4.3**	9.4*	7.7*	1.3	–18.3**	D
	X	Raj 821	43.6	–5.8**	5.2	4.9	–6.0	–0.6	D
Janak	X	Arjun	52.1	–6.0**	–2.6	–0.5	–12.2**	4.8	D
Arjun	X	S 331	53.8	–1.7	–16.1**	–14.8**	–4.7*	25.2**	D
HD 2021	X	Raj 821	50.2	2.1	–4.5	–7.2	–0.2	21.6*	D
	X	S 331	56.6	–5.6*	–8.4	–11.0	–11.4*	11.7	D
Raj 821	X	S 331	51.7	–8.0**	–3.9	–2.3	–11.8**	–3.2	C
			Grain weight of 3 spikes						
Kalyan Sona	X	Moti	5.0	0.6	2.8**	2.1**	–0.4	–2.4	D
	X	Janak	5.9	–0.1	2.7	1.7	0.6	0.0	C
	X	HD 2021	6.1	–0.8**	0.8	0.3	–1.1*	2.9	C
	X	Raj 821	5.7	–0.1	5.1**	4.7**	0.5	–6.2**	D
	X	S 331	4.9	0.6**	3.8	2.7	–0.0	–1.9	D
Sonalika	X	Moti	5.0	0.8**	3.3**	3.4**	–0.7**	–4.8**	D
	X	Janak	6.2	–1.2**	2.9**	2.5**	–2.4**	–2.4**	D
	X	HD 2021	6.4	–1.2**	–0.9	–0.8	–2.8**	1.6	D
	X	Raj 821	6.3	–0.6	–0.6	0.4	–1.2	–1.1	C
Janak	X	Arjun	5.5	–0.1	2.1	1.2	–2.5	–0.7	D
	X	S 331	5.5	0.7	2.3	1.4	–0.5	–0.7	D
Arjun	X	HD 2021	5.5	–0.6	–0.4	–0.3	0.9	–0.2	C
HD 2021	X	Raj 821	6.0	0.1	0.9	0.4	0.5	2.0	C
Raj 821	X	S 331	5.9	–0.1	0.1	–0.2	–2.3	–0.2	D

(Contd.)

Table 1. *(contd.)*

Cross			$\hat{m}$	$\hat{d}$	$\hat{h}$	$\hat{j}$	$\hat{i}$	$\hat{l}$	Type of epistasis
					Yield/plant				
Kalyan Sona	X	Janak	14.7	1.3	10.5	6.8	7.4	–3.6	D
	X	Raj 821	12.4	1.2	16.9**	14.3**	4.6	–17.2*	D
	X	S 331	12.0	0.5	16.0**	9.6**	–0.4	–5.8	D
Sonalika	X	Janak	13.6	–4.3*	13.9**	13.0**	–5.4	13.8	D
Moti	X	Raj 821	12.3	–4.7**	11.8**	11.3**	–6.7**	–15.7**	D
Janak	X	Arjun	12.8	0.6	15.6**	13.2*	–4.5	–13.0*	D
	X	Raj 821	15.4	1.3	2.0	5.3	–0.1	–13.1	D
	X	S 331	12.4	2.2	20.0**	18.6**	–1.9	–25.6**	D
Raj 821	X	S 331	12.8	–1.6	2.6	2.7	–6.8	–3.6	D
					100-grain weight				
Kalyan Sona	X	Sonalika	3.7	–1.1*	0.4	–0.1	–0.5*	0.6	C
	X	Arjun	2.9	–0.2	0.2	–0.2	–0.5	0.5	C
Sonalika	X	Arjun	3.5	0.6**	0.6	0.4	–0.7**	–0.1	D
Janak	X	Arjun	3.3	0.3*	1.2*	0.9	–0.7**	–0.1	D
	X	HD 2021	3.8	0.3*	0.0	–0.1	0.5	0.7	C
	X	S 331	3.3	0.3	1.2**	0.8	–0.6**	–0.6	D

Note: $\hat{m}$—F_2 population mean, $\hat{d}$—additive gene effect, $\hat{h}$—dominance gene effect, $\hat{i}$—additive x additive interaction, $\hat{j}$—additive x dominance interaction, $\hat{l}$—dominance x dominance interaction, C—complementary epistasis, and D—duplicate epistasis.

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

Graphical analysis showed the absence of nonallelic interactions (nonsignificant deviation of b from unity), and complete dominance. Component analysis showed significant estimates of additive components ($\hat{D}$), dominance components ($\hat{H}_1$ and $\hat{H}_2$), $\hat{h}^2$ $\hat{F}$ and $\hat{E}$. The estimate of ($\hat{H}_1$ was higher than that of $\hat{H}_2$, and $\hat{D}$ appeared to be more important than $\hat{H}_1$ and $\hat{H}_2$.

YIELD PER PLANT

Nine crosses were detected to exhibit epistasis by the scaling test; of these, seven crosses displayed significant epistatic gene effects. All the nine interacting crosses exhibited duplicate type of epistasis. The contributions of $\hat{h}$ and $\hat{i}$ were more pronounced than those of the other gene effects. The component $\hat{d}$ was significant only in two crosses and these estimates were negative. On the other hand, most of the significant estimates of $\hat{h}$ were positive. Out of the epistatic components, $\hat{l}$ was negative in all the cases where it was significant.

Graphic analysis exhibited nonallelic interaction, partial dominance and asymmetrical gene distribution among the parents. Component analysis exhibited significant estimates of $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{F}$ and $\hat{E}$. The magnitude of nonadditive component was higher than that of the additive one.

100-GRAIN WEIGHT

Epistasis was observed in six crosses, of which four showed significant epistatic gene effects. Additive gene effects ($\hat{d}$) and additive dominance interaction effects contributed more to the mean effect than the other gene effects. However, the significant estimates of $\hat{d}$ were generally positive, while those of $\hat{j}$ were negative.

Table 2. Estimates of genetic components of variation in F_1 diallel progenies for four characters in breadwheat

Component of variation	Grains per spike	Grain wt. of three spikes	Yield per plant	100-grain weight
$\hat{D}$	32.6^{**}	1.34^{**}	6.74^{**}	0.64^{**}
	±4.9	±0.07	±0.86	±0.01
$\hat{H}_1$	24.4	0.96^{**}	8.31^{**}	0.15^{**}
	±11.2	±0.15	±1.98	±0.02
$\hat{H}_2$	19.0	0.59^{**}	4.45^{*}	0.11^{**}
	±9.7	±0.13	±1.73	±0.02
$\hat{h}^2$	−1.4	0.84^{**}	1.79	0.25^{**}
	±6.5	±0.09	±1.16	±0.01
$\hat{F}$	−17.7	0.90^{**}	7.09^{*}	0.34^{**}
	±11.5	±0.16	±2.04	±0.02
$\hat{E}$	3.4	0.10^{**}	2.69^{**}	0.01^{**}
	±1.6	±0.02	±0.29	±0.01

Note:- $\hat{D}$—Component of variation due to additive effects of genes, $\hat{H}_1$—component of variation due to dominance effects of genes, $\hat{H}_2$—proportion of dominance variance, $\hat{h}^2$—net dominance effect, $\hat{F}$—relative frequency of dominant and recessive alleles in parents, and $\hat{E}$—expected environmental component.

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

Graphic analysis suggested independent distribution of genes, partial dominance and absence of epistasis. Component analysis exhibited significant estimates of $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{h}^2$, $\hat{F}$ and $\hat{E}$, the magnitude of $\hat{D}$, being considerably greater than those of H_1 and H_2.

The scaling tests indicated 18, 14, 9 and 6 crosses to be interacting for grains/spike, grain weight of spikes, yield/plant and 100-grain weight, respectively, while the estimates of epistatic components were significant in 14, 6, 7 and 4 crosses. It is, thus, obvious that the scaling test of Mather [4] tends to overestimate the number of interacting crosses.

The estimates of gene effects showed that the additive ($\hat{d}$) gene effect was the most important contributor to the inheritance of grains/spike and 100-grain weight. On the other hand, dominance ($\hat{h}$) gene effects were predominant for grain weight of 3 spikes and yield/plant. Among the epistatic interactions, additive x additive ($\hat{i}$) effects were more pronounced for all the characters, except for 100-grain weight, for which $\hat{j}$ was more important. Generation mean analysis in wheat indicated the presence of additive gene effects for number of grains per ear, grain weight per ear, 100-grain weight and yield per plant [8]. Similar results were also obtained for all the characters except grain weight per ear [9, 10]. But other workers significant epistasis for yield has also been reported in wheat [11, 12]. In the presence of epistasis, especially of the complementary type, the additive component is often relatively underestimated, while the dominance effects tends to be over-estimated [13]. Therefore, it is likely that the additive gene effects were more prominent in these crosses than is evident from the present study.

A comparison of the findings from the generation mean analysis with those from the diallel analysis reveals only a partial agreement between the two. Graphic analysis was unable to detect the presence of interacting crosses for grain weight of 3 spikes and 100-grain weight, while generation mean analysis did detect interacting crosses for these traits. The agreement with the component of variance analysis was considerably greater. It indicated the predominance of additive gene effects for these of the four traits of which only one (grain weight of 3 spikes) differed from the findings of generation mean analysis. In the remaining case (yield/plant) both the analyses revealed the preponderance of additive gene action.

REFERENCES

1. B. I. Hayman. 1958. The separation of epistatic from additive and dominance variation in generation means. Heredity, **12**: 371–390.

2. J. L. Jinks and R. M. Jones. 1958. Estimation of the components of heterosis. Genetics, **43**: 223–234.

3. F. E. Gamble. 1962. Gene effects in corn (Z. *mays* L.). I. Separation and relative importance of gene effects for yield. Can. J. Pl. Sci., **42**: 339–348.

4. K. Mather. 1949. Biometrical Genetics. Metheun, London.

5. J. L. Jinks. 1954. The analysis of continuous variation in a diallel cross of *Nicotiana rustica* varieties. Genetics, **39**: 767–788.

6. R. Aksel and L. P. V. Johnson. 1963. Analysis of a diallel cross: a worked example. Advancing Frontiers Pl. Sci., **2**: 37–53.

7. J. L. Jinks and B. I. Hayman. 1953. The analysis of diallel crosses. Maize Genet. Crop. Newsl., **27**: 48–54.

8. B. I. Hayman. 1954. The theory and analysis of diallel crosses. Genetics, **39**: 789–809.

9. R. S. Paroda and A. B. Joshi. 1970. Genetic architecture of yield and component of yield in wheat. Indian J. Genet., **30**: 298–314.

10. Subedar Singh. 1978. Intermatings in early segregating generations and characterisation of genetic parameters in self-pollinated crops (abstract). J. Indian Soc. Agric. Stat., **30**(2): 159.

11. H. Ketata, E. L. Smith, L. H. Edwards and R. W. McNew. 1976. Detection of epistatic, additive and dominance variation in winter wheat (*Triticum aestivum* L. em Thell). Crop Sci., **16**: 1–4.

12. G. S. Bhullar, K. S. Gill and A. S. Khehra. 1979. Combining ability analysis over F_1–F_5 generations in diallel crosses of bread-wheat. Theor. Appl. Genet., **55**(2): 77–80.

13. R. S. Pathak and R. B. Singh. 1970. Genetics of yield characters in upland cotton. Indian J. Genet., **30**: 679–689.

14. I. S. Pawar, R. S. Paroda, M. Yunus and S. Singh. 1985. A comparison of three selection methods in two wheat crosses. Indian J. Genet., **45**(2): 345–353.