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EPISTATIC GENE EFFECTS FROM THE TRIPLE TEST-CROSS ANALYSIS IN F_2 POPULATION OF OATS FOR FORAGE YIELD AND QUALITY

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ABSTRACT

A triple test-cross analysis in F_2 population of forage oats detected both complementary as well as duplicate epistatic gene effects for green fodder and dry matter yield. For quality traits viz., protein content and in vitro dry matter digestibility (IVDMD), however, only duplicate type epistasis was observed. Both additive and dominance gene effects were involved in the inheritance of green fodder yield, dry matter yield, and digestibility. But protein content was controlled mainly by dominant gene effects. Overdominance was indicated for these characters. Dominant increasers were in higher proportion than dominant decreasers for all the characters. The breeding procedures to exploit the various types of gene effects observed for genetic improvement of forage yield and quality are suggested.

Key words: Triple test-cross, epistasis, *Avena sativa* L., forage yield, quality.

Oat (*Avena sativa* L.), an important cereal of the world, is a dual purpose crop of temperate and subtropical areas. Being highly nutritious, it is used for human consumption as well as for feed and fodder. This crop has also gained importance due to multicut system which ensures regular fodder supply over a long period of time. Breeding of oat for high fodder yield with improved quality has, therefore, gained importance for increasing quality forage production.

Various biometrical methods have been used in different crops in the past to estimate various types of gene effects. In most of the designs used, it is assumed that nonallelic interactions are absent, whereas the fact is often contrary to the assumption. Information on genetics, especially on epistatic gene effects, of important characters in oats is extremely limited. The triple test-cross technique which specifically tests the nonallelic interactions, and also provides equally precise estimates of the additive and dominance components of genetic variation, has been used for genetic analysis of forage yield and quality attributes.

MATERIALS AND METHODS

The material for this study comprised F_2 population of a cross between two homozygous and genetically diverse varieties of oats, namely, OS 7 and Flamings Gold. Fifteen plants were selected at random from the F_2 population and used as male for crossing with their respective female testers (P_1, P_2 and F_1). Thus, 45 crosses were produced (L_{1i}, L_{2i} and L_{3i}) in the form of a triple test- cross. The experimental lines were grown in single 3-m long row with 30 x 20 cm spacing in randomized block design with three replications. Five competitive plants from each row in a replication were randomly picked up to record data on green fodder and dry matter yield/plant. Crude protein content was estimated using the method proposed by McKenzie and Wallace [1], whereas IVDMD was determined by the modified method of Tilley and Terry [2, 3]. The triple test-cross analysis was done using the orthogonal set of comparisons of Jinks and Perkins [4] separately for all the four characters.

RESULTS

The mean squares due to epistasis (Table 1) indicated that i type epistasis was significant for green fodder and dry matter yields, whereas j and l type epistasis was significant for all the four characters studied.

Table 1. Analysis of variance of triple test-cross progenies for the test of epistasis

Source	d.f.	Mean squares			
		green fodder yield	dry matter yield	crude protein	IVDMD
Epistasis	15	18661.6^{**}	700.2^{**}	0.54^{**}	35.25^{**}
i type epistasis	1	156625.9^{**}	1627.5^{**}	2.91	2.82
j and l types epistasis	14	8807.1^{**}	634.0^{**}	0.37^{**}	37.56^{**}
Replicate error	30	172.0	6.7	0.08	0.69
1 type x replicate	2	83.4	0.5	0.19	0.35
j and l types x replicate	28	178.3	7.2	0.07	0.72

**Significant at $P = 0.01$.

The mean squares obtained from the analysis of sums and differences along with the correlation (of sums and differences) are presented in Table 2. Mean squares due to both, the sums and the differences, were highly significant for all the characters. This indicates that both additive and dominance components were important in the inheritance of these characters. The correlation coefficient was also significant, indicating the presence of directional dominance element in the characters studied.

Table 2. Analysis of variance for sums and differences of triple test-cross progenies

Source	d.f.	Mean squares			
		green fodder yield	dry matter yield	crude protein	IVDMD
Sums ($\bar{L}_{1i} + \bar{L}_{2i}$)	14	9283.9^{**}	471.9^{**}	0.76^{**}	15.82^{**}
Sums x replicates	28	633.8	22.3	0.26	2.80
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	14	15644.3^{**}	667.2^{**}	1.94^{**}	16.59^{**}
Differences x replicates	28	135.6	3.2	0.29	1.75
r (sums/differences)	—	-1.3^{**}	-0.9^{**}	-1.07^{**}	-1.43^{**}

**Significant at P = 0.01.

The components D and H were significant for all the characters except for crude protein for which D component was nonsignificant (Table 3). In the present study, H component was more important than D component for all the characters. The average degree of dominance for all the characters indicated the preponderance of dominance component resulting in overdominance.

Table 3. Estimates of additive and dominance components, degree of dominance and direction of dominance

Source	Green fodder yield	Dry matter yield	Crude protein	IVDMD
D	11533.4^{**}	599.5^{**}	0.64	17.4^{*}
H	20678.3^{**}	885.4^{**}	2.24^{*}	19.8^{*}
$(H/D)^{\frac{1}{2}}$	1.4	1.2	1.87	1.1
F	9908.2	342.7	0.64	15.04

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

The estimate of F was positive (Table 3) and had significant correlations for all the characters (Table 2). This indicated that the dominant increasers were in higher proportion than dominant decreasers for all the characters.

DISCUSSION

The triple test-cross is independent of gene correlation, mating system, and allelic frequency [5]. The sampling of large F_2 population of a cross involving homozygous lines and random selection of males further meets the assumption of equal gene frequencies and multiple allelism. Robinson et al. [6] pointed out that multiple alleles, even if present, would increase the dominance variance but would not affect the additive genetic variance. In the present study, epistatic effects have been detected for all the characters. The i type (additive x additive) and j and l type (additive x dominance and dominance x dominance) epistasis were present for green fodder and dry matter yields. Only j and l type of epistatic effects were detected for crude protein and digestibility (IVDMD). Complementary type of epistasis was observed for dry matter and protein content [7]. Solanki et al. [8] observed epistatic interaction mostly of digenic nature for green fodder and dry matter yield.

The estimates of genetic components of variance revealed that additive and nonadditive genetic variances were significant for all the characters. These results confirm the earlier findings in oat [9, 10]. Overdominance was recorded for all the characters. Both green fodder and dry matter yield were governed by additive as well as nonadditive gene effects, the latter being predominant. Paroda et al. [9] also found that these traits were governed by nonadditive gene effects. On the contrary, partial dominance was also reported for these traits in oats [8, 10]. Since both additive and nonadditive gene effects were detected in this material, recurrent selection which could utilise both the gene effects, may be employed for evolving high yielding oat cultivars.

Crude protein and digestibility were found to be under the control of nonadditive gene effects. Manga and Sidhu [11] also reported similar results in oat. Therefore, the conventional breeding methods, which exploit only additive genetic variation, may not be of much help for the improvement of quality traits. Since gene expression is known to vary from environment to environment, multienvironmental approach is suggested for such studies. More investigations on this aspect would be helpful to specify the genetic architecture of these traits.

To sum up the results of the present study, it is obvious that the forage yield in oats is under the control of both additive and nonadditive gene effects. Also, digenic interactions were detected. Predominance of nonadditive gene effects was evident for all the traits including the quality traits. Therefore, breeding procedures which could exploit both types of gene effects may be employed in the present base population of oats. Hence reciprocal recurrent selection and diallel matings might give fruitful results for developing high yielding oat cultivars with improved quality.

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