

## A DIALLEL ANALYSIS OF HEIGHT IN WHEAT, *TRITICUM AESTIVUM L.*

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### ABSTRACT

F<sub>1</sub> data from a complete seven-parent diallel cross for the study of inheritance of height in wheat, *Triticum aestivum L.*, were analyzed. Differences among F<sub>1</sub> families were highly significant. No significant differences between reciprocals were obtained. The data showed that dwarfness was conditioned mostly by recessive genes. 'Genesee' (the tallest variety) and line A1 (the shortest) had the highest and lowest amounts of dominant genes, respectively. Estimates of D (additive genetic variance), H<sub>1</sub>, and H<sub>2</sub> (dominance variances) were found to be 35.10, 49.13, and 31.84, respectively. Differences within pairs of reciprocals used as an estimator of environmental variance (E) had a value of 16.30. The average degree of dominance was 1.18, denoting slight overdominance. Heritability values were 74% (broad sense) and 24% (narrow sense).

### INTRODUCTION

Development of short-stawed cultivars of wheat, *Triticum aestivum L.*, during the last decade has had a great impact on production in many parts of the world. Dwarfness, resistance to lodging, disease resistance, and insensitivity to photoperiod are the main differentiating characteristics of these cultivars (2). This study aims to provide some information on the genetic aspect of dwarfness in wheat.

### MATERIALS AND METHODS

In the winter of 1968 a complete 7x7 diallel cross was made in the greenhouse. The materials included three standard cultivars: 'Genesee' (CI 12653), 'Avon' (CI 13477), and 'Monon' (CI 13278) and four advanced generation lines. CI abbreviations for Cereal Investigation represent the accession numbers of cultivars in the U.S. Dept. of Agriculture World Wheat Collection. The four advanced generation lines, A1-A4 (all dwarf selections), had the following pedigrees:

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A1 NY 5726-AB-3B-23

A New York Agricultural Experiment Station selection with a complex pedigree involving the cultivars 'Redcoat', Genesee, 'Yorkwin', 'Brevor', 'Norin 10', and 'Heine VII',

A2 Genesee \*3/3 Norin 10/Brevor// Yorkwin

A3 Norin 10/Brevor //2\* Genesee

A4 Norin 10/ Brevor // Yorkwin /3/ Genesee

The method used in writing the pedigrees is that suggested by Purdy *et al.* (5). In this method slash symbols (/, //, or /2/, /3/, etc.) denote the successive crosses in the pedigree of the line. Backcrosses are denoted by numbers at the "/" symbols which are placed on the same side of the symbols as the recurrent parent. An asterisk "\*" separates the number and the recurrent parent. Genesee is a tall, soft, white, winter wheat; Norin 10 (CI 12699) is a short, soft, red, spring wheat; Brevor (CI 12385) is a short, soft, white, winter wheat; Yorkwin (CI 11855) is a tall, soft, white, winter wheat; Redcoat (CI 13170) is a tall, soft, red winter wheat; Heine VII is a medium tall, red, winter wheat.

The F<sub>1</sub> seeds from the 42 crosses, including reciprocals and the seven parents were planted in wooden flats in greenhouse. The resulting plants were vernalized in the vernalization chamber for a period of 8 weeks. The vernalized plants were transferred to the greenhouse and were planted individually in clay pots. The number of plants for each of the crosses and the parents ranged from 3 to 20 with an average of 14.5. After full development of the spikes, height measurements were made on the individual plants. Height was measured (in centimeters) as the distance between the soil line and the tip of the spike. The means for the 42 crosses and the parents were calculated and measurements for each pair of reciprocals were replaced by their common mean prior to the diallel analysis.

The analysis of the diallel cross and the symbols used are those described by Hayman (4). The diallel analysis is based on several assumptions whose validity must be met before proceeding with the analysis. These assumptions are: (a) homozygous parents, (b) diploid segregation, (c) no reciprocal differences, (d) no epistasis, (e) no multiple allelism, and (f) independent distribution of genes between parents. The estimated genetic parameters included: D, additive genetic variance; H<sub>1</sub> and H<sub>2</sub>, dominance variances; and F, covariance of dominance and additive effects. Bartlett's test of homogeneity of variance was used to test differences among variances associated with parents and F<sub>1</sub> families. No significant differences were obtained; thus, a common E (the environ-

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mental component of variation) was calculated on the basis of differences between reciprocals. With estimates of  $D$ ,  $H_1$ ,  $H_2$ ,  $F$ , and  $E$ , it was possible to calculate:

$(H_1/D)^{1/2}$ :	Average degree of dominance over all loci
$\frac{pq}{4H_1} = (H_2/4H_1)$ :	Relative frequency of negative versus positive alleles in the parents
$\frac{K_D}{K_R} = \frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$ :	Ratio of dominant to recessive genes in the parents
$H_N = (\frac{1}{4} D)/(V_{ILI})$ :	Heritability in a narrow sense
$H_B = \frac{V_{ILI} - (n+1)E/2n}{V_{ILI}}$ :	Heritability in a broad sense, where $n$ = number of parents, and $V_{ILI}$ = mean variance of the arrays(1).

The assumption of parental homozygosity (a) is assured by the history and cleistogamous nature of the parents. Genesee, Avon, and Monon were standard varieties. A1-A4 were pure, advanced generation lines which had been under natural self-pollination for at least seven generations. The assumption of diploid segregation (b) is met by the fact that inheritance in this species is uniformly disomic (3). No differences between reciprocals were noted (c). The validity of assumptions (d), (e), and (f) can be tested by the slope of ( $W_r, V_r$ ) regression line, where  $W_r$  = covariance of the offspring in each parental array with the nonrecurring parents, and  $V_r$  = variance of all the offsprings of each parent.

A slope of unity is an indication of fulfillment of the assumptions. A balanced failure of the assumptions would also lead to a slope of unity; therefore, reduction due to regression should be tested. A slope of unity and a significant regression are indications of fulfillment of the postulated hypotheses.

## RESULTS AND DISCUSSION

In the present study a slope of the magnitude of  $b = 0.44 \pm 0.21$  was significantly different from unity. Inspection of the data revealed that the array of line A3 had the highest amount of variation a probable indication of non-allelic interaction. Elimination

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of this array resulted in a substantial improvement in the slope of the regression line ( $b = 1.0$ ) and a significant reduction due to regression. Materials were selected deliberately and did not constitute a random sample from any population.

Differences among  $F_1$  families in the analysis of variance were highly significant. Differences within pairs of reciprocals, used as an estimator of environmental variation, had a mean square value of 16.30. Values of  $D$ ,  $H_1$ , and  $H_2$  were found to be 35.10, 49.13 and 31.84, respectively. Covariance between additive and non-additive effects ( $F$ ) had a value of  $-21.37$ .

The value obtained for the average degree of dominance over all loci (1.18) indicated slight overdominance which could be due to close linkage. The estimate for average frequency of negative versus positive alleles was 0.16, indicating that distribution was not equal in the parents. This is also evidenced by the  $K_D/K_R$  ratio of 0.59. Equality of positive and negative gene frequencies should lead to a ratio of unity. The negative sign of the  $F$  is an indication of an excess of recessive genes.

The correlation coefficient between parental measurements ( $Y_p$ ) and ( $W_p + W_r$ ) was equal to  $-0.70$ . This suggests that dwarfness is mostly conditioned by recessive genes. The order of dominance of the parents was Genesee, A4, Monon, Avon, A2, and A1. The rank of their mean performances was Genesee, Monon, Avon, A4, A2, and A1. Thus, Genesee, (the tallest variety) and A1 (the shortest) had the highest and lowest amount of dominant genes, respectively. The advanced generation lines (all dwarf selections) had in their pedigrees Norin 10 and Brevor, and with the exception of A4 showed similar gene action.

Heritability in a broad sense, defined as the ratio of total genotypic variance to total phenotypic variance, was 74%. The value of heritability in a narrow sense, defined as the ratio of additive genetic variance to total phenotypic variance, was 24%. Since dwarfness is controlled by recessive genes, the effectiveness of selection would be greater in the later than in the earlier generations.

Our observations of the present materials have shown that dwarfness is associated with shrunken kernels. This has resulted in undesirable characteristics of low-kernel weight and low-test weight.

## LITERATURE CITED

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