

GENETICS OF PLANT HEIGHT IN SPRING WHEAT

Tanwir Ahmad Malik, Khurshid Alam and Manzoor Khan

Department of Plant Breeding and Genetics, University of Agriculture,
Faisalabad.

Genetics of plant height was studied in crosses of three isogenic lines of wheat (*Triticum aestivum* L.) having different levels of height with a tripple dwarf variety Olsen dwarf. Analysis of data revealed two to three genes responsible for plant height. Genetic components estimated from generation means (parental F_1 and F_2 indicated both additive and non-additive gene action for the inheritance of plant height.

INTRODUCTION

Short statured wheat varieties are resistant to lodging and thus ensure better development of yield components consequently resulting in enhanced grain yield. A better understanding of the genetics of plant height is, therefore, essential for the breeders to synthesize new cultivars incorporating the height reducing genes. Isogenic analysis is an efficient and reliable technique for the inheritance study of height. Although studies have already been conducted in the past (Markle and Atkins, 1964; Jorrel *et al.*, 1967; Amaya *et al.*, 1972; Fick and Qualset, 1973; Saakyan, 1981; Pochaba, 1985), these are usually based on the generations of the crosses between varieties and not on the generations of the crosses of isogenic lines having different height levels. For this reason the present study was conducted and the results are reported in the present paper. Genetic information thus derived would be a valuable tool for tailoring new dwarf varieties of wheat.

MATERIALS AND METHODS

The experimental population was derived from three crosses of isogenic lines (Isogenic line I, Isogenic line II and Isogenic line III) of wheat (*Triticum aestivum* L.). The F_1 and F_2 generations of these crosses alongwith their parents were space planted in the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the year 1985-86 using randomized complete block design of layout with three replications. Two

hundred and forty plants from each F_2 population and 24 plants from each of F_1 and the parents were selected at random. The data were recorded for :

1. *Plant height (cm) :*

Length of the central tiller from the soil surface upto the tip of the spike excluding awns.

2. *Number of nodes per culm ;*

The number of nodes of the central tiller of selected plants.

3. *Internode length (cm) :*

The length of individual first three internodes (below peduncle) of the central tiller.

Analysis of variance was run as per method given by Steel and Torrie (1980). The data of plant height were analysed to get an estimate of the minimum number of genes involved in controlling this character using the formula given by Sewall Wright (1921).

Simple correlation coefficient between internode length and plant height was calculated by the following formula :

$$r = \frac{\frac{\sum XY - \frac{\sum X \cdot \sum Y}{n}}{(\sum X^2 - \frac{(\sum X)^2}{n}) (\sum Y^2 - \frac{(\sum Y)^2}{n})}}{\frac{\sum X^2 - \frac{(\sum X)^2}{n}}{n}}$$

RESULTS AND DISCUSSION

The analysis of variance (Table 1) indicated significant differences among generations for plant height and internode length while for number of nodes the results were non-significant meaning thereby the differences of height in the lines were not due to the number of nodes.

The mean values of all the F_2 hybrids were greater than the respective mid parents (Table 2) showing positive heterosis and partial dominance of positive genes for plant height. Similar findings were reported by Markle and Atkins (1964). Pochaba (1985), however, observed incomplete dominance of short

Table 1 *Mean performance of parents and analysis of variance for various characters.*

Character	Isogenic line I	Isogenic line II	Isogenic line III	Olsen dwarf	Replication mean squares	Generation mean squares
Plant height (cm)	117.55	107.39	79.6	49.81	28.10**	11.23**
Number of nodes	7.04	7.08	6.94	6.86	0.325**	NS 0.033
1st internode length (cm)	22.92	22.00	18.4	10.6	0.202	37.59**
2nd internode length (cm)	17.18	15.00	10.15	9.08	9.47**	13.52**
3rd internode length (cm)	12.4	10.58	7.44	6.06	NS 0.645	10.69**

NS = Non-significant

* = Significant at 5% level of probability

** = Significant at 1% level of probability

Table 2. Means (\bar{X}), standard deviations (S. D.) for parental, F_1 and F_2 generations and number of genes controlling plant height in three wheat crosses.

Crosses	P_1		P_2		F_1		F_2		Number of genes for plant height
	\bar{X}	S. D.	\bar{X}	S. D.	\bar{X}	S. D.	\bar{X}	S. D.	
1. Isogenic line I x Olsen dwarf	117.55	3.14	49.81	2.78	87.57	3.96	84.72	15.49	3
2. Isogenic line II x Olsen dwarf	107.39	3.34	49.81	2.78	76.75	3.26	77.24	13.98	2
3. Isogenic line III x Olsen dwarf	79.60	3.00	49.81	2.78	64.6	5.24	63.24	7.87	3

plant stature in wheat.

The mean heights of all the F_2 populations approximated to mid parents (Table 2) which indicated the presence of additive gene effects for the inheritance of this character, an observation consistent with the findings of Amaya *et al.* (1972). Additive gene action points to the possibility of obtaining desirable plant stature with relative ease from the population under study.

Minimum number of genes involved for the inheritance of plant height in the crosses Isogenic line I x Olsen dwarf and Isogenic line III x Olsen dwarf were three while in the cross Isogenic line II x Olsen dwarf were two (Table 2). These results find support from the studies conducted by Saakyan (1981) and Pochaba (1985). However, Fiek and Raalet (1973) observed four genes responsible for plant height in wheat.

As is evident from the data in Table 1, the length of the first, second and third internode below peduncle for the tall line (Isogenic line I) was greater as compared to the dwarf line (Isogenic line III). Moreover, the tall genotype also had greater mean internode length than the dwarf one. The values of simple correlation coefficients of plant height with the first, second, and third internode length below peduncle were 0.963, 0.968 and 0.964, respectively and were positive and significant. These observations suggest that height in wheat primarily increased through increasing internode length rather than the number of nodes. These conclusions are in agreement with the findings of Markle and Atkins (1964) and Jerrel *et al.* (1967).

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