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Inheritance of Plant Height in Cotton. I. A Cross Between Lubbock Dwarf and Texas Marker-1[1]

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ABSTRACT

In Upland cotton (*Gossypium hirsutum* L.), plant height is determined primarily by the number and length of the main stem internodes, but it can be significantly modified by variation in the node on the main stem where fruiting branches are first initiated. F_1, F_2, and backcross populations from a cross between the inbred lines of Lubbock Dwarf and Texas Marker-1 provided estimates about the inheritance of plant height, number of main stem nodes, length of main stem and fruiting branch internodes, and node of the first fruiting branch. Phenotypic correlations were computed from the F_2 population for all character combinations.

The parental lines differed in plant height, main stem and fruiting branch internode lengths, and the node of the first fruiting branch. The parental lines were not different in the number of main stem nodes; only environmental variation occurred for this character. Each of the other characters were quantitatively inherited with additive genetic effects, without any indication of significant dominance genetic effects. Plant height was shown to be associated with the number of main stem nodes ($r = 0.57$), main stem internode length ($r = 0.88$), and node of the first fruiting branch ($r = 0.38$). A significant association was also found between the number of main stem nodes and node of the first fruiting branch ($r = 0.34$). The lack of significant association between the main stem internode length and the fruiting branch internode lengths suggested that these characters can be manipulated by traditional breeding techniques independently of each other.

Additional index words: ***Gossypium hirsutum*** **L., Cotton breeding, Internode length.**

THE main stem of a cotton (*Gossypium hirsutum* L.) plant has monopodial growth, prominent nodes and internodes, and a growing point at the apex. Leaves arise at the nodes on the main stem in an alternate order; they are arranged about this stem in regular spirals. Two types of side branches occur, these are i) the spirally ascending fruiting branches that are sympodial in growth and ii) vegetative branches that are monopodial in structure and usually arise from the lower nodes of the main stem. The length of the main stem and the side branches are determined by the number of nodes, the length of the internodes, or both. Brown and Ware (1958) suggest that main stem length is generally determined by nutritional or environmental conditions, but they recognized that some variation may be due to cultivars.

In some cotton cultivars, the full growing season is not used in plant growth. This is because of the "determinate" fruiting and growth habit bred into these cultivars during the process of selecting for earliness of crop maturity (Brown and Ware, 1958). Although the terms "determinate" and "indeterminate" are often used in reference to cotton cultivars, it is recognized by cotton workers that all cotton cultivars are indeterminate in their growth and fruiting habits and that these adjectives express only degrees of indeterminate habit. The "determinate" cultivars initiate sympodia (fruiting branches) at lower main stem nodes than do "indeterminate" or full-season cultivars. Fruiting begins early in "determinate" cultivars and development of flowers and bolls gradually retards growth of the main stem and branches. When such cultivars become fruited to capacity, apical growth ceases. This cessation of terminal-growth is referred to as the "cut out" point or date. Thus height achieved during a growing season is generally less in "determinate" cultivars than in "indeterminate" cultivars.

The preceding discussion has presented some of the genetic factors that can produce differential plant heights in cotton. Other environmental factors that can modify plant height are mechanical, insect, or disease damage to the terminal growing point, fertilizer deficiencies, or water stress. The purpose of this research however was to evaluate the inheritance and relationships among plant height, number of main stem nodes, internode lengths, and node number of the first fruiting branch.

LITERATURE REVIEW

Balls (1919) reported the inheritance of plant height from an F_2 population of a cross between *Gossypium barbadense* L. 'Sultani' and *Gossypium hirsutum* L. 'King.' He found that plant height exhibited continuous variation from one parental extreme to the other and that excessively high night temperatures tended to cause the cotton plant to flower at a higher main stem node, thereby producing a taller plant.

Ray and Richmond (1966) studied the inheritance of the number of nodes to the first fruiting branch. They indicated that this character was quantitatively inherited and controlled primarily by additive gene action. They also found that the character was highly associated with earliness of crop maturity.

Studies on the main stem node number of the first fruiting branch have shown that the character is extremely sensitive to changes in temperature (Low, Hesketh, and Muramoto, 1969). Cool temperatures caused the first fruiting branch to form at a lower node.

MATERIAL AND METHODS

The parental lines used in this study were Lubbock Dwarf and Texas Marker-1 (TM-1). Lubbock Dwarf has reduced plant height, earliness of crop maturity, short, fine, and weak fiber, and low yield of lint/plant. The TM-1 line is a genetic standard that often has been used in genetic studies in cotton (Kohel, Richmond, and Lewis; 1970). This line (in terms of plant height, crop maturity, fiber quality, and yield/plant) is typical of those cotton cultivars grown in the Mississippi Delta. Both lines are highly inbred and should be relatively homozygous and homogeneous. Crosses between these lines were used to generate F_1, F_2, and both backcross populations (B_1 and B_2). These populations, along with the parental lines, were used to provide information on the inheritance of the characters measured. The extent to which these estimates can be applied to other cotton varieties is unknown.

In 1973, three plots of each of the six entries (P_1, B_1, F_1, F_2, B_2, and P_2) were planted in the genetics nursery at Lubbock,

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Tex. Each plot was a single 10-m row with 40 to 60 plants/row. A preplant and a summer irrigation were applied and normal tillage and cultural practices were utilized.

Five characters were measured on each plant in every plot. These were plant height, number of main stem nodes, length of the main stem and fruiting branch internodes, and node of the first fruiting branch. Each of the characters was measured at the end of the growing season after a freeze had killed the plants and all leaves had fallen. Damaged plants were not measured. *Plant height* (cm) was from the cotyledonary node (node number one) to the last easily recognized node on the main stem. The *number of nodes* on the main stem was counted by beginning at the cotyledonary node and ending at the last easily recognizable node on the main stem. Average *main stem internode length* was estimated by dividing plant height by one less than the total number of main stem nodes. Average *fruiting branch internode length* was the average length of the first three internodes of the fruiting branch at the ninth main stem node. If a fruiting branch at the ninth main stem node did not have three internodes, or if the fruiting branch was damaged, the fruiting branch below or above the ninth main stem node was measured. The *node of the first fruiting branch* was determined by counting from the cotyledonary node up the main stem to the first fruiting branch.

These above mentioned features were tested by a joint scaling test to determine if an additive-dominance model could adequately evaluate the variation present (Mather and Jinks, 1971). This test consisted of estimating the parameters *m*, (*d*), and (*h*) from the means of the available generations. The parameter *m* was the estimated mid-point between the parental means, (*d*) was the fixable or additive portion of the genetic variation, and (*h*) reflected the dominance properties of the genes and represented the contribution to the unfixable heritable variation. The observed generation means were compared with the expected values derived from the estimates of these three parameters. These parameters were estimated by weighted least squares and the comparisons between observed and expected generation means were conducted by asuming that the sum of squares minimized in the fitting process were distributed as χ^2.

Phenotypic correlation coefficients were calculated among the characters measured from the individual plants of the F_2 population. A significant phenotypic correlation (r) suggested that the two characters being measured were associated, although not necessarily demonstrating a cause and effect or linkage relationship.

Table I. Mean separation of parental and F_1 generations for the features measured.

Entry	Feature: Plant ht.	No. of nodes	Internode lengths: Main stem	Internode lengths: Fruiting branch	Node of first fruiting branch
	cm		cm		
P_1 (Lubbock Dwarf)	73.4 a*	21.9 a	3.4 a	4.6 a	5.7 a
F_1	83.3 b	21.4 a	3.9 b	7.3 b	6.4 b
P_2 (TM-1)	93.8 c	21.7 a	4.4 c	9.2 c	7.5 c

* Means within columns followed by different letters are significantly different at the .05 level, according to a Duncan's multiple range test.

Table 2. Generation means with standard errors and the results of the joint scaling test for the adequacy of the additive-dominance model.

Generation	N	Feature: Plant ht.	Internode lengths: Main stem	Internode lengths: Fruiting branch	Node of first fruiting branch
		cm			
P_1	60	73.4 ± 4.44	3.4 ± 0.23	4.6 ± 1.38	5.7 ± 0.70
B_1	120	78.6 ± 7.68	3.7 ± 0.33	5.9 ± 1.44	5.8 ± 0.76
F_1	60	83.3 ± 5.23	3.9 ± 0.21	7.3 ± 1.31	6.4 ± 0.72
F_2	180	82.1 ± 10.38	3.8 ± 0.49	7.4 ± 1.94	6.2 ± 1.08
B_2	120	89.8 ± 8.51	4.2 ± 0.26	8.6 ± 1.58	7.1 ± 1.06
P_2	60	93.8 ± 4.44	4.4 ± 0.25	9.2 ± 1.39	7.5 ± 0.57
m		83.7 ± 2.99	3.9 ± 0.16	6.6 ± 0.98	6.5 ± 0.42
(d)		9.9 ± 2.89	0.5 ± 0.15	3.1 ± 0.95	0.9 ± 0.17
(h)		-0.06 ± 5.86	0.04 ± 0.27	0.4 ± 1.83	-0.2 ± 0.83
χ^2(3)		0.0825	0.1653	2.3914	0.1822
P range		0.99	0.97-0.99	0.3-0.5	0.97-0.99

Table 3. Phenotypic corelations among the feature combinations in the F_2 population of Lubbock × TM-I.

Feature	Feature: Plant ht.	No. of nodes	Internode lengths: Main stem	Internode lengths: Fruiting branch
	cm		cm	
No. of nodes	0.57*	--	--	--
Internode lengths				
Main stem	0.88*	0.11	--	--
Fruiting branch	0.10	0.10	0.11	--
Node of first fruiting branch	0.38*	0.34*	0.11	0.15

* Significantly different from zero at the 0.01 level.

RESULTS AND DISCUSSION

The parental lines (Lubbock Dwarf and TM-1) were statistically different in plant height, main stem internode length fruiting branch internode length, and node number of the first fruiting branch (Table 1). The number of nodes on the main stem did not differ between the lines and only environmental variation occurred; therefore this character was not included in the genetic analyses. Lubbock Dwarf had reduced plant height, short main stem and fruiting branch internodes, and a low node of the first fruiting branch. In comparison, TM-1 was taller in plant height, had longer main stem and fruiting branch internodes, and had a higher node of the first fruiting branch. The F_1 hybrid was intermediate between the parental lines in all characters (Table 1).

Frequency distributions of the parental, F_1, F_2, and backcross (B_1 and B_2) populations for all characters were typical of those expected of quantitatively inherited characters. Means from the F_1 and F_2 generations generally took an intermediate position between the parental means and the means from the backcross generations produced values nearer those of the parents to which they had been crossed (Table 2).

The χ^2 values from the joint scaling test showed that all characters adequately fit an additive-dominance model and that the estimates of m, (d), and (*h*), were not biased to any significant extent by effects not attributable either to the additive or dominance action of the genes (Table 2). For all characters, the estimates of (*d*) were significantly different from zero, and the estimates of (*h*) were not significantly different from zero. Therefore we concluded that dominance genetic effects were not a major factor in the inheritance of any of the characters and that the expression of each character was caused primarily by additive genetic effects.

Significant phenotypic associations were found in the F_2 population between plant height and number of main stem nodes, main stem internode length, and node of the first fruiting branch (Table 3). Plant height was not correlated with fruiting branch internode length. Main stem internode length was not associated with the number of main stem nodes, fruiting branch internode length, or node of the first fruiting branch. The length of the fruiting branch was not associated with the number of main stem nodes or the node of the first fruiting branch. The node of the

first fruiting branch was significantly associated with the number of main stem nodes.

The results of this study have shown that two of the factors that cause differential plant height in cotton (length of the main stem internode and node of the first fruiting branch) are inherited in an additive fashion and that the two genetic systems are probably inherited independently of each other. The lack of significant association between the length of the main stem internode and the length of the fruiting branch internode suggests that these two internode lengths are independently controlled genetically and that independent genetic manipulation of each internode length should be possible.

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