Phenotypic Effects of Nine Height Mutants in *Sorghum vulgare*

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The inheritance of height in sorghum is not yet completely understood, but present knowledge indicates that at least four major genes are involved. These genes have been designated as dw1, dw2, dw3, and dw4 (5). One of the genes is unstable in the recessive state and reverts to the dominant allele at a very high rate. The unstable gene has not been definitely identified, but has been postulated to be dwv.

The mere fact that the gene reverts from the recessive to the dominant condition does not necessarily imply that all mutations produce identical alleles. That is to say, it does not preclude the possibility of mutation to varying levels or grades of the same effect and the consequent establishment of a multiple allelic series. The comparison of several mutants from a homogeneous source should indicate, at least, whether the unstable gene ordinarily reverts to a common allele. This approach was utilized in the present study, which was designed to compare the phenotypic effects of some height mutations within each of three different sources of material.

**REVIEW OF LITERATURE**

Quinby and Karper (5) considered as true height genes in sorghum only those genes which influence length of internodes. Genes which affect the time of floral initiation, and consequently the number of internodes, were classified as maturity genes. These authors observed differences in height among plants of similar genotype with respect to both major height genes and maturity genes. The differences were attributed to the presence of a modifier complex which apparently has approximately the same effect on height as a single homozygous recessive gene.

Karper (4) noticed the regular occurrence of a dominant mutation in a parental stock of Standard Blackhall kafr in which head selection was practiced for 15 years. The mutations were identical to the parental lines in every respect except height, and the increase in height was due entirely to an increase in length of internodes. The unstable gene has been assumed to be dw1; however, the variety Early Hegari has an unstable dwarfing gene, but is not recessive for dw1 (5). Apparently, therefore, dw1 is not the only unstable gene.

Karper (4) suggested that the mutation probably occurs during gametogenesis of the parental plant. Blakeslee (1) noted a similar unstable recessive dwarfing gene in *Portulaca grandiflora* and concluded that reversions in *Portulaca* can occur at any stage from gametogenesis to maturity.

According to Goldschmidt (2) a mutant gene has an action different from the original gene but always affects the same kind of process. This is asserted by Goldschmidt for any number of mutational changes or multiple alleles which give rise to several alternative states or variants of the same gene.

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**MATERIALS AND METHODS**

Seed from nine tall mutants were obtained from J. R. Quinby. Four of the mutants were from the variety Combine 7078, 3 were from line B-600, and 2 were from line B-602. Subsequently, mutants from the same variety or line will be considered to constitute a family. The nine mutants were included in a test to determine if the changes within each family resulted from the reversion of the unstable gene to a common allele.

Each of the nine mutant plants was assumed to be heterozygous for the mutant gene. Two replications of the F1 selfed progenies from the 9 mutants were planted in a randomized complete block design at Urbana, Ill., on May 14, 1958. Measurements were taken on height and days to anthesis. Height was measured as inches from the ground to the collar of the flag leaf, and days to anthesis were counted from planting to the first exsertion of anthers from the florets. All plants were selfed, and seed from different plants were placed in separate packets. The recessive plants were easily distinguished, but tall plants did not fall into discrete groups corresponding to heterozygous and homozygous genotypes.

Expansion of the binomial revealed that if seed were planted from at least 12 tall (Dw-) plants from the segregating F2 generation of each mutant, the odds of obtaining 2 or more DwDw progenies would be about 19:1. Since dominance does not appear to be complete (3), the probability of obtaining DwDw progenies should be enhanced by selecting seed from the taller F1 plants. On this basis seed from the 10 tallest F1 plants from each mutant were planted in 1959 in a randomized complete block design with 4 replications. Plot size varied from 7 to 14 plants with all but 2 plots having at least 10 plants. Individual plant measurements of days to anthesis and plant height were taken on 10 plants from each plot.

Four recovered dwarfs from each F1 progeny were included in a similar test to determine if the genetic backgrounds of mutants within a family were homogeneous. If the mutants were from homogeneous material and if no other changes occurred in conjunction with the height mutations, no difference should exist among the recovered dwarf plants within each family. The time of planting and field conditions were similar to those for the DwDw progenies, and measurements were taken in the same manner.

The genotypes of the F1 plants were determined by classifying the F2 progenies. Degree of dominance was calculated for each of the mutants by utilizing the following method which was suggested by H. W. Norton: (3)

Degree of dominance = \[ \frac{H - DwDw}{2DwDw + DwDw} \]

where DwDw is the mean height of homozygous tall plants, DwDw is the mean height of heterozygous tall plants, and DwDw is the average height of dwarf plants. The variance of dominance expression is calculated as follows:

\[ V(H) = \frac{V(DwDw)}{n_1} + \frac{V(DwDw)}{n_2} + \frac{V(DwDw)}{n_3} \]

where \( n_1, n_2, \) and \( n_3 \) are the numbers of observations in the respective classes and the numerators represent the variances of these three groups. A statistical weight \( w \) is derived by taking the reciprocal of the variance of \( H \). Sums of squares are calculated in the usual manner. For example, the total sum of squares is found as follows:

\[ \text{Total SS} = \sum \text{H}^2 - (\sum \text{H})^2/n \]

Differences between mutants within families are indicated if the within-families mean square deviates significantly from unity.

All results were submitted to analysis of variance and only those results which differ at the 5% level will be considered as significant throughout the context of this paper unless specifically stated otherwise.

**RESULTS AND DISCUSSION**

The F2 progenies from each of the 9 mutants segregated in a ratio of 3 tall to 1 dwarf as expected for a single