2. The brown-midrib mutants of maize.

Several years ago here at Purdue we found that the basis of the $\frac{bm_1/bm_1}{bm_1}$ and the $\frac{bm_2/bm_2}{bm_2}$ phenotypes was the production by these mutants of lignins which are quite different from that produced by normal plants. These altered lignins are responsible for the midrib color in mutant plants. Later we found that Jorgensen, who isolated the $\frac{bm_1}{bm_1}$ mutant, reported that the pigment responsible for the color was either lignin or a pigment indissociably bound to lignin.

Our discovery stimulated a program to attempt to learn something about the biosynthesis and structure of lignin using the mutants as tools as has been done so successfully in Neurospora, E. coli, and other microorganisms. The chemistry of lignin is still poorly understood in spite of much research. Lignin is known to be a polymer of various phenylpropanoid (C6-C3) building blocks (depending on the species). Since this is so, a mutant affecting lignin production could affect either a step in the production of a phenolic building block or a step in the synthesis of the polymer itself.

The current consensus of opinion regarding lignin synthesis (after Freudenburg) is that the only enzymatically mediated step in the synthesis of the polymer itself is a dehydrogenation of the building blocks. The result of this dehydrogenation for a given building block is a radical which can exist in various mesomeric forms. These mesomers can combine at random in all possible combinations to form a disorderly type of polymer. If this view is correct, then the origin of the very different bm1 and +bm1 lignins must be found in different pools of phenolic compounds in which this random polymerization is proceeding. This should be experimentally verifiable, and we are now investigating this point.

The bm₁ and +bml lignins differ in many ways. In the first place, there is a lower content of Klason lignin in bm₁/bm₁ plants (lk percent) as compared to +bm/+bm plants of roughly comparable genotype which have 21 percent lignin. Alkali lignin from +bml plants is a light tan amorphous powder which melts at ca 172° C. Alkali bm₁ lignin is a deep reddish-brown paracrystalline substance which chars at 236° C before melting. Oxidative degradation of native lignins with nitrobenzene in an alkaline medium shows a marked deficiency of p-hydroxy-phenyl residues (p-oH cinnamic acid, p-oH benzoic acid, and p-oH benzaldehyde) in bm₁ lignin as compared to +bml lignin. This reduction has not been determined quantitatively as yet, but there may be only one fourth as much in bm₁ lignin.

The grasses are the only group of plants in which p-hydroxy phenylpropanoid building blocks are incorporated into the lignin polymer. The grasses are also the only group in which added tyrosine will serve as a lignin precursor. It was suspected at first that the block in bmi might be in one of the steps between tyrosine and p-oH cinnamyl alcohol

which is apparently the p-oH phenylpropenoid building block. Accordingly tracer experiments were conducted in which both bm1/bm1 and +bm/+bm plants were allowed to take up either UL Cll phenylalanine or UL Cll plants were allowed to take up either UL Cll phenylalanine or UL Cll phenylalanine or UL Cll the tyrosine and then frozen 24 hours later for analysis. Estimation of the specific activity of the isolated alkali lignins indicated that both amino acids were equally good lignin precursors for both bm1/bm1 and +bm/+bm plants. This would appear to rule out the hypothesis suggested above.

If anyone has a brown-midrib mutant which is known not to be 1, 2, 3, or 4, we would be most interested in obtaining it.

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3. The location of the Hm2/hm2 locus.

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In the 1951 News Letter (25) we reported a second locus affecting susceptibility to Race I, Helminthosporium carbonum. This locus has now been designated as Hm2/hm2 and located on chromosome 9. Its location is probably on the long arm of the chromosome since in a 3-point test (CS) the order of the genes is sh wx hm2 with recombination between wx and hm2 approximating 25 percent.

The data on the location of $\frac{\text{Hm}_2}{\text{hm}_2}$ substantiate those collected earlier from a RS progeny. The F₂ progeny investigated in 1960 was derived from $\left(\frac{\text{hm}_1}{\text{hm}_1} \frac{\text{Sh}}{\text{sh}} \frac{\text{Wx}}{\text{km}_2} + \frac{\text{Hm}_2}{\text{km}_2}\right)$ The data are given in Table I.