UNIVERSITY OF MISSOURI
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and
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1. Mass selection for seedling survival in a shrunken-2 (sh_2) population.

Our population of southern corn belt material has undergone 8 cycles of selection for seedling survival. Additional selection pressure was applied in the last 4 cycles for kernel weight and kernel density. The population now expresses greatly improved seedling survival, kernel weight, and kernel test weight when compared with corn belt inbred lines homozygous for the sh_2 gene or genetic stocks currently in use.

Seed stocks can be obtained from the Missouri Agricultural Experiment Stations.

	Seedling[+] survival	Kernel weight	Test weight
Mo sh_2 population	55%	.16g	54 kg/hl
(N15 sh_2 x B37 sh_2)F_1	19%	.08g	39 kg/hl
Corn Belt SX (dent)	86%	.60g	72 kg/hl

[+]Average of 13 planting date - corn belt locations in 1971.

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1. Complex regulatory scheme for catalase in early maize development*.

Maize catalase (H_2O_2:H_2O_2 oxidoreductase, EC 1.11.1.6) is a

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tetrameric enzyme containing four heme prosthetic groups. It catalyzes the breakdown of hydrogen peroxide to water and molecular oxygen although its precise physiological function is unknown. The enzyme exists in several isozymic forms, and has been well characterized genetically (Scandalios, 1968, 1969). In the liquid endosperm of the immature kernel, a single catalase species is present, and is the homotetrameric gene product of the $\underline{Ct_1}$ locus. At seed maturation, a second and distinct locus is activated ($\underline{Ct_2}$), and shortly after imbibition of the seed, five isozymes can be distinguished (the homotetramers of each locus plus three heterotetramers). The product of the $\underline{Ct_1}$ locus disappears during the first few days of development, and the $\underline{Ct_2}$ homotetramer becomes the primary species by days 7-10 (Scandalios, 1970). In addition to this differential activation of two distinct loci, there appear to be several other mechanisms controlling catalase expression during early maize development. The enzyme is subject to changing patterns of compartmentation (Longo and Longo, 1970), and the isozyme balance is controlled in part by differential rates of synthesis and degradation (Quail and Scandalios, 1971; Ganapathy and Scandalios, manuscript in preparation). Preliminary evidence indicates that at least two other mechanisms may be active during this same period, namely that one isozyme appears to be preferentially secreted from isolated scutella in response to gibberellic acid, and that there appears to be a catalase specific inhibitor present shortly after imbibition, but absent by the fourth day of germination. We are presently attempting to characterize this inhibitor, and relate it to the overall scheme of catalase regulation in maize.

Experiments in which crude day 1 and day 4 scutellar extracts were mixed showed that the catalase activity of the mixture was less than the sum of the activities added. Similar results were obtained in all three inbred lines tested (W64A, T21, 229). Dilution effects and proteolysis were ruled out as causes of the lowered activity, and the inhibitory factor was found to be in the day 1 extract. This factor has since been shown to be heat labile and non-dialyzable, leading to speculation that it may be a protein. The factor has been shown not to inhibit peroxidases (a group of catalytically related hemoproteins), indicating an apparently high degree of catalase specificity. An attempt is presently being made

to purify this inhibitory factor, and to determine if it differentially inhibits the various catalase isozymes.

References:

Longo and Longo, Plant Physiol. 45:249 (1970).

Quail and Scandalios, PNAS 68:1402 (1971).

Scandalios, J. G. Annals N. Y. Acad. Sci. 151:274 (1968).

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John C. Sorenson
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2. De novo synthesis of soluble and mitochondrial forms of genetically determined isozymes of malate dehydrogenase.

Three classes of malate dehydrogenase (MDH) have been identified according to their subcellular location: those found in the soluble fraction (s-MDH), those associated with the mitochondrial fraction (m-MDH) and those associated with glyoxysomes (g-MDH). Seven electrophoretic variants of m-MDH have been found among 35 inbred lines examined.

The developmental control of the two s-MDH's and the five m-MDH's has been studied using the inbred strain W64A. During early sporophytic development (dry seed - 10 days), all of the scutellar s-MDH's and m-MDH's follow the same developmental pattern; however, the total m-MDH activity is only 60% that in the cytosol. Chloramphenicol (CAP) and cycloheximide (CH), two known inhibitors of protein synthesis, were employed to determine whether the MDH isozymes are affected during the course of development. CAP (0.5-2.0 mg/ml) did not have an inhibitory effect on MDH, whereas CH (2-10 μg/ml) inhibited 60-65% of the MDH activity in scutella by 96 hrs. after treatment. Both s-MDH's and m-MDH's are inhibited to the same extent. It is thus apparent that protein synthesis in the cytoplasm is essential for the increase seen in both s-MDH and m-MDH activities during development. This result is quite consistent with our earlier findings that mitochondrial MDH's are controlled by nuclear genes (Longo and Scandalios, 1969, PNAS 62:104).

In order to test whether the increased MDH activities in the developing scutella result from activation of pre-existing MDH molecules or