1. Mass selection for seedling survival in a shrunken-2 (sh<sub>2</sub>) 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<sub>2</sub> gene or genetic stocks currently in use.

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

<table>
<thead>
<tr>
<th></th>
<th>Seedling survival</th>
<th>Kernel weight</th>
<th>Test weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mo sh&lt;sub&gt;2&lt;/sub&gt; population</td>
<td>55%</td>
<td>.16g</td>
<td>54 kg/ha</td>
</tr>
<tr>
<td>(N15 sh&lt;sub&gt;2&lt;/sub&gt; x B37 sh&lt;sub&gt;2&lt;/sub&gt;)&lt;sub&gt;F&lt;sub&gt;1&lt;/sub&gt;&lt;/sub&gt;</td>
<td>19%</td>
<td>.08g</td>
<td>39 kg/ha</td>
</tr>
<tr>
<td>Corn Belt SX (dent)</td>
<td>86%</td>
<td>.60g</td>
<td>72 kg/ha</td>
</tr>
</tbody>
</table>


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

Maize catalase (H<sub>2</sub>O<sub>2</sub>:H<sub>2</sub>O<sub>2</sub> oxidoreductase, EC 1.11.1.6) is a

*A portion of this work was completed at Michigan State University under AEC Contract AT(11-1)1338.
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 pro-
duct of the $\text{Ct}_1$ locus. At seed maturation, a second and distinct locus
is activated ($\text{Ct}_2$), and shortly after imbibition of the seed, five iso-
zymes can be distinguished (the homotetramers of each locus plus three
heterotetramers). The product of the $\text{Ct}_1$ locus disappears during the
first few days of development, and the $\text{Ct}_2$ homotetramer becomes the pri-
mary species by days 7-10 (Scandalios, 1970). In addition to this differen-
tial activation of two distinct loci, there appear to be several other
mechanisms controlling catalase expression during early maize develop-
ment. The enzyme is subject to changing patterns of compartmentation (Longo and
Longo, 1970), and the isozyme balance is controlled in part by differen-
tial rates of synthesis and degradation (Quail and Scandalios, 1971;
Ganapathy and Scandalios, manuscript in preparation). Preliminary evi-
dence 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:
Quail and Scandalios, PNAS 68:1402 (1971).

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John G. Scandalios

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