a high affinity for the basic amino acids. On the other hand, the B and C forms have lower K_ms and higher affinities for the non-polar side chains of some of the neutral amino acids. As mentioned previously, the LpA and LpD genes are linked (approximately 13 map units apart). The linkage relationships of the B and C loci and of the B and C loci to the A and D loci will be investigated, and we plan to determine the chromosomal locations of the aminopeptidase genes. The maize aminopeptidase system represents a potentially good system for correlating structural, biochemical and genetic information in an effort to understand possible evolutionary relationships between the aminopeptidase loci.

Lila A. Ott and John G. Scandalios

Quantitative catalase inhibitor variants — We have previously reported on a catalase-specific inhibitor in maize scutella which is involved in catalase regulation

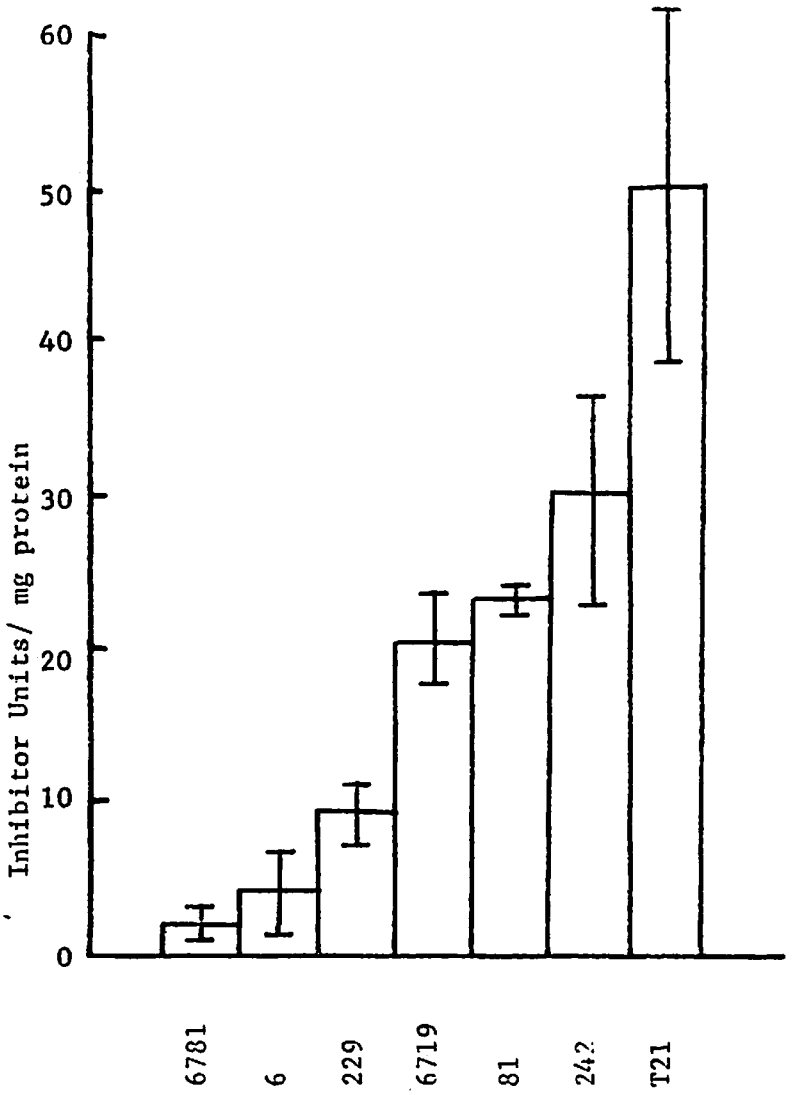

Fig. 1. Levels of inhibitor in various inbred maize strains. Error bars represent standard deviations of at least four replicates in two or three independent experiments.

during early seed germination (MGCNL Vols. 47, 48). The inhibitor has since been purified by affinity chromatography on immobilized catalase (Sorenson and Scandalios, Biochem. Biophys. Res. Comm., in press), and we have determined that it is a protein. We are currently screening inbred maize lines for quantitative inhibitor variants in hopes of defining the structural gene for the inhibitor. The results of the first screening series are shown in Figure 1 (preceding page). The inhibitor levels in these lines fall into three groups, 0-10 inhibitor units/mg protein, 20-30 i.u./mg and a high level group of approximately 50 i.u./mg for which the range has not yet been defined. Although there is only one inbred line in this category in the data presented, initial measurements of a second group of inbreds show several more lines which fall into the high inhibitor category.

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Effect of ethanol on meiotic chromosome behavior — Ethanol was introduced on filter paper into the tassel area at meiotic stages during a three-hour temperature elevation from about 25°C to 36°C. Microsporocyte samples were collected just before treatment, immediately following treatment, and at 5 hours, 7 hours, 24 hours and 48 hours following treatment initiation. Pre-treatment samples were found to be normal.

Desynapsis at synizesis and pachytene was common in all post-treatment samples, occurring with a distribution which suggests treatment damage of existing synaptonemal complexes. Decondensation was often found in chromosomes fixed at diplotene to metaphase I at all intervals following treatment. Bivalents were often dissociated to dyads or monads at metaphase I in 24-hour and 48-hour samples; nearly complete separation of bivalents to univalents was occasionally found at diakinesis in 24-hour samples. Polyspory was found at the quartet stage in a 24-hour sample.

Chromosome 10 rod bivalents at diakinesis were studied in material heterozygous for K10, collected and fixed immediately following treatment (material was therefore at late pachytene to diakinesis during treatment). In such rod bivalents open at the K10 end, the knob sometimes appeared to be disjunctionally separated and sometimes to be equationally separated (with a K10 knob at each end). This is considered to be evidence of treatment-induced chiasma failure following crossing