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1. Malate dehydrogenase in maize endosperm.

In a previous report (M.G.C.N.L. 44:189-90), the ontogenetic changes associated with the isozyme pattern of malate dehydrogenase during the development of the endosperm were described. Two isozymes comprised 45% and 35% of the total activity, respectively, and were the subject of further investigation. The use of differential and density gradient centrifugation established that both isozymes were of particulate origin. The organelles were identified as mitochondria and peroxisomes, and the latter were further examined both in situ and in cell homogenates. In addition to a single MDH isozyme, they also contained most of the catalase present in the tissue. This was verified by incubating pieces of endosperm in a medium containing diaminobenzidine, which cytochemically localizes catalase activity. Electron-microscopic examination of incubated tissue demonstrated that catalase was localized within these organelles alone, with some staining evident in the cytoplasm.

Homogeneous preparations of the two major isozymes, designated m-MDH and p-MDH, were obtained using anion-exchange chromatography; and these preparations were then used directly to determine several physical and kinetic parameters. Data from gel filtration experiments indicated that both m-MDH and p-MDH had Stokes (molecular) radii of about 34Å and were hence indistinguishable on the basis of molecular size. An investigation of some kinetic parameters did, however, provide evidence that the two isozymes were catalytically distinct. Among the parameters used were nucleotide analogue ratios, K m's and pH dependency curves.

Since the isozymes have different catalytic properties and are differentially compartmented within the cell, it is safe to assume that they have specific and unique physiological roles. The mitochondrial isozyme is most certainly involved in Krebs Cycle activity; and while a truly accurate assessment of the role of p-MDH must await further biochemical characterization of maize endosperm peroxisomes, it is probable that these organelles function in much the same way as peroxisomes

(glyoxysomes) in castor bean endosperm. It has been established that these organelles, containing the enzymes of the glyoxylate cycle, are involved in the mobilization of lipid reserves and their subsequent conversion to carbohydrate. The intimate association between lipid bodies and peroxisomes in maize endosperm, observed during the present study, would support the contention that maize peroxisomes function in a similar fashion.

It may be concluded then, that m-MDH and p-MDH are distinct molecular species with catalytic differences and unique metabolic functions.

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2. Data analysis and maize cytogenetics.

The application of standard statistical tests is generally well understood and the techniques have been described in many elementary texts. Less well known are a number of techniques which in the biological field are more commonly used by numerical taxonomists and ecologists. In general, these are techniques which are concerned not so much with validating hypotheses as with the manipulation of data to bring to light information not apparent in the original data. Information in this sense may well include new problems or the rephrasing of old questions in a way which allows of more productive experimental design in subsequent investigations.

Perhaps the greatest problem is the difficulty which is faced in evaluating a large body of diverse data which contains many simultaneous variables. Presented with such a mass of data, one's tendency is to examine it in parts, looking, the while, to see if the rest of the data supports impressions gained from the part. This is a notoriously unreliable procedure, and consequently the whole basis of the investigative method rests on the sequential examination of limited hypotheses. While reliable, the method suffers from the fact that very frequently one is examining the wrong hypothesis. Clearly, any technique which will extract more information from a mass of multivariate data will enable specific hypotheses to be formulated much more efficiently. It is possible, indeed, that a meaningful answer can only be obtained by taking the mass of data as a whole.