μliters of solution C and 3 μliters of TEMED, (iii) *4% acrylamide stacking gel:* 1.5-cm layer of a mixture composed of 0.665 ml of solution A, 1.250 ml of solution B, 3.085 ml of water, 30 μliters of solution D, and 5 μliters of TEMED.

Electrophoresis.—The electrophoresis was run in a 4-C air cooled chamber at constant current (20 mA) for about 2.5-3.0 hr. The apparatus and the electrode buffer (Tris, 20.16 gm; glycine, 4.3 gm; SDS, 0.7 gm in 700 ml H_2O) used were essentially those described by Studier (9,10). After electrophoresis, the gels were fixed overnight in an aqueous solution of 12.5% TCA (w/v), 25% isopropanol (v/v), stained 24 hr with a 0.1% aqueous solution of Coomassie brilliant blue G, and destained in water.

RESULTS AND DISCUSSION

The method described was applied to a number of protein preparations from different sources and generated in various ways, ranging from green plant (*Gynura aurantiaca*) protoplasts and tissue homogenate to *Xenopus laevis* oocyte and nematode proteins.

A comparative study of the proteins obtained from lysed protoplasts and homogenized tissue was carried out to detect the variation in the corresponding profiles. The patterns (Fig. 1 and 2), are quite similar in the number, relative intensity, and position of the bands along the profile. The quality of the patterns achieved also is quite similar, indicating that the proteins derived from tissue homogenization and those prepared from protoplast lysates reflect a common distribution of protein species.

Polypeptides with apparent molecular weights of 10^4 to 10^5 daltons were observed in the resolving gel after a relatively short time of electrophoresis, without leaving significant amounts of protein of the highest molecular weights at the gel interface or in the spacer gel. Despite the great number of bands of the patterns, they are finely separated, and sharp along the whole profile. Even though the number of distinct protein bands that can be detected per 50 μg of protein in the photographs taken after destaining the gel is about 60-90, the actual resolution by direct observation is greater. Furthermore, we have observed excellent reproducibility, from aliquots of preparations made before SDS treatment, common samples analyzed in different positions of the same gel, and comparable preparations from distinct experiments.

The electrophoretic system also was applied to study the ^{14}C-labeled proteins of subcellular fractions from *Gynura aurantiaca* leaves. After leaf pieces had been vacuum-infiltrated with the labeled amino acids, the proteins detected both by Coomassie staining and the fluorographic (1) patterns indicated the distribution of the newly-synthesized protein species (Fig. 3).

It should be noted that the preparations which have been used to obtain the protein profiles presented in this paper were very crude. This feature is especially notable in the case of *Gynura aurantiaca* extracts, in which the interference of the great amount of pigments present has been overcome, and emphasizes the general application of this procedure in analysis of plant proteins. The utilization of this technique in the comparative analysis of healthy and diseased systems already has been demonstrated in the detection of the proteins associated with viroid infection (2).

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ERRATA, VOLUME 67

Page 844, second column, eighth line from bottom—the authors wish to change "$E^{0.01\%}_{260\ nm}$" to "$E^{0.1\%}_{260\ nm}$."

Page 847, first column, under "*Note added in proof*" the authors wish to change:

line 3—to make "volunteer soybean plants" read "hoary tick clover, Desmodium canescens (L.) DC."; and

line 7—to make "soybeans" read "*D. canescens.*"

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