Two-Dimensional Gel Electrophoresis of Proteins

Methods and Applications

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METHODS AND APPLICATIONS

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Eight years have elapsed since O'Farrell first introduced twodimensional gel electrophoresis as a high-resolution technique for the separation of thousands of proteins from a given cell type. Since then there have been many technological advances that have led to improvements in the methods of detecting, quantifying, comparing, characterizing, and storing information contained in the gels. The technique, however, has not been fully standardized, and various laboratories use slightly different gel running conditions and sample preparation procedures. In most fields in which this technique is being applied there is no. consensus as to how gels should be presented (e.g., with respect to the direction of the pH gradient). Despite these minor drawbacks it is timely to publish a volume on two-dimensional gel electrophoresis of proteins, especially because no comprehensive compilation of these techniques or data is available. This book attempts to present an overview of current procedures and to review a few areas of research in which this technique is currently being applied.

The book has been divided into three sections: General Methodology, Applications, and Protein Catalogs. The first chapter in Section I describes the methodology of two-dimensional gel electrophoresis. The following chapters describe computerized two-dimensional gel electrophoresis, silver staining, immunoblotting, and one- and twodimensional peptide mapping. In most cases, a step-by-step guide to the techniques is given so that procedures may be easily repeated. Section II is dedicated mainly to applications of two-dimensional gel electrophoresis. Because of space limitations, it has not been possible to review all fields in which this technique is currently being applied. Rather we have chosen to reflect current research interests by paying special attention to expanding subjects. These include applications in clinical and cancer research, human genetics, protein biosynthesis, and gene expression in plants. Section III presents current protein catalogs of Escherichia coli and human HeLa cells. A catalog of mouse fibroblast

proteins is also presented in Section I.

reface Preface

The book is suitable for young researchers as well as for senior scientists working with a wide variety of problems in molecular and cell biology, basic biochemistry, genetics, and clinical research.

We would like to thank the authors for their readiness to write the chapters and for their punctuality in providing manuscripts. Our gratitude is also due to the staff of Academic Press for their aid and cooperation in the completion of this work.

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J. E. Celis R. Bravo

Contents

Contributors x Preface xv

PART I. Methods and Satellite Techniques

- Two-Dimensional Gel Electrophoresis: A Guide for the Beginner RODRIGO BRAVO
 - I. Introduction 4
 - II. Materials and Solutions 5
 - III. Experimental Procedures 7
 - IV. Hints and Comments 15
 - V. Concluding Remarks References 34
- 2. The QUEST System for Computer-Analyzed
 Two-Dimensional Electrophoresis of Proteins
 JAMES I. GARRELS, JOHN T. FARRAR, AND CARTER B. BURWELL IV
 - I. Introduction 38
 - II. Problems to Be Faced in Development of Computerized Protein Data Bases 7 39
 - III. Strategy for the QUEST System 40
 - IV. The QUEST System As Seen by the User 45
 - V. Program Descriptions 75
 - VI. Perspectives 88 References 90

3.	Detection of Polypeptides in Two-Dimensional Gels Using Silver Staining CARL R. MERRIL AND DAVID GOLDMAN
	I. Introduction 93 II. Staining Procedures 95 III. Mechanisms of Silver Stains 104 IV. Potential and Real Problems in Silver Staining 107 References 108
4.	Applicability of Color Silver Stain (GELCODE® System) to Protein Mapping with Two-Dimensional Gel Electrophoresis D. W. SAMMONS, L. D. ADAMS, T. J. VIDMAR, C. A. HATFIELD, D. H. JONES, P. J. CHUBA, AND S. W. CROOKS
	 I. Introduction 112 II. Variables that Affect Sensitivity and Reproducibility of the Color Silver Stain (GELCODE System) 113 III. Application of Color Silver Staining (GELCODE System) to Two-Dimensional Mapping of Proteins 117 IV. Computerized Data Acquisition of Color-Stained Images: Test for Stoichiometric Staining 122 V. Concluding Remarks 125 References 125
5.	Electrophoretic Transfer of Proteins from Two-Dimensional Gels to Sheets and Their Detection JANEY SYMINGTON
	I. Introduction 128 II. Electrophoretic Transfer of Proteins 131 III. Probing the Transfer 146 IV. Removal of Probes 153 V. Examples and Applications of Protein Transfer Analysis 155 VI. Concluding Remarks 162

6. Correlation between Mouse and Human Two-Dimensional Gel Patterns: Peptide Mapping of Proteins Extracted from Two-Dimensional Gels STEPHEN J. FEY, RODRIGO BRAYO, PETER MOSE LARSEN, AND JULIO E. CELIS

163

- I. Introduction
- II. Methods 170

References

III. Correlation between the Mouse and Human Two-Dimensional Gel Patterns 177

IV. Concluding Remarks References

PART II. Applications of Two-Dimensional Gel Electrophoresis

7. Clinical Applications of Two-Dimensional Gel Electrophoresis

RUSSELL P. TRACY AND DONALD S. YOUNG

daman Cultured Calls and Tamo 401

II. The Electrophoresis System 196

III. Serum and Plasma 211

IV. Urine 220

V. Blood Cells 226

VI. Solid Tissue 230

VII. Other Specimens 233

VIII. Conclusions 234 References

8. Two-Dimensional Gel Electrophoresis for Studies of Inborn Errors of Metabolism DAVID GOLDMAN AND CARL R. MERRIL

I. Introduction

II. Detection of Protein Polymorphism

III. Protein Mutation by Two-Dimensional Gel Electrophoresis

IV. Characteristic Patterns of Polypeptide Modulation

254 255 V. Conclusion References

9. Adapting Two-Dimensional Gel Electrophoresis to the Study of Human Germ-Line Mutation Rates J. V. NEEL, B. B. ROSENBLUM, C. F. SING, M. M. SKOLNICK, S. M. HANASH, AND S. STERNBERG

I. Introduction

II. Some Basic Facts Concerning Mutation III. Why Attempt to Use 2-D Gels to Study Mutation

IV. Some General Considerations in the Design of a Program to Detect

Mutations

V. Selection of Most Appropriate Material for Study

VI. Technical Considerations

	VII. A Statistical Analysis of Factors Influencing Spot Location VIII. Ability of the System to Detect Genetic Variants 274 IX. Nomenclature 282 X. Gel Analysis 288 XI. Steps Necessary to Identify a Putative Mutant 292 XII. Data Management 296 XIII. The Selection of Populations for Study 299 XIV. Concluding Comments 302 References 303
10.	Expression of Cellular Proteins in Normal and Transformed Human Cultured Cells and Tumors: Two-Dimensional Gel Electrophoresis as a Tool to Study Neoplastic Transformation and Cancer JULIO E. CELIS, RODRIGO BRAVO, PETER MOSE LARSEN, STEPHEN J. FEY, JAIME BELLATIN, AND ARIANA CELIS
	I. Introduction 308 II. Transformation-Sensitive Polypeptides in Cultured Epithelial and Fibroblast Human Cells: Work in This Laboratory 311 III. Transformation-Sensitive Polypeptides of Known Identity 323 IV. Variation in the Expression of Mutant Actins in Chemically Transformed Human Diploid Fibroblasts: Actin in General 334 V. Phosphoproteins 337 VI. Polypeptide Synthesis in Human Tumors and Normal Tissue 343 VII. Conclusions 347 References 353
11.	Application of Two-Dimensional Polyacrylamide Gel Electrophoresis to Studies of Mistranslation in Animal and Bacterial Cells JEFFREY W. POLLARD I. Introduction 363 II. Detection of Error-Containing Proteins by Two-Dimensional Polyacrylamide Gel Electrophoresis 364 III. Quantification of the Error Frequency of Protein Synthesis 373 IV. Assessment of the Error Frequencies of Protein Synthesis under Varying Physiological Conditions 379 V. Other Uses of the Two-Dimensional Gel Assay 388 VI. Two Out of Three Reading 390 References 392

12.	Application of Two	-Dimension	al Gel l	Electrop	horesis
	in Studies of Gene	Expression	during	Early P	lant
	Development		_		
	7 P SUNC				

I. Introduction 397 II. Gene Expression during Early Embryogenesis

398

III. Somatic Embryogensis

IV. Gene Expression during Somatic Embryogenesis

V. Coordinate Regulation of Sets of Biochemical Phenotypes VI. Gene Expression in Temperature-Sensitive Cell Lines Impaired in

405 Embryogeny

VII. Gene Expression during Late Embryogeny

VIII. Gene Expression in Cotton Cotyledons

406

406

IX. Gene Expression in Germinating Seeds

407

X. Conclusion References 412

Part III. Protein Catalogs

13. The Protein Catalog of Escherichia coli FREDERICK C. NEIDHARDT AND TERESÅ A. PHILLIPS

I. Introduction 417

II. Identification of Proteins

III. Current E. coli Catalog

IV. Applications in E. coli Research References 442

439

418

14. Catalog of HeLa Cell Proteins RODRIGO BRAVO AND JULIO E. CELIS

I. Introduction

445

II. Two-Dimensional Gel Electrophoretic Separation of HeLa Cell **Proteins**

III. Some Characteristics of HeLa Cell Proteins 447 474

IV. Transformation-Sensitive Polypeptides V. Conclusions 474 References 475

Index

477

PART I Methods and Satellite Techniques

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Methods and Satellite Techniques

CHAPTER 1

Two-Dimensional Gel Electrophoresis: A Guide for the Beginner seem out at GED and monopoleous to seep a determine in the stat discretizion and slab sel electrophopesis under dena

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I.	Introduction.	1
II.	Materials and Solutions.	5
	A. Materials.	5
411	B. Stock Solutions and Buffers for the First Dimension	
	C. Stock Solutions and Buffers for the Second Dimension	6
III.	Experimental Procedures	. 7
		7
	A. Labeling of Cells with [35S]Methionine. B. Sample Preparation. C. Determination of Trichloroacetic Acid (TCA)-Precipitable.	7
	C. Determination of Trichloroacetic Acid (TCA)-Precipitable	
	Radioactivity in Samples.	- 8
	D. Procedures for the First Dimension	. 8
	E. Procedures for the Second Dimension	11
	F. Fluorography.	13
	E. Procedures for the Second Dimension. F. Fluorography. G. Quantitation of Spots.	15
IV.	Hints and Comments.	15
	A. Effect of Storage or Heating on the Sample.	15
	B. Loading Capacity	17
	C. A Simple Device for Casting the First Dimension Gels	17
	D. Equilibration Time of the First Dimension	18
	E. Simplifying the Assembly and Casting of the Slab Gels	18
	F. Fluorography. 17. 17. A DARWING THE LOT ON BURNE SHOP	19
	G. Sensitivity of Detection.	21
	H. Percentage of the Initially Applied Radioactivity Recovered	
	in the Second Dimension	22
	I Comparison of Complex Protein Mixtures.	24
	J. The Use of Coordinates and Markers	24
	K. A Few Common Problems in Two-Dimensional Gels	28
V.	Concluding Remarks.	34
	References	34

J. Introduction

The two-dimensional gel electrophoresis system that gives the best resolution for separating a complex mixture of proteins combines the techniques of isoelectrofocusing (IEF) in the presence of urea and a neutral detergent in the first dimension and slab gel electrophoresis under denaturing conditions using sodium dodecyl sulfate (SDS) in the second dimension (Klose, 1975; O'Farrell, 1975; Scheele, 1975; Iborra and Buhler, 1976). The separation makes use of two independent protein characteristics: one is the charge, which is reflected by the isoelectric point (pl), and the other is the molecular weight, which determines the mobility of the SDS-protein complexes in polyacrylamide gels (Weber and Osborn, 1969).

O'Farrell (1975) first demonstrated the great potential of such a technique when using isotopically labeled proteins by resolving more than a thousand polypeptides and detecting components as minor as 0.001% or less of the total cellular protein. This method has been extensively applied in resolving proteins from both prokaryotic and eukaryotic organisms and can be used for the separation of many types of cellular proteins [for references, see special issue of Clinical Chemistry (Vol. 28, No. 4, Part II, pp. 737–1092, 1982) and other chapters in this volume]. Unfortunately, basic proteins are not well separated in the IEF/SDS system, because in general they enter the IEF gel poorly. Even when more basic ampholytes are included, the extension of the pH gradient is very small, because in the presence of urea the basic region of the gradient is unstable. Furthermore, the few basic proteins that enter the IEF gel under these conditions alway; produce streaks. However, it is possible to overcome these problems using a nonequilibrium pH gradient electrophoresis (NEPHGE) in the first dimension as described by O'Farrell et al. (1977). The main differences between NEPHGE and IEF are that in the former the samples are applied to in the acidic side of the gel and the voltage x time product is smaller than it is in IEF. Under such conditions the pH gradient does not reach full equilibrium. As a result the proteins are not totally focused at their isoelectric point as they are in IEF gels. Nevertheless, most proteins in NEPHGE gels are separated according to their charge differences.

In general, special, not easily attainable apparatus is needed to improve the resolution of the technique, making an initial start difficult for the beginner (Garrels and Gibson, 1976; Garrels, 1979; N. G. Anderson and N. L. Anderson, 1978; N. L. Anderson and N. G. Anderson, 1978). Nevertheless, it is the author's experience that many studies can be done using the standard equipment found in any laboratory. However,