Preface

Identification of the chromosomal coordinates of every human gene is now a realistic goal. The technical advances in nucleic acid biochemistry, enzymology, biophysics, biostatistics, and instrumentation have brought us to the threshold of this new era in the biological sciences. It is anticipated that the benefits of gene-mapping technology and information will extend beyond human medicine to agriculture and other life sciences. The mission of this book is to explain current strategies for mapping genomes of higher organisms and also to explore applications of gene mapping to agriculturally important species of plants and animals. We hope that this book will satisfy those who seek information on state-of-the-art strategies and techniques for gene-mapping research and its applications.

The first section includes four chapters by leading investigators on strategies for gene mapping in plants and animals. Womack gives an overview of mapping strategies currently in use and presents a rationale for the comparative gene-mapping approach. While the basic objective of comparative mapping is to relate chromosomal evolution to speciation, the high level of conservation of linkage relationships across mam-

malian species allows projection of mapping data from one species to another. The following chapter, by Soller, discusses a theoretical framework and some statistical approaches for mapping genes affecting quantitative traits (QTL), with particular emphasis on livestock populations. The chapter by Hetzel reviews the advantages of establishing a common set of "reference families" for linkage mapping in humans and other species. This particularly useful section explores the power of different family structures for linkage analysis. In the final chapter of this section, Nelson reviews methods for "reverse genetics," i.e., how to go from a genetic marker for a disease gene to localizing it on a chromosome and the eventual cloning and characterization of the genetic lesion. Approaches used for physically isolating the genes responsible for Duchenne muscular dystrophy and cystic fibrosis are contrasted, and new strategies that will employ yeast artificial chromosomes and the polymerase chain reaction are presented.

The chapters in the next section explore in further detail the experimental techniques used for genetic and physical mapping of genes. DNA-sequencing strategies and methods are not considered in this section. In the first chapter, the development of hypervariable genetic markers and their uses in experimental genetics, with particular emphasis given to QTL mapping in domestic animals, is outlined by Georges. Chrisman et al. give a detailed review of in situ hybridization techniques, with a description of the new and powerful methods for high-resolution chromosome banding. Bensaid et al. discuss physical mapping by pulsed-field gel electrophoresis. Included in this chapter is a description of one of the first applications of this technique to a domestic animal species—the physical mapping of genes within the major histocompatibility complex of cattle. The chapter by Fries et al. explores variations of in situ hybridization for monitoring the spacing of markers in species with developing gene maps. Next, Lathrop et al. introduce the concepts and methodologies for statistical evaluation of linkage mapping data, with consideration given to qualitative and quantitative phenotypes.

Current and potential applications of gene mapping are presented next. Beckmann reviews mapping problems and projects with plants, and Watkins discusses identification and use of restriction fragment length polymorphism (RFLP) in the development of human chromo-

some linkage maps. As a window to the future in animal genetics, Kessler and Schuler present a detailed summary of their studies on the organization and physiological importance of the bovine prolactin gene family. Lewin et al. review the mapping of genes that influence resistance to infectious diseases in humans and domestic animals and discuss experimental designs and strategies for detection and utilization of such genes in livestock species. The final chapter, by Weller and Fernando, describes methodological approaches to achieve the ultimate goal of gene mapping in species of agricultural importance: the improvement of animals through the utilization of genetic marker information. Such methods for "marker-assisted selection" incorporate molecular genetic information into classical animal breeding schemes, thus permitting more accurate selection that is based on genotype as well as phenotype.

We would like to acknowledge the scholarly efforts of our contributors, who have made our task stimulating and rewarding by providing timely and creative articles. Our appreciation also goes to Helen Gawthorp for her assistance in the preparation of this book. The support of our families, colleagues, and students in this effort is gratefully acknowledged.

This book is dedicated to the memory of Dr. C. Larry Chrisman.

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