
Preface

In recent years, there has been phenomenal progress in the understanding of the genetic architecture of normal and disease-related complex phenotypes. The progress has been fueled by an explosion of research activities related to the Human Genome Project and subsequent sequencing projects, and the nonhuman primate comprehensive sequencing projects. Advances in molecular genetics, statistical genetics, medical genetics, and bioinformatics have accompanied this progress.

Tracing its roots back to the laws of inheritance established by Mendel, which continue to be the basic tenets underlying modern genetics, the field of genetics has expanded tremendously and has richly diversified over the years. Gene mapping efforts and genomic research on humans and nonhuman primates have generated an enormous amount of information relevant for studies of evolution, phylogenetics, human genetics, anthropological genetics, and for biomedical research. Elucidation of gene function, expression, and regulation and of genetic variation and conservation among primate species has exciting potential for informing research in the areas of biology, evolution, population genetics, anthropological genetics, and biomedicine. The huge increase in the amount of available genomic information and advances in the tools available to analyze that data have already had a tremendous impact on disciplines such as evolutionary biology, bioinformatics, genetic epidemiology, medicine, pharmacogenetics, pharmacogenomics, and anthropology.

This volume is an attempt to provide researchers and academicians with a review of advanced methodologies and applications in gene mapping and genomics of humans and nonhuman primates, with an emphasis on genetics of complex phenotypes and diseases. As a part of the “Genome Mapping and Genomics in Animals” series (Dr. C. Kole, Editor), this volume is designed to illustrate ongoing research activities related to gene mapping and genomics in human and nonhuman primates. The topic of this volume is broad and a full coverage of such a huge area of research would be impossible. Therefore, we limited the volume to 16 chapters that illustrate the amazing changes in genomic studies that have occurred since the Human Genome Project. From the initiation and expansion of the Human Genome Project to revolutionary next generation sequencing approaches, we have seen dramatic improvement in the understanding of the genetic architecture of complex phenotypes in human and nonhuman primates.

This volume constitutes an overview of the impact of the genomic revolution on research related to human and nonhuman primate populations. It also reviews the state-of-the-science with respect to the molecular, statistical genetics, and genetic epidemiologic techniques that are used to dissect the genetic architecture of normal and disease-related complex phenotypes using data from human and nonhuman primates. We present examples of successful applications of genomic methods to traits of particular interest in biomedical research and evolutionary biology, and provide discussions of future directions in human and nonhuman primate genomics.

Since genetic investigation of complex phenotypes is by nature multidisciplinary, efforts were made to provide readers with review papers which illustrate the full range of methodological and analytical approaches being applied to human and nonhuman primate population data sets. Examples and applications were drawn from diverse areas including evolutionary genetics, population structure, genetic epidemiology, transcriptomics, copy number variation, molecular ecology, comparative genomics, and gene mapping for phenotypes related to behavior, skeletal biology, and cardio-metabolic disease in human and nonhuman primate populations.

We are in the midst of an exciting scientific era with constantly changing technology revolutionizing genomic research approaches over and over again. The advances will ensure continued interest in explorations of genomics and other “omics” approaches as they relate to normal variation and disease-related traits in human and nonhuman primate populations. Progress in gene mapping and genomic sequencing will add further momentum to progress in comparative genomics, evolutionary genomics, and biomedical research as it corresponds to disease prevention and treatment, pharmacogenomics, and personalized medicine.

We are grateful to the contributors to this volume who have prepared comprehensive and informative reviews of advanced, complex genomics-related topics. We thank Drs. Vidya S. Farook, Sobha Puppala, Geetha Chittoor, and Laura Cox for reviewing one or more chapters of this volume. The editors also express their gratitude to Ms. Maria Messenger whose expert skills in proofreading and formatting greatly improved the quality of this volume.

Ravindranath Duggirala
Laura Almasy
Sarah Williams-Blangero
Solomon F.D. Paul
Chittaranjan Kole

Genome Mapping and Genomics in Human and
Non-Human Primates

Duggirala, R.; Almasy, L.; Williams-Blangero, S.; Paul,
S.F.D.; Koe, C. (Eds.)

2015, VIII, 305 p. 39 illus., 10 illus. in color., Hardcover

ISBN: 978-3-662-46305-5