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Post-Genome Biology of Primates

 Springer

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Cover illustration:

Front cover: *Top:* An adult male white-handed gibbon (*Hylobates lar*) at the Nakhon Ratchasima (Khorat) Zoo, Thailand. Photo by Hirohisa Hirai. *Center left:* Hybridization of a human bacterial artificial chromosome shows split signals (*red*) on two chromosomes of the white-cheeked gibbon, revealing an evolutionary breakpoint. Photo by Roscoe Stanyon. *Center middle:* A proboscis monkey metaphase counterstained in *blue* and hybridized by human chromosome paints: 1 in *green*, 3 in *yellow*, and 19 in *red*. Photo by Roscoe Stanyon. *Center right:* Screenshot of an alignment of short nucleotide reads produced by next-generation sequencing (NGS). Photo by Yasuhiro Go.

Back cover: Grooming by Japanese macaques (*Macaca fuscata fuscata*) at the Primate Research Institute, Kyoto University, Japan. Photo by Hirohisa Hirai.

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Foreword

It is a great pleasure and honor to be asked to write a foreword to this volume, which addresses the *Post-Genome Biology of Primates*. It is hard to believe that just over 10 years ago there was a raging debate as to which primate genome should be selected for sequencing next, after the human, mouse, and rat genomes had been completed. The chimpanzee eventually won out, based on feedback from the academic community, but a strong minority believed that a better studied and more experimentally tractable animal such as the rhesus monkey or baboon should have had priority. In hindsight, all these arguments turned out to be meaningless, as the pace of genome sequencing increased so rapidly and the costs fell so dramatically that many primate genomes have been partially or completely sequenced within the past decade.

There is still a long way to go before one can say that we have covered all genomes that would be worth sequencing (one even could argue that all of them are), and population-level genomic information is still very limited for most primate genomes. But I think it is safe to say we are now indeed in an era where the genomic sequences that are already available can be used to explicate the genetic and genomic contributions toward primate evolution and phenotype. Indeed, we are now in a situation in which it is the phenotypic information that has become rate limiting. In this volume, the editors have brought together an excellent collection of papers covering a wide variety of topics relevant to primate genomes, including evolution, genome structure, chromosome genomics, bioinformatics, and functions. Although it is impossible to do justice to all possible topics in this huge area of research, this book covers many that should be of interest, not only to those who study primate and primate genomes, but also for those wishing to understand human origins (“anthropogeny”) and the remarkable phenotypic diversity of primates. Also included are somewhat more theoretical papers about issues of interest to other readers.

This valuable resource will undoubtedly catalyze further sequencing of primate genomes as well as studies of primate phenotypes. Thus, although we are in a “Post-Genome Era,” we will also continue to be in the “Genome Era” for some time yet. Meanwhile, please enjoy reading this timely and informative volume.

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