

Preface to the Series

The deciphering of the sequence of a gene for the first time, the gene for bacteriophage MS2 coat protein to be specific, by Walter Fiers and his coworkers in 1972 marked the beginning of a new era in genetics, popularly known as the genomics era. This was followed by the complete nucleotide sequence of the same bacteriophage in 1976 by the same group; DNA sequencing of another bacteriophage (Φ -X174) in 1977 by Fred Sanger, Walter Gilbert, and Allan Maxam, working independently; and first use of any DNA marker in gene mapping in 1980 for the human system by David Botstein. These landmark discoveries were immediately embraced by the life science community and were followed by an array of elegant experiments leading to the development of several novel concepts, tools, and strategies for elucidation of genes and genomes of living organisms of academic and economic interests to mankind.

The last two decades of the twentieth century witnessed the invention of the polymerase chain reaction; several types of molecular markers; techniques of cloning large DNA segments in artificial chromosomes; approaches to isolate and characterize genes; and tools for high-throughput sequencing, to name just a few. Another noteworthy development had been the formulation of different computer software to analyze the huge amount of data generated by genome mapping experiments, and above all deployment of information technology to store, search, and utilize enormous amounts of data particularly of cloned genes, transcripts, ESTs, proteins, and metabolites. This sweet and swift marriage of biology and information technology gave birth to bioinformatics and the new “omics” disciplines such as genomics, transcriptomics, proteomics, and metabolomics.

The tide of genome mapping and genomics flooded all phyla of the animal kingdom and all taxa of the plant kingdom and most obviously the prokaryotes. In the animal systems, we already had the gene sequence for the CFTR protein in humans in 1989; genome sequence of the model organism *Caenorhabditis elegans* in 1998; genetic maps of many higher animals with map positions of genes and gene-clusters during the nineties. We also happily witnessed the beginning of genome sequencing projects of three domestic animals (cow, dog, and horse) and poultry in 1993. All these achievements and endeavors culminated in the whole-genome sequence of the fruit-fly *Drosophila*, the garden pea of the animal system, in 2000 declaring a successful and pleasant ending of the genome science efforts of the twentieth century. The new millennium in 2001 started with the publication of the draft sequence of the human genome on February 15th by The International Human Genome Mapping Consortium and on February 16th by The Celera Genomics Sequencing Team.

A flurry of new concepts and tools in the first few years of the first decade of the twenty-first century has enriched the subject of genomics and the field has broadened to include the young and fast-growing disciplines of structural genomics, functional genomics, comparative genomics, evolutionary genomics, and nutraceutical genomics, to name just a few. We now have more, faster, cheaper, and cleverer mapping and sequencing strategies, association mapping and the 454 for example; several tools, such as microarrays and cDNA-AFLP to

isolate hundreds of known and unknown genes within a short period, elegantly assisted by transcript-profiling and metabolic-profiling; identifying new genes from the knowledge-base of homologous genomes; and precise depiction of the road map of evolution of human and other members of the animal kingdom and their phylogenetic relationships with members of other species or genera. Within less than a decade of the deciphering of the first complete genome sequence for an animal species in 1998, we have complete sequences of some seventeen species of the animal kingdom including nematodes (2), arthropods (4), domestic animals and poultry (2), marsupial (1), wild animals (2), aquatic animals (4), human (1), and non-human primate (1). Many more genome mapping projects are progressing rapidly and their results are expected to be published soon.

The list of achievements in the fields of genome mapping and genomics in human and other members of the animal kingdom is enormous. It is also true that in today's world, in the global village of the new millennium, we have access to almost all information regarding the initiation, progress, and completion of all endeavors of animal genome sciences and can enrich our knowledge of the concepts, strategies, tools, and outcomes of the efforts being made in animal genome mapping and genomics. However, all this information is dispersed over the pages of periodicals, reviews on particular types of animals or their specific groups in hard copy versions, and also in electronic sources at innumerable links of web pages for research articles, reports, and databases. But we believe that there should be a single compilation, in both hard copy and electronic versions, embodying the information on the work already done and to be done in the fields of genome mapping and genomics of all members of the animal kingdom that are of diverse interests to mankind: academic, health, company, or environment.

We, therefore, planned for this series on Genome Mapping and Genomics in Animals with five book volumes dedicated to Arthropods; Fishes and Aquatic Animals; Domestic Animals; Laboratory Animals; and Human and Non-Human Primates. We have included chapters on the species for which substantial results have been obtained so far. Genomes of many of these species have been sequenced or are awaiting completion of sequencing soon. Overview on the contents of these volumes will be presented in the prefaces of the individual volumes.

It is an amazingly interesting and perplexing truth that only four nucleotides producing only twenty amino acids in their triplet combination could create anywhere between five to thirty million species of living organisms on the earth. An estimated number of about a half million vertebrate animal species have been described so far! Genomes of the few animal species from this enormous list that we know today are also too diverse to elucidate. It is therefore daring to edit a series on depiction of the diverse genomes we are presenting in over sixty chapters in the five volumes. Seven globally celebrated scientists with knowledge and expertise on different groups of animal systems, and human and non-human primates provided me with the inspiration and encouragement to undertake the job of the series editor. Wayne (Wayne B. Hunter), Tom (Thomas D. Kocher), Noelle (Noelle E. Cockett), Paul (Paul Denny), Ravi (Ravindranath Duggirala), Tony (Anthony G. Comuzzie), and Sarah (Sarah Williams-Blangero) were always available for consultations and clarifications on any aspect while editing the manuscripts of this series. During working on this series, I have been a student first, a scientist second, and an editor third and last, with the mission to present a comprehensive compilation of animal genome mapping and genomics to the students, scientists, and industries currently involved and to be involved in the study and practice of animal genome sciences.

I express my thanks and gratitude as a humble science worker to these seven volume editors for giving me an opportunity to have an enriching and pleasant view of the wide canvas of animal genome mapping and genomics. I also extend my thanks and gratitude to all the scientists who have generously collaborated with their elegant and lucid reviews on the rationale, concepts, methodologies, achievements, and future prospects of the particular systems they are working on, and for the subtle touches of their own experiences and philosophies.

As expected, the editing jobs of this series comprised communication with the volume editors, authors, and publishers; maintenance of the files in hard and soft copies; regular internet searches for verification of facts and databases; and above all maintenance of an environment to practice and enjoy science. My wife Phullara, our son Sourav, and our daughter Devleena were always with me on my travels as a small science worker on a long road of “miles to go before I sleep,” not only for the successful completion of this series but also in all my efforts for teaching, research, and extension wherever I worked and stayed in my life.

We have already completed a seven-volume series on Genome Mapping and Molecular Breeding in Plants with Springer that has been very popular among students, scientists, and industries. We are also working on a series on Genome Mapping and Genomics in Microbes with Springer. It was, is, and will be enriching and entertaining to work with the experienced and wonderful people involved in the production of this series, including Sabine (Dr. S. Schwarz) and Jutta (Dr. J. Lindenborn) among many from the Springer family. I record my thanks and gratitude to them, here (and also submit in the databanks for future retrieval) for all their timely co-operation and advice when publishing these volumes.

I trust and believe that we must have missed deliberations on many significant animal species and left many mistakes on the pages of these volumes. All these lapses are surely mine, and all the credits must go to the volume editors, the authors, and the publisher. In the future these errors will be rectified on receipt of suggestions from the readers, and also there will be further improvement of the contents and general set-up of the volumes of this series.

Clemson
January 10, 2008

Chittaranjan Kole

Preface to the Volume

Over the past century, humans have used an expanding knowledge of genetics to improve the functionality and wellbeing of animals. The field of quantitative genetics has led to the selection and breeding of domesticated animals possessing superior genes for desirable traits. Enhanced animal selection, as well as a clearer understanding of the genes and genetic regulation underlying traits, is now possible through the study of genomics.

The nine chapters in this volume focus on genome mapping and genomics research that has been conducted in domesticated and farm species. Topics include the development of genome maps, descriptions of available genomic resources, phylogenetic analyses, domestication patterns, and genetic control of traits. While each chapter serves as a stand-alone description of genomics for that particular species, when read as a whole, the breadth of the research in domesticated and farm species is remarkable, particularly in the light of the limited funding, resources, and personnel as compared to the investment on humans and laboratory species. These limitations have resulted in the development of collaborations and consortiums that cross the globe. Clearly, the pooling of funding and expertise has expanded genomic resources for these species, and allowed prioritization of needs through a collective and iterative process.

While not all domesticated and farm species are included in the volume, the ones that are described here allow a comparison of the outcomes and approaches that were used across the various species. To encapsulate, the amount of genomics research that has occurred to date differs dramatically across the species. For example, there are only a limited number of molecular markers and a rudimentary genome map in cervids and water buffalo while full genome sequences are publicly available for cattle, chickens and dogs. And while there are limited outcomes from the research in some species, the impact of genomics research in livestock and domestic species has resulted in critical information. Direct outcomes have been the identification of genetic regions and in some cases, the causative mutation, that control a spectrum of traits including fertility, reproduction, growth rate and efficiency, milk production, carcass quality and composition, fitness, immune function, and disease traits. This progress is remarkable given that it has only been since the early 1990s, when genome linkage maps containing molecular markers were developed, that genome-wide studies for economic trait loci became feasible.

Comparative genomics is a critical component in the advancement of genomics for livestock and domesticated species. Anchoring the genome of one species to another has allowed an exchange of information and resources, particularly important when one of the species has limitations in funding and researchers, or is at an earlier stage in the discovery process. In addition to leveraging resources across species, an equally important outcome of the comparative genomic efforts is the comparison of locus order in mammalian species, providing additional information for understanding chromosomal evolution.

As mentioned, whole genome sequences for several species are now available or soon to be available, including cattle, dogs, chickens, horses and swine. Certainly

a fully sequenced genome will advance the progress of research in every species but the utilization and impact of genomics resources is tempered by the number of active scientists working on that particular species. The economic impact of a species is also a major determinant of the emphasis placed on genomics resources. Several farm species, such as sheep and rabbits, are now used as models for biomedical studies, which has increased attention on securing genomics information.

It is important to note that the genomics research being conducted on these species is not static. With each passing week, more information is added. Therefore, the chapters included in this volume serve as a “snapshot” of the existing information available at the time that the chapter was written. Each author has included a section that highlights areas of future work and needs.

It has been a pleasure to work with the 23 authors who have contributed the chapters in this volume. These authors were invited to participate because they are experts within their field of study. As expected, they have added their own style and interpretation to the work conducted in their assigned species. The authors are affiliated with institutions from around the world, highlighting the global impact of the work being conducted. We appreciate the hard work and perseverance of the authors in the preparation of their chapters and contribution to the volume.

Logan, UT, USA
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