

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 neutraceutical 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 six book volumes dedicated to Food and Fiber Animals; Wildlife and Companion Animals; Fishes and Aquatic Animals; Arthropods; 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 six 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. Noelle (Noelle E. Cockett), Paul (Paul Denny), Wayne (Wayne B. Hunter), Tom (Thomas D. Kocher), 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. While 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), Jutta (Dr. J. Lindenborn), and Cornelia (Mrs. C. Gründer), 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
September 5, 2007

Chittaranjan Kole

Preface to the Volume

The field of genomics continues to provide new and inspiring answers to the most intriguing questions about life on earth and beyond. This influence will most likely continue even as humans turn toward the colonization of space. Genomics and bioinformatics have accelerated the rate of discovery in all fields of science, but even more so in those fields related to entomology. Arthropods, such as insects, greatly impact our world, yet few really understand how insects affect our lives. Most have seen the pollinators, bees and butterflies, and can see their roles in the production of fruits, food, and fiber crops. Few have seen the benefits we all receive when the parasitoid lays its eggs inside of a pest insect. The numerous, invisible, and never-ceasing interactions of insects and arthropods entwined with their host plants, pathogens, and as food for other animals within the chain of life are as common and as necessary as the air we breathe.

Insects and arthropods contribute hundreds of billions of dollars to our well-being. However, they also cost us hundreds of millions of dollars each year in lost yields, structural damage, and in efforts to manage them and/or in reducing the diseases they spread. Estimates suggest that for every *single dollar* spent in biological control of insect pests the general public receive a *\$5 return* or more in benefits to their quality of life. When you factor in the other benefits that agricultural research has produced, which include more nutritious foods, reduced use of insecticides, environmentally safer herbicides and pesticides, development of new products in fiber, food, feed, and products that impact human health, one can see that this has been and will continue to be one of the best investments to maintain the growth and welfare of our world. The combination of biology, genomics, and computers in bioinformatics has changed the face of entomology forever. The wonder of these advances have yet to be fully realized, but are only a small jump from “thought” to “understanding” as we continue to explore all the possibilities. *Genomics* has opened a new gateway to examine existing and emerging questions concerning arthropods. While insects as a group make up more species walking on the earth than all other animal groups combined, very few species have had any genomic data produced. We are still only at the beginning in our quest to understand insects and other arthropods.

The completion of the *Drosophila* genome initially demonstrated the broad applications of using an insect as a model system to conduct functional genomics studies, thereby elucidating gene functions which were also found to be present in many non-dipteran species. Now several insect genomes have been completely sequenced such as of fruit flies and mosquitoes, the honey bee, the flour beetle, the silkworm, the pea aphid, and a parasitic wasp, with others scheduled to follow: a medfly, the hemipteran *Rhodnius prolixus*, a bedbug, a body louse, and two-spotted spider mites, as well as other agricultural pests such as whiteflies. These studies on the evolution and phylogeny of insects will continue to advance our understanding of their similarities and differences, which was not possible using traditional methods.

The insects covered in this volume are only the early stages of some of the projects that are being pursued in genomics of insects, ticks, and other arthropods. In the preparation of this volume we wish to express our gratitude to all of the authors for their contributions and expert cooperation. The experience allowed us to grow professionally and it was a pleasure to work with Dr. Jutta Lindenborn, Life Science Editorial Springer. We also wish to acknowledge and thank many publishers and authors for their generosity and goodwill to permit authors to gain permission of previously published works. We wish to acknowledge and thank Dr. Xiomara Sinisterra for her patience and assistance in many levels in the completion of this project.

Clemson and Fort Pierce
September 5, 2007

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