Preface

As a result of the development of technologies allowing access to, and analysis of, the complete genetic material of an organism, a new field of study—genomics—was established in the late twentieth century. It has flowered to encompass many different taxa, but the laboratory animals in this volume are of particular interest, because of their role as models for human disease and biology (Aitman et al. 2011). These model organisms are disparate and their adoption for scientific study was typically for pragmatic reasons, e.g., they are relatively small, have short life cycles for their particular taxonomic class, and breed well in the laboratory environment. In many cases, these organisms were not selected as "models," but because they were easy to maintain in a laboratory and so were amenable to academic study. This has meant that the chapters herein are disparate, yet there are many common themes.

The sea urchin has played a central role in developmental biology, a field in which the other invertebrates described in this volume, the nematode worm (*C. elegans*) and the fruitfly (*Drosophila*), have also been important. Amongst the vertebrates, the frog, *Xenopus*, and the mouse can also make excellent claims for critical roles in the study of development. The nematode worm, *C. elegans*, is perhaps the best characterized of all the multicellular eukaryotic organisms, with a completely described cell lineage from egg to adult. Furthermore, the worm was the first multicellular organism for which there was a finished genome sequence. Much of twentieth century genetics could be seen as a series of footnotes to the genetics of *Drosophila*, so we make no excuse for the detail and content of this chapter. One of the marvelous things about editing this volume was the amount that we learnt—we were not aware that Darwin had studied ascidians (sea squirts) and considered them important in understanding chordate evolution. Another surprise was that William E. Castle of Harvard University has good claim to be considered as the founding father of the genetics and genomics of both *Drosophila* and the laboratory mouse. But we digress—the fishes are well represented in this volume, covering the pufferfishes, fugu and *Tetraodon*, with their amazingly compact genomes and the medaka, a freshwater fish. The large size of oocytes from the frog, *Xenopus*, and the ease of obtaining large numbers of oocytes has enabled their use in studies of a wide range of molecular, cellular, and developmental processes. The mouse was the second mammal for which a draft genome sequence was assembled and, taking a historical viewpoint, almost became the subject of Mendel's genetic studies,

only to be replaced by the pea-plant at the suggestion of his Abbot (Paigen 2003). Rats are not simply "larger mice," but may be qualitatively a more relevant or faithful model of disease in humans, in some cases.

Two model animals missing from this volume have been covered in other volumes in the Genome Mapping and Genomics in Animals series: zebrafish—reviewed in another volume as a cyprinid fish (Kocher and Kole 2008) and the chicken as a domestic animal (Cockett and Kole 2009).

In future, the new high-throughput technologies, e.g., ultra-deep sequencing, will mean that the distinction between an established "laboratory" animal and almost any wild species will start to become less clear—complete genome sequences and transcriptomes can be derived quickly and then annotated using systems derived from the public genome browsers, such as Ensembl. Assisted reproductive technologies can also be adapted for many species, allowing biological experimentation that might otherwise be difficult. However, the accumulated literature, experimental techniques, and the expertise of the scientists studying the classical laboratory animal species mean that many will remain the foci of biomedical research for years to come.

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