PREFACE

Understanding the history of life on Earth has become invigorated by technological advances in molecular evolution, in fossil inference, and in geology and by comparative descriptions of anatomy, physiology, and behavior. The earliest mammals were the morganucodontids, mouse-sized insectivores that scurried around in the shadows of dinosaurs across the Triassic and Jurassic epochs. With articulated jaws and squared forelimbs adapted for running, the tiny shrewish creatures never got much bigger than a cat since their first appearance in the fossil record 210 million years ago (mya) until an asteroid or comet blackened Earth 65 mya and eliminated the giant dinosaurs forever. By the early Eocene (55 mya), recognizable adaptations to the world ecological niches were appearing in precursors to the 26 orders of modern mammals.

Recently, sophisticated phylogenetic analyses of large deoxyribonucleic acid (DNA) sequence datasets across mammalian species, interpreted in the context of paleontological remains and tectonic movements, have revealed an evolutionary hierarchy we call the mammalian radiations (see end papers). The timing and rationale for taxon divergence, for species isolation, and for adaptation remain imprecise, but genomic tools have already exceeded modest expectations in revealing secrets of our ancestors. Today, around 4700 species of mammals survive on Earth. They range from the smallest 1.5-g Kitti's hog-nosed bat to the 190,000-kg blue whale, the largest species to ever live. They reflect as diverse an assemblage of anatomic, behavioral, and physiological adaptation as the world has ever seen. The assembly instructions, retained for each species by natural selection across a 200-million-year history, are preserved in modern genomes. The field of comparative genomics is providing a new opportunity to annotate the distinctions, divergence, and genetic occurrences that have sculptured modern genomes. (O'Brien et al., 1999; Murphy et al., 2005)

The rich diversity of living mammals is aptly chronicled in several outstanding monographs that describe adaptive specialization and taxonomic classification (Ewer, 1973; Eisenberg, 1981; Novak, 1999; Wilson and Reeder, 1993; 2005; MacDonald, 2001). Further, the paleontological literature reveals *the anatomic transitions that characterize each lineage of mammal evolution* (McKenna and Bell, 1997; Savage and Russell, 1993). The genetic scripts for each of evolution's creations are encoded in the chromosomes of living species, organized in genomes containing nearly 3 billion nucleotide letters as instructions to make a manatee, a naked mole rat, a vampire bat, a lion, an elephant, or a cognitive human being. We present in this atlas a sampling of 815 species karyotypes, most (but not all) G-banded, providing a view of chromosomal bar codes of homologous segments among related species. The karyotype photographs provide a starting point for genomic inquiry, a platform for genetic discovery.

This *Atlas of Mammalian Chromosomes* is a sequel to the pioneering volumes edited by T. C. Hsu (now deceased) and Kurt Benirschke (author of the foreword). In 10 editions, unbanded karyotypes for hundreds of species were archived. Here we extend that beginning with the best karyotypes available for 815 species. We asked experts on cytogenetics for each order of mammals to compose a short overview on the biology, genetics, cytogenetic accomplishments, and analyses for each order. For each species we present the best karyotype available, the common and Latin name for the species, the published citation, and contributing author(s). The collection offers in one place an unabridged description of mammalian cytogenetics from a half century of work by hundreds of cytogenetic artisans.

The Human Genome Project, an international collaboration to determine the full DNA sequence of a human genome, published a near-finished version in October 2004 (International Human Genome Sequencing Consortium, 2004). The dense genome-mapping annotation and redundant sequencing immediately elevated the human genome as the primary mammal for genomic studies. The new human sequence showed our genomes to be 2.85 billion base pairs in length, around 2% protein coding, around 50% repetitive elements, and containing 20,000–25,000 protein-coding genes. Full genome sequences of other mammalian species recently sequenced (mouse, rat, bovine, dog) showed that other mammals had very similar composition statistics and gene order, affirming the indisputable unity of all living mammals. Our genomes all descend from an ancient 200-million-year-old ancestor, the tiny insectivore of the Triassic.

Comparative genomics of mammals is a fast-moving new field empowered by the vastness of genome information, by powerful computer routines developed to quantify DNA divergence, and by a potential to unlock the hidden secrets in the human and related species genomes. Comparative genomics seeks two broad goals: annotation of the mysterious operatives of the human genome and unraveling the changes and adaptations that led to mammalian species diversification. These are heady issues and only very recently have geneticists actually had the opportunity, data, and tools to pursue such profound genetic challenges. Chromosome identification is a century old, while G-banding and homology segment identification first appeared in the 1970s. Chromosome painting (also called Zoo-FISH, for fluorescent in situ hybridization) has allowed the characterization of homologous chromosome segments virtually by direct observation. Over 50 species of mammals have been "painted" with flow-sorted human and other mammalian chromosome libraries as the discipline of phylogenomics (the study of chromosome exchanges that characterize mammalian ordinal lineages) is beginning to bear fruit (O'Brien et al., 1999; VandeBerg and Marshall Graves, 1999).

The ultimate comparative genomics tool, an assembled whole genome sequence, has been proposed and developed for 10 species of mammals: human, chimpanzee, orangutan, macaque, mouse, rat, cow, dog, opossum, and platypus (www.nhgri.nih.gov). Whole-genome sequence coverage has been funded for eight species in order to capture the evolutionary diversity of eight additional mammal species: African savanna elephant, lesser hedgehog tenrec, nine-banded armadillo, rabbit, domestic cat, hedgehog, guinea pig, and European common shrew. Before long a new mammal genome will appear every month or even each week. A deluge of genomic sequence data has geneticists of all specialties anticipating the assembly, comparison, analysis, and mining of mammalian genomes. The atlas presented here is an early salvo in the compiling of genomic information. Our understanding of the details of species formation of developmental specialization, of the exact targets of natural selection, of life's darkest secrets is one step closer than before.

STEPHEN J. O'BRIEN
JOAN C. MENNINGER
WILLIAM G. NASH

Frederick, Maryland
February 2006