

BOOK REVIEW

Molecular cytogenetic evolution of mammals

Chromosomal evolution

Evolutionary Dynamics of Mammalian Karyotypes.

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This volume reviews and synthesizes the cytogenetic results obtained in the numerous studies of mammalian chromosome evolution including the recent advances in molecular cytogenetics.

The study of animal karyotypes showed that animals have a great diversity in number and morphology of chromosomes despite that their genomes are remarkably conserved. How can this conservation be resolved? This volume tries to answer to this question.

The first contribution of the volume, written by the Editors with a bringing of MA Ferguson-Smith, is an overview and a history of the cytogenetic techniques used in the analysis of mammalian karyotypes including the results obtained, with an emphasis on chromosome painting in mammals. Chromosome banding (Q-, G-, R-, and C-banding) allowed the workers looking for between-species homologies. However, the homologies established between distantly related species remained speculative until the advent of molecular cytogenetics and especially chromosome painting in the late 1980s and early 1990s. Then it became possible to search for ancestral karyotypes, and to offer original perspectives on genome evolution in mammals and in other vertebrates, as well as on syntenic and associational evolution.

The second contribution is devoted to genome size as the evolution of the main genome signature is its size. However, the genome size of several taxa vary over a broad

range and do not correlate with the complexity of the organisms (the C-value paradox). The biology of transposable elements may explain some of the molecular mechanisms that are involved in genome size variation and novelties.

The other 13 contributions of the volume, written by leading experts in the field, details the cytogenetic findings in Marsupialia and Monotreme, Xenarthra, Afrotheria, Eulipotyphla, Chiroptera, Carnivora and Pholidota, Cetartiodactyla, Perissodactyla, Sciuromorpha and Lagomorpha, Non-Sciuromorpha Rodentia, Strepsirrhine Primates, Dermoptera and Scandentia, new-world monkeys (Platyrrhini), and Catarrhine Primates (old-world monkeys, apes and humans).

In this volume, a consistent view of chromosome evolution in mammals is proposed. However, more work is needed as there is an insufficiency of taxa sampling. Even in the more studied mammalian orders, primates and carnivores, only a few species have been studied. The study of more species for enormous orders such as rodents and bats should be done as well for other species all over the mammalian tree, including smaller clades such as Afrotheria and Xenarthra.

Painting comparisons of humans and other primates displayed that there is no molecular clock for chromosome evolution. Different rates of chromosome evolution were reported, for example, the high chromosome conservation in felids and whales, and the

rapid chromosome evolution in canids, skunks, pigs, and equids.

The molecular cytogenetic method commonly used is chromosome painting. Few species, mostly primates, have been studied with higher resolution methods such as BAC-FISH (fluorescent *in situ* hybridization using BAC), which are able to define intrachromosomal rearrangements and inversions. There is much work to be done at this level. However, chromosome painting has allowed a large sampling of taxa, whereas sequencing studies have been performed mainly in species of economic interest or in species that are of peculiar significance for understanding human evolution such as the higher primates. Nonetheless, with the next-generation sequencing, the number of vertebrate species sequenced will highly increase. It is probable that the integration of cytogenetic and sequencing information will be extremely important for resolving issues in cytogenetics such as the reconstruction of ancestral karyotypes, the elimination of homoplasmy that can plague cytogenetic reconstructions, and the distinction of convergent associations and homologous associations.

Those searching for an answer to the question what makes us human, will not find it in this volume. However, one can imagine that understanding the forces responsible for different rates of chromosome evolution and the peculiar characteristics of the mammalian genome will be possible at the sequencing level in the near future. Will this mean that cytogenetics is no more relevant in evolutionary studies? The Editors of this volume do not think so, they think that a closer integration between cytogenetics and sequencing efforts will be necessary if cytogeneticists want to maintain their relevance in evolutionary studies.

This book, available in hardback and in electronic format, is recommended to those interested in the evolution of the vertebrate genome and for researchers involved in mammalian evolution, comparative cytogenetics, molecular cytogenetics, comparative genomics, primatology, and zoology ■

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