

## Book Reviews

THE EVOLUTION OF THE GENOME. Edited by T. Ryan Gregory. Burlington, MA: Elsevier Academic Press. 2005. 740 pp. ISBN 0-12-301463-8. \$66.50 (cloth).

In many regards, “genomics” has become synonymous with the collection and study of genome sequences, reducing an organism to a linear collection of bases. Gregory’s volume is an argument for retaining the genome itself as an important biological level of organization with its own structure, content, and evolutionary dynamics. This book explores many interesting genomic phenomena, such as polyploidy in animals, parasitic chromosomes, transposable elements, and genomic expansions, summarizing information from a wide taxonomic sample in every instance. Indeed, anthropologists, who are more likely to be familiar with the *Alus*, fissions, fusions, and translocations common in primates, may be surprised by the multiplicity of other paths to genome change. Though this book only occasionally addresses the evolution of the primate genome directly, it provides an excellent background for anthropologists interested in a wider understanding of genomic and karyological evolution, and the connections between evolutionary theory and genomics.

This text is organized into six parts, examining genome size, genomic parasites (e.g., transposable elements), duplications, polyploidy, sequence comparisons, and genomic macroevolution. The genome-size chapters (by Gregory, and Bennett and Leitch) review the debate on the C-value paradox (the disconnect between genome size/weight and complexity) and reframe it as a puzzle. These chapters provide an informative taxonomy-based review of C-values, along with graphs and tables. The many organismal correlates of C-value are also examined (e.g., the correlation between developmental complexity and C-value in insects), detailing the debate on each. Overall, these chapters open the book with a compelling argument, insisting that genomes cannot be reduced to strings of letters and that studies of genome itself as a level of biological organization have value for understanding diversity and evolution.

The chapters on genomic parasites treat both genetic elements, such as *Alus*, and parasitic chromosomes, known as B chromosomes. Kidwell reviews many classes of transposable elements, including details on how they work, as well as their genomic and taxonomic distribution. Insights into the relationships between organismal attributes and the rate of parasitism are especially intriguing, because these phenomena may relate to the differences in distributions of such elements in primates. Perhaps more attention could have been paid to the usefulness of these elements for resolving phylogenetic questions. Camacho’s chapter on B chromosomes, a type of “dispensable” parasitic chromosome, offers a clear example of how evolutionary games can be played at the level of the karyotype. Both chapters provide useful taxonomically organized tables detailing their respective phenomena.

The first section on duplications (Taylor and Raes), treating small- and large-scale genome duplications, comes at a particularly interesting time in the debate on evolution by gene duplication. Ohno’s (1970) classic

theoretical framework on duplications, where gene duplications either gain a new function or lose function, has been reframed in light of new data by Lynch and Conery (2000), who contend that duplicated genes may both partially lose function, and sometimes require one another. This latter model is known as subfunctionalization. Taylor and Raes place this debate into a broader historical framework, specifically examining gene duplications. Van de Peer and Meyer treat larger-scale duplications, from block to whole-genome duplications. This chapter contains a useful section explaining methods that can detect and reconstruct genomic changes between organisms. Both chapters present excellent reviews of recent debates in the literature, and clearly show how future work will impact the field, both experimentally and theoretically.

The second duplication section, on polyploidy, examines both plants and animals. While polyploidy is well-known in plants, Gregory and Mable’s taxonomic review of polyploidy in animals shows that it is more frequent than often presumed. Many examples are described, including several cases of recent polyploidy in fish, where it is common. The only case of mammalian polyploidy, in a South American rodent, is well-described. As is the case in the other chapters, this section includes informative tables and figures describing polyploidy, serving as an excellent reference.

The fifth section treats genome sequence comparisons in both pro- and eukaryotes. Filipinski and Kumar review the history of genomics from the inception of karyology to the Human Genome Project and beyond, to future genome-sequencing targets. A brief passage highlights the interesting genomic aspects of many eukaryote-sequencing targets. Also, this chapter summarizes many of the sequence-based comparisons between human and mouse, reviewing many of the studies with the most direct relevance to anthropologists. Gregory and DeSalle’s chapter on prokaryotes similarly reviews each completed genome sequence project, and shows how these data sets have been harnessed for different types of analyses than in eukaryotes. Having these chapters back-to-back is useful, though more direct comparisons between the two groups would have been helpful.

Gregory’s final chapter, on genome macroevolution, fits genome-level thinking into the debate between micro- and macroevolution. The chapter explores many contentious aspects of the debate, resolving that higher-level processes are at play in the evolution of genomes, organisms, and ecosystems. In the second part of the chapter, the role of genome-level changes is linked to major transitions, such as immunity, the evolution of vertebrates, and human uniqueness. *Alu* elements are indicated as a particularly interesting line for future research within primates. While the chapter provides interesting arguments, more data must be marshaled in the future to more definitively assess these issues.

Overall, Gregory’s volume does an excellent job of reviewing and detailing genomic-level phenomena across all living (and even some fossil) organisms. Each chapter is taxonomically comprehensive, with many references and excellent tables. Though there is little treatment of the karyological changes that are important to primatologists, this book provides a wider view for framing such

studies. For example, understanding the hypotheses for the differences in C-values and polyploidy among animals will help anthropologists formulate and refine hypotheses for explaining genomic diversity among primate groups (e.g., the conservative papionins vs. the diverse *Cercopithecus* species). Aside from the analogies to primates, this text provides a comprehensive view of the genome as an evolving level of biological organization that significantly enhances and complements the view of the genome as a string of letters.

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