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BOOK REVIEW

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Evo-devo in anthropology: the value of flies, mice, and biologists, our surprisingly close relatives

DEEP HOMOLOGY?: UNCANNY SIMILARITIES OF HUMANS AND FLIES UNCOVERED BY EVO-DEVO

By Lewis Held, Jr.

New York: Cambridge University Press. 272p. \$39.99 (paperback). ISBN: 9781316601211

DEVELOPMENTAL APPROACHES TO HUMAN EVOLUTION

Edited by Julia C. Boughner and Campbell Rolian.

New York: Wiley-Blackwell. 344p. \$129.95 (hardcover). ISBN: 9781118524688

The field of evolutionary developmental biology (evo-devo) is relatively new; the application of evo-devo theory and methods in anthropology is even more recent. While the perspectives of evo-devo are being used more widely within anthropology, it can be a difficult subject area to become familiar with. The field of evo-devo is hard to define precisely, but encompasses a wide range of research related to how the evolution of genetic and developmental processes is associated with driving or limiting the evolution of various traits. The modern field of evo-devo is frequently associated with the use of genomic approaches to trace the evolution of genes and gene networks across macroevolutionary scales, as well as the use of developmental-biology approaches to visualize and manipulate gene expression patterns during development to determine how genomic variation leads to phenotypic variation. The great value of evo-devo largely rests on the fact that distantly related animals share a surprisingly high number of homologous or orthologous gene regulatory networks and fundamental developmental systems.

Lewis Held's *Deep Homology*? reflects a macroevolutionary evodevo perspective. In it, he reviews the state of knowledge regarding homologous genetic networks that underlie general development of body plan, brain, limb, heart, and sensory traits across a wide range of animal taxa. This is the third evo-devo book written for a broad scientific audience by a clearly knowledgeable and well-read fly geneticist and educator. While this short book is fun and informative, it is written with the assumption that readers are familiar with terms and concepts typically covered within an introductory genetics or developmental biology course. With this assumption in mind, the book succeeds as a valuable resource for advanced students and researchers who are less familiar with evo-devo because it provides well-written introductory passages on several major examples of ancient genetic homology. These passages include a multitude of references to primary literature (half of the book is a reference list).

The presentation of material is well balanced in that it acknowledges gene network, developmental, and phenotypic differences between taxa alongside the strong evidence for general genetic homology. After all, evo-devo is not merely a reification of homologous gene regulatory systems like hox gene clusters, but the study of how homologous systems have evolved, been co-opted, and modified to produce new phenotypes, as well as how genetic and developmental variation relates to phenotypic differences between modern species.

While some anthropologists might find the jargon challenging at first, Deep Homology? is an excellent starting point for anyone seriously interested in taking a deep dive into the basic genetic and developmental underpinnings of the phenotypes covered by the book. However, in only a few minor instances does this book include speculation on how genetic or developmental networks have been modified to produce specifically primate or human phenotypes. While the book is framed as a comparison of flies and humans, it might be more appropriately described as a comparison of flies and mammals, with most of the mammalian data coming from studies of lab mice. Given that mammals share many fundamental genomic and developmental networks, the use of mice as a model for humans within a broad macroevolutionary perspective is appropriate. The fundamental homologies between humans, mice, and other model organisms also underpin a range of successful biomedical studies on human disease and are now more frequently being leveraged to answer anthropological questions.

The value of animal models in anthropology is among the many topics discussed within Julia Boughner and Campbell Rolian's edited volume, entitled *Developmental Approaches to Human Evolution*. This volume is a valuable survey of current and innovative approaches aimed at uncovering how developmental process can be modified to produce the evolutionary changes noted among primate and hominid species. Chapter one is a great, however brief, introduction to the history and current state of research on biological development within the context of primate and human evolution. The following chapters represent a variety of perspectives, include a wide breadth of research topics and methods. Each should provide some inspiration to any anthropologist interested in the interaction of genes, development, and evolution. Alongside interesting results and perspectives, readers should expect significant discussion of next steps and future directions rather than final answers about how a given evolutionary change occurred. This partially reflects the recent application of modern evo-devo perspectives to anthropology and partially reflects the relative youth of the field of evo-devo as a whole. As discussed by Dr. Held throughout his book, there are still many open questions regarding the evolution and function of gene regulatory systems within even the most wellstudied traits and organisms. By working within the wide interdisciplinary field of evo-devo, anthropologists have the opportunity not only to leverage previous work and tools to answer questions on primate evolution, but also to contribute to a deeper understanding of developmental systems across many taxa.

An interest in the connection between development and evolution is not new within anthropology. Some chapters within Boughner and Rolian's volume illustrate approaches that use recently developed genomic and developmental genetic methods or previous results generated by these methods. However, other chapters represent interesting reframing of methods and perspectives more traditionally used by anthropologists. The use of descriptive comparisons, quantitative genetics, and concepts such as integration, allometry, and heterochrony reflect both their continuing value within the study of developmental systems and the fact that applying many developmental genetic approaches to primates is not practically or ethically feasible. Moving forward, comparative guantitative studies of primate and fossil species remain a critical foundation on which anthropological evo-devo will be based. As discussed in the introductory chapter of Boughner and Rolian's edited volume, the results of primate and fossil studies must be used to test and validate the developmental hypotheses generated within studies of model species or from computational and statistical models.

One experimental pipeline that was proposed within multiple chapters of the edited volume illustrates how molecular methods and anthropological knowledge might be combined to illuminate the genetic basis of evolutionary change. In some cases, developmental genetic work within model species has identified variation in certain regulatory genes that is associated with phenotypic variation reminiscent of variation among primate species. Genomic comparisons of published or new primate genome sequences could be used to identify sequence differences in those regulatory genes between representative species. After using statistical models to predict which sequence variation might cause significant changes in gene expression, the specific primate regulatory sequences (such as enhancers) can be placed within mouse populations using transgenic technologies. If the phenotypic differences between the transgenic mouse lines are similar to those between the representative primate species, this regulatory sequence difference is a good candidate for explaining, at least partially, the phenotypic differences noted between primate species. Further experiments within model organisms might be required to validate the role of this regulatory factor and to determine how it interacts with other relevant genes to produce the phenotype of interest. In this proposed pipeline, which is a variant on common methods to identify the role of genes in developing model organisms, research success depends on an interdisciplinary combination of modern molecular methods and careful quantitative comparisons of phenotype within primates and model organisms.

As discussed by Drs. Weiss and Buchanan in the final chapter of the edited volume, incorporating evo-devo approaches into the anthropological toolkit promises to allow researchers to determine the genetic and developmental basis (or reasons) for evolutionary changes in phenotype. Because most phenotypes of interest are complex traits influenced by a large number of interacting protein coding and regulatory genes, a careful combination of approaches will likely be necessary to parse the causal networks underlying evolutionary variation. However promising, a degree of skepticism is required when extrapolating from model organisms and computational models to explain human and primate evolution. The collaboration of anthropologists of various stripes will be critical to properly design and validate the results of evo-devo research in anthropology.

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