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EVOLUTION, DEVELOPMENT, & THE PREDICTABLE GENOME.

By David L. Stern. *Greenwood Village (Colorado): Roberts and Company Publishers*. \$40.50. xvi + 264 p.; ill.; index. ISBN: 978-1-936221-01-1. 2011.

This slim volume begins with a fascinating question: Why are the alleles responsible for repeated adaptations, such as changes in flowering times in local populations of *Arabidopsis thaliana*, often restricted to one or two loci, when studies reveal dozens of candidate genes with potentially adaptive phenotypic effects? Stern builds toward an answer with lucid chapters on pleiotropy, epistasis, and population processes, each filled with clearly described empirical examples. These chapters accomplish the subtle but important mission of knitting together population genetics and developmental biology. Rather than talking about the need for such a synthesis, Stern has done it: pleiotropy and epistasis are demystified through an exploration of their genetic and biochemical roots, and population size is clearly linked to the developmental roles of those mutations favored by selection.

In the book's later chapters, the author returns to the question of mutational hotspots and argues that such predictable changes result from both the sorting processes of selection, and the structures of developmental networks. Stern introduces the idea of "pathworks"—traces through the developmental network from differentiated cells backward in time—as a new way to parse complex networks to reveal the causes of predictable evolutionary change. Although I did not find that he quite made the case that pathworks are a uniquely useful perspective, I was inspired by his enthusiastic arguments for the central roles of networks in a predictive theory of genome evolution.

Although there is much here for experienced scientists, I would recommend this book most strongly to graduate students. With such a clear, and laudably compact, presentation, Stern's volume has the potential to influence a generation of students to think deeply on how selection sorts and networks shape the raw materials of adaptation.

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EPIGENETICS: LINKING GENOTYPE AND PHENOTYPE IN DEVELOPMENT AND EVOLUTION.

Edited by Benedikt Hallgrímsson and Brian K. Hall. *Berkeley (California): University of California Press*. \$68.00. viii + 459 p.; ill.; index. ISBN: 978-0-520-26709-1. 2011.

Epigenetics is a difficult term, and one whose meaning has changed and diversified much over the decades. Epigenetics is used narrowly to refer to heritable modifications of genes and genomes just other above the level of the nucleotide sequence. Such changes, exemplified by methylation of cyto-

sine nucleotides or histones, have the potential to alter gene function heritably across cell divisions, thus enabling developmental changes, and sometimes across generations, possibly enabling evolutionary changes. Its broadest definition, in contrast, expands to include all mechanisms, including differential gene expression, that enable the emergence of organismal form, function, and complexity in development and evolution. It is this broader view that is taken in *Epigenetics: Linking Genotype and Phenotype in Development and Evolution*, a volume edited by Benedikt Hallgrímsson and Brian K. Hall and consisting of 23 chapters grouped in four parts.

Part I includes two chapters aimed at highlighting the historic and philosophical foundations of epigenetic mechanisms and inheritance. The next part, consisting of five highly diverse chapters, showcases different empirical and conceptual approaches to the study of epigenetic mechanisms and their consequences. Parts III and IV then form the bulk of the volume. Part III includes seven chapters devoted to the epigenetics of various aspects of vertebrate organ development. These chapters illustrate vividly how form, function, and complexity emerge through development, contingent upon previously established developmental landscapes and enabling subsequent landscapes in the process. Part IV is similarly engaging. Devoting eight chapters to the topic of epigenetics in evolution and disease, this part highlights how an appreciation of epigenetic processes enriches our understanding of why and how novel phenotypes and pathologies may emerge in development, altering evolutionary trajectories in the process.

Throughout this book, readers may wonder sometimes if and how the study of epigenetics really differs from the study of development and evolutionary developmental biology (evo-devo). The answer may be that the study of epigenetics emphasizes what the study of development and developmental evolution used to include, but seemed to have lost sight of over the decades. Contemporary developmental biology, and much of evo-devo, have become devoted to the study of developmental genes as the regulators and determinants of form and function. It is this mindset that the study of epigenetics opposes, arguing instead that organisms and their traits are first and foremost the emerging properties of development. Genes and their products enable developmental processes, but they do not make traits and organisms. If we want to understand why and how development produces the traits it does, why developmental evolution takes the directions it takes, and why disease emerges when it does, the study of epigenetics deserves to take center stage. This vol-