

Evolutionary botanists need to look elsewhere for answers, especially to the roles of gene duplications, where polyploidy is the most dramatic case, in driving drift, mutation, linkage, epistasis and pleiotropy.

This book is not aimed at botanists. In fact, Lynch knowledgeably covers all life and even life's progenitors. The chapter on gene duplications, which are prevalent in plants, will probably be most useful to plant scientists, especially his discussions of neo- and sub-functionalization, which is greatly strengthened by Keith Adams' beautiful work on reciprocal epigenetic silencing of homeologous genes in cotton.

Alex Haley's Autobiography of Malcolm X was ironically not an autobiography. Charles Darwin's Origin of Species was ironically not about the origin of species. Lynch follows in this grand tradition. His book is not is much about the origins of genome architecture, but rather about ramifications of that architecture to evolutionary trajectories.

The only faults that I could find with this book are extremely minor. More extensive coverage of epigenetic effects would have been nice. His discussion of centromeres omitted mention of karyotypic fission and perpetuated the inaccurate suggestion that only one of four products of meiosis survives in most female organs (cf Ed Klekowski's wonderful diagrams of angiosperm megagametophytes, which show more than just the textbook Polygonum type). While Lynch's index is moderately good, a more comprehensive index would be a great addition to any revision.

This is not a book for the meek. The genetic and population genetic details, while accessible, are still extraordinarily rich in detail. Many of the arguments are cumulative throughout the volume. But it is worth the effort wading through these details, which, while important in their own right, add up to an expected synthesis that selection is not the primary driver of plant (or animal) evolution. Casting the hand-waving aside, Lynch shows that it is only by looking at the details of genome architecture and associated population genetics that we can really see how important non-adaptive evolutionary explanations can be. While most botanists abhor mathematics, it is worth trying to understand the nicely presented and simplified mathematics herein. Read Lynch's book, have your students read it, and let's revise our views of evolution.

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The Origins of Genome Architecture. Lynch, Michael. 2007. ISBN 978-0-87893-484-3 (cloth US\$59.95) 494 pp. Sinauer Associates, Inc. P.O. Box 407, Sunderland MA 01375-0407.

This is a truly remarkable book, which will forever change your view of evolutionary biology. Anyone with even tangential interest in evolution needs to read the preface, epilogue, and especially the fourth chapter on population size. Lynch takes a detailed knowledge of molecular genetics and genomics, combined with a refined fluency in population genetics, to create sound sweeping descriptions and predictions about evolution.

Lynch shows how modern genomic data imply that large eukaryotes - e.g. plants and animals - are largely immune from selection. Drift and mutation are much more salient drivers of their evolution, virtually mocking adaptationist explanations. Empirically, he shows how small effective population size also results in reduced recombination, increased linkage disequilibrium, greater genetic hitchhiking, and increased mutation rates. By contrast, with small eukaryotes with few cell types, selection reigns supreme. This does create tension. Rich Lenski pioneered experimental evolution in prokaryotes, a field that others have expanded to protists and fungi, showing that selection drives evolution of large populations. For better or worse, Lynch shows that such results cannot be extrapolated to larger, more complex eukaryotes. He thereby resurrects Sewall Wright's early vision that drift matters. Botanists need to heed his words and stop always looking for adaptationist explanations. For example, why are angiosperm radiations invariably thought to be adaptive?