

Preface

The recombination of genetic information has long been recognized as an important process in evolution. However, genomic and metagenomic analyses, particularly of prokaryotic cells, have revealed a hitherto unexpected number of horizontal gene transfer (HGT) events. Divergent organisms exchange genes and the traits they encode; vast amounts of genetic information only sometimes reside within the chromosomes, but perhaps can be found more frequently in plasmids and phages. The importance of HGT was first recognized in pathogenic bacteria, but it plays an equal role in the evolution of non-pathogenic Bacteria and Archaea. Studies have also revealed the transfer of parasitic, selfish genes between the mitochondria of different plant and fungal species; genetic material was found to be exchanged between parasitic plants and their hosts; and many studies have identified genes that were transferred between pro- and eukaryotes, including transfers from symbionts to multicellular animals.

HGT events encompass not just a transfer of one or a few genes but the evolution of organelles by symbiosis can be viewed as an extreme instance where whole genomes were acquired by another organism. The transfer of genes from the symbiont to the host genome was crucial in eukaryogenesis, and these types of transfers continue to shape the evolution of eukaryotes, including multicellular plants and animals.

This book provides advanced undergraduates, graduate students, researchers, and professors with an overview of HGT concepts, as well as specific case histories that highlight current progress in the field. Where possible, molecular biology (wet-lab) protocols as well as overviews on *in silico* methods are provided to allow researchers to incorporate the methods of recognizing and characterizing HGT in their own research systems. This volume will be of interest for molecular biologists, geneticists, evolutionary biologists, bioinformaticians, and computational scientists.

Written by prominent contributors to the field, this volume is divided into three sections following the Introduction: Definitions, philosophy and Implications; Methods and Case Studies. Chapters provide an overview of the terminology, concepts, and implications of HGT, and current evolutionary thought and philosophy. Discussions of microbial species concepts and the possibility to reconstruct evolutionary history have frequently focused on HGT. Throughout this book, we attempt to include different and often controversial viewpoints to provide the reader with an impression of the excitement surrounding HGT. Contributions of gene transfer, often as a consequence of symbiosis, in the origin and evolution of eukaryotic cells are highlighted, as well as the role of HGT in assembling biochemical pathways, and the difficulties that HGT creates for tracing metabolic capabilities through life's history.

Methods used in exploring HGT encompass both computer and bioinformatics analyses of genomic data as well as molecular biology techniques for identifying, quantifying, and differentiating instances of HGT. These methods allow the characterization of mobile agents of HGT in modern communities as well as the identification of ancient transfers that have contributed to genome evolution.

Case Studies provide detailed accounts of how HGT has shaped evolution across the diversity of organisms and organismal lineages. In prokaryotes, transfer events in thermophiles as well as organisms that had to adapt to increased atmospheric oxygen are discussed. From a biogeochemical point of view, organisms leave a mark on the geological record in a variety of ways, including changing the isotopic composition of rocks. The metabolic pathways and their building blocks responsible for these isotopic discriminations are scattered throughout the phylogenetic web of life in distantly related lineages, suggesting their origin and distribution by HGT. The extent of plasmid ecology in marine and subsurface niches as well as mathematical modeling approaches to HGT in continuous and batch culture conditions are examined. The impacts of gene transfer on our ability to clearly define prokaryotic species and strains, our ability to accurately reconstruct phylogenetic trees, and how transferred genes or genomes undergo adaptation are also discussed. Finally, HGT has impacted evolution of eukaryotic genomes through organellar evolution. Contributions highlight the evolution of anaerobic pathogenic protozoa, plastid evolution in algae and plants, and HGT events in other eukaryotic genomes.

Taken as a whole, this book provides not just an introduction. It is a detailed compendium of how HGT has impacted genome evolution and how understanding HGT impacts our ability to accurately reconstruct and comprehend the web-like evolutionary history. It also gives a toolbox of methods to help recognize HGT events in genome analysis as well as in extant microbial communities. It is our hope that all scientists who are interested in genome evolution and microbial ecology will benefit from this new paradigm and make use of the tools and ideas presented here to further their own research.

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