Preface

The horizontal transmission of nucleic acids is thoroughly documented, especially with viruses and other host–parasite relationships. With the increasing body of information deposited in the sequence databases, DNA transfer between distinct groups of organisms and between kingdoms is becoming apparent. In this book, we include examples of gene transfer involving all of life's kingdoms. This necessitated bringing together a highly disparate group of active scientists to discuss and review the current understanding of horizontal gene transfer. This brings into a single volume such disparate subjects as movement of DNA into bacterial cells, mobile genetic elements in metazoans, plant and animal infection mechanisms, molecular evolution, and macroevolutionary theory. An underlying interest in this subject concerns the safety of releasing genetically engineered organisms into the environment.

The motivation for bringing people from different areas together at the Fallen Leaf Lake Conference in September, 1996, was to assess a single hypothesis. It has been conjectured that horizontal gene transfer plays a significant role in evolution. If this is true then three conditions must be realized. First, can genes, or more specifically DNA, move from one species to an unrelated one? Thus, a section of this book is devoted to the subject of transfer mechanisms, a phenomenon well documented in bacteria. The discovery of plasmid transfer laid the basis for our current thinking about horizontal gene transfer. Transfer mechanisms also include microorganisms that transfer DNA to eukaryotic cells; hence a number of papers are given on *Agrobacterium*, on bacterial transfer to yeast, on actinomycetes, and on eukaryotic parasites that inject their genomes into their host's cells.

Second, what is the evidence that genes transfer in nature? The primary evidence supporting evolutionarily significant horizontal transfers involves phylogenetic reasoning. This is an area where the evidence is accumulating in the gene and protein sequence data bases. Two problems

are repeatedly encountered: defining the topology of a gene tree and estimating divergence times following molecular clock assumptions. There are several contributions discussing results obtained from phylogenetic analysis and problems associated with this approach.

The third question raised by the central hypothesis is that if the mechanisms exist and events can be documented, does horizontal gene transfer actually play any significant evolutionary role? Or, is a theory that incorporates migrant DNA useful in explaining more general biological phenomena? To this end, there are chapters that directly address macroevolutionary patterns and trends.

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