Preface

Evolutionary biology has been experiencing an exciting time with a wealth of continuously emerging new data since DNA technology became widely available about ten years ago. Although characteristic features of molecular evolution such as constancy of the evolutionary rate and the conservative nature of mutant substitutions have been recognized for two decades, they can now be examined under a new light. This has led many biologists to regard the neutral theory, put forward in 1968 by one of us, as a powerful guiding principle. A new biological topic, *molecular evolution*, has also become popular, and a new discipline devoted to its study has been growing steadily. At the same time, however, it has become clear that genomic evolution is not so simple as one might previously have thought. It has apparently taken place in a complex manner, involving various mechanisms in addition to mutation and random drift. These include gene conversion, unequal crossing-over, duplicative transposition, functional and structural changes caused by selfish DNAs such as segregation distorters and transposons, as well as natural selection at both the individual and population levels. Not only the genome as a whole but also individual genes are shuffled and parts of the genome or genes may undergo hitherto unrecognized modes of change. One such mode often observed among members of a

multigene family is termed concerted evolution. The extent of such change depends strongly on functional and structural requirements.

Confronted with such rapid accumulation of new molecular data, we felt around 1987 that it would be timely to promote further molecular evolutionary studies in Japan, employing population genetical methods to assess the evolutionary significance of newly found genetic factors and mechanisms at the molecular level. We therefore proposed the project entitled "Development of evolutionary and population genetics incorporating newer molecular findings" in collaboration with the late Dr. Terumi Mukai, and also with Dr. Takashi Miyata and Dr. Sadao I. Chigusa. Fortunately, the project was approved by the Japanese Ministry of Education, Science and Culture and we received a special priority grant (#63618004) for three years. Thanks to enthusiastic efforts of about 40 individuals who participated in this project, we believe that it has been quite successful and has produced a number of significant results, many of which have already been presented at international symposia and published in international journals. Noteworthy among them are: (i) establishment of the neutral theory as a scientific hypothesis, and full recognition of its usefulness in evolutionary thinking, and (ii) clues for the future direction of research in molecular evolutionary biology. It is our great pleasure to now be able to publish these accomplishments in a single volume.

This publication contains 19 papers which, for convenience, are classified into six sections. The first consists of three theoretical papers on population genetics and molecular evolution with special reference to the neutral theory (Kimura), multigene families (Ohta), and gene or allelic genealogy (Takahata). These papers may be read in their own rights, but also they serve as a guide to understanding population genetical aspects of the subsequent papers treating experiments or data analyses.

One of the main interests in molecular evolutionary studies is the molecular bases of adaptive evolution as observed at the morphological or phenotypic level, and this is covered in the second section. Mukai's paper is based on his work on population genetics of *Drosophila melanogaster*. The other two contributions consider molecular adaptation found in δ-crystallin (Mori *et al.*) and aminohexanoate hydrolases (Okada *et al.*). The third section contains papers on DNA variation which represents the ultimate level of genetic variation within populations. Two papers in this section review DNA variation in relation to

human genetic disorders associated with steroid 21-hydroxylase genes (Sasazuki *et al.*) and the hemoglobin β cluster (Fukumaki and Fucharoen). The other two discuss mitochondrial DNA variation in the *D. melanogaster* subgroup (Satta and Chigusa) and in humans (Horai) with special emphases on their evolutionary histories as inferred from DNA sequence data. The GC content often differs greatly from species to species, or between different regions within one genome. The fourth section is concerned with genomic evolution, focusing on codon and anticodon evolution by biased mutation pressures (Muto *et al.*) and on the mosaic structure of warm-blooded animal chromosomes (Wada *et al.*). The prevalence of repetitive sequences, retroposons, and transposons raised various questions about the origin, the mechanisms involved, and the evolutionary implications. In the fifth section, it is shown that: W chromosome-specific repetitive DNA sequences have the ability to bend and interact with a non-histone protein (Mizuno); three families of short interspersed sequences in the genome of salmonid species are all derived from a lysine or lysine-like tRNA (Okada); translational frameshifting in a bacterial insertion element IS1 is involved in the expression of the transposase genes encoded by other IS elements (Sekine and Ohtsubo); and the open reading frame 3 in the *P* element harbored in the *D. melanogaster* genome may be essential in determining the so-called *P* or *M* cytotype (Nitasaka and Yamazaki). The final section concerns data analyses of DNA sequences and species phylogenies. Through sequence comparisons of duplicated genes shared by organisms belonging to the three kingdoms, a rooted phylogeny was constructed, unambiguously determining the phylogenetic position of archaebacteria (Miyata *et al.*). Two other topics are the recent history of human immunodeficiency viruses with the conclusion that recombinants between simian or simian-like immunodeficiency viruses are the likely origin (Moriyama and Gojobori), and the divergence time of humans from African apes using a new maximum likelihood method appropriate to variable substitution rates (Hasegawa *et al.*)

Shortly after our project term was finished, Dr. Mukai died quite unexpectedly at his home due to lung failure. He was not only one of the chief promoters of our project during its three year period, but also one of the world's leaders in experimental population genetics. We are saddened that his contribution in this volume turned out to be his last writing, and deeply mourn his untimely death. It is especially sad that this came just as his laboratory had been organized to better fulfill his

aims. We also regret that his recognition as the second recipient of the Duke of Edinburgh Prize from the Japan Academy came too late, although there is some consolation in knowing that he learned of the forthcoming award while he was still active. As editors of this volume as well as his longtime friends, we hope and expect that Mukai's contribution will be remembered well into the future. It is fitting that this volume be dedicated to his memory.

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