

## 講座大師李文雄 ( Wen-Hsiung Li ) 演講與對談

I shall give two lectures on the mathematical theory of molecular evolution, which is a relatively new branch in biology. Molecular evolution encompasses two areas of study: (1) the evolution of DNA sequences and protein sequences, and (2) the evolutionary history of organisms and genes. The first area includes the rates and pattern of change in the genetic material (e.g., DNA sequences) and its encoded products (e.g., proteins) during the evolutionary time and the mechanisms responsible for such changes. In classical evolution, morphological changes in time are the primary concern and the major mechanism of evolution is commonly believed to be natural selection as proposed by Darwin. Such theories are not sufficient for explaining evolution at the molecular level. So, new theories are needed. The second area, also known as “molecular phylogeny” or “molecular phylogenetics”, deals with the evolutionary history of organisms or genes. A phylogeny is an evolutionary tree that shows the evolutionary relationships among the organisms under study. A major effort in classical evolution is to understand the evolutionary relationships among the organisms on earth and dates of evolutionary divergences such as the divergence between human and chimpanzee. The materials used to infer evolutionary relationships of organisms were again morphological features. Such materials are limited and their evolutionary changes are difficult to be quantified. In contrast, molecular data are much more abundant and much more amenable to mathematical treatments. Therefore, the study of molecular evolution has led to enormous progress in the study of evolution.

## 講座大師李文雄 ( Wen-Hsiung Li ) 演講與對談一

### Mathematical Models for DNA Sequence Evolution

Abstracts:

Evolution of DNA sequences is a basic topic in molecular evolution. To understand how DNA sequences evolve we need mathematical models. I shall first explain what DNA sequences are. I shall then present several mathematical models of DNA sequence evolution and their mathematical treatments. I shall also give some examples.

## 講座大師李文雄 ( Wen-Hsiung Li ) 演講與對談二

### Methods of Phylogenetic Reconstruction

Abstracts:

Molecular data have been widely used to study of evolutionary history of organisms and genes. For this purpose we need to have mathematical (statistical) methods. The inference of the phylogenetic relationships among organisms is commonly known as phylogenetic reconstruction, implying the reconstruction of history from data. I shall present several methods for reconstructing phylogenetic trees from molecular data. I shall also present several examples where the relationships were of great interest but were not resolved by classical studies – indeed, classical views turned out to be very wrong!