《**International Symposium**》

Let's Talk about Trees

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Abstract

Phylogenetic analysis in evolutionary genetics

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In the field of evolutionary genetics, researchers estimate phylogenetic relationships between populations by constructing molecular phylogenetic trees. So far, numerous methods to construct an accurate phylogenetic tree have been developed. On the bases of data to be used (distance matrix or nucleotide sequences) and principles to select the best tree, these methods are classified into three approaches: 1) minimum evolution, 2) maximum parsimony, and 3) maximum likelihood estimations. In addition, stepwise reconstruction methods have been proposed since exhaustive search of innumerable possible trees is inefficient. One example of such methods is the neighbor-joining method that is widely used at present.

However, there are cases when phylogenetic relationships between populations are not consistent with a molecular phylogenetic tree even if the tree is accurate, which is called "incomplete lineage sorting". When incomplete lineage sorting is observed, an analysis of a number of loci is required to obtain accurate phylogenetic relationships between populations. The points in which whole genome analysis is superior to conventional mitochondorial DNA analysis are to include not only a large number of nucleotides but also a large number of loci that transmit independently.

A phylogenetic tree cannot represent any confluence between lineages but depict only splits. Here, confluence between lineages indicates recombination in molecules and gene flow and admixture in populations. The shape of phylogenetic trees is distorted in the presence of gene flow and admixture. In contrast, construction of phylogenetic networks is an effective solution to represent the presence of gene flow and admixture between populations. In these cases, however, it is difficult to search innumerable possible demographic models. Therefore, the best model is chosen based on the likelihood from only limited candidates. In recent studies of evolutionary genetics, such model-based analyses are usually adopted to reconstruct a complicated demographic history of populations.