

Speculating the characteristics of ancestral organisms by analyzing the inferred ancestral gene sequence

Akihiko Yamagishi[1]

[1] Dep. Mol. Biol., Tokyo Univ. Pharm. Life Sci.

Based on the phylogenetic tree constructed from the sequences of contemporary organisms, it is possible to obtain information on evolution of life. By utilizing the phylogenetic tree, sequence of the ancestral genes can be inferred. The reliability of the inferred sequence depends on the degree of information retained in the contemporary sequences. Though it is not easy to infer the sequence of the gene of Commonote, the common ancestor of all the living organisms, it is possible to infer the partial sequence of the Commonote. The recombinant genes were constructed by introducing the sequence of the Commonote to the gene of the contemporary organisms. The proteins were produced from the recombinant genes. By analyzing the characteristics of the proteins, the characteristics of the Commonote were speculated. The results obtained from the analysis of recombinant proteins having partial sequence of the Commonote supported the hypothesis that the Commonote was hyperthermophilic.