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Genome structure analysis by molecular genealogical tree comparisons of metabolic system genes

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1 Purpose of research

So far, we know that evolution of biological life depends on genes. On account of this, it is difficult to understand evolution of a biological life as an aggregate of genes. Beside process of the functional evolution of genes is usually very hard to clarify. Our purpose is to find an original gene of the citrate cycle which plays an important role for energy production by investigating a group of genes coding the citrate cycle. For the investigation we applied molecular phylogeny to data from publicly available gene databases in order to find evolutionary bias of gene mutations.

2 Information obtained from data base

In this research, we selected 26 species of which complete genomic sequence data are available. Many of these species lack citrate cycle functionality. But there are genes which belong to a part of the citrate cycle. In general, one chemical reaction about which the enzyme genes bring is used in several different metabolism. Therefore we believe that the citrate cycle genes in species lacking the citrate cycle functionality are used for other metabolic systems. Then they built the citrate cycle. Based on the above belief, we investigate other functions of the citrate cycle genes by database. In order to analyze the citrate cycle, it is more appropriate to categorize genes coding the citrate cycle based on characteristics of enzymes which are functional units rather than to investigate gene

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data for each species. So we used KEGG(Kyoto Encyclopedia of Genes and Genomes); a database for metabolism and enzyme information. As a result, the citrate cycle was classified into four descendant of Reductive carboxylate cycle, descendant of amino acid metabolism, descendant of carbohydrate metabolism and the citrate cycle native. There are correlations between these classifications and position of the citrate cycle map.

3 Analysis by molecule phylogenetic trees

We made molecular phylogenetic trees for descendant of Reductive carboxylate cycle, descendant of amino acid metabolism, and descendant of carbohydrate metabolism, the citrate cycle native. As a result, molecular phylogenetic trees of gene of amino acid metabolism preserve tree form in close relatives and have high reliability. On the other hand, molecular phylogenetic trees of Reductive carboxylate cycle do not preserve tree form and have low reliability. These facts can be explained as follows. In this research, many of species lack the citrate cycle functionality. Reductive carboxylate cycle is main root of The Citrate cycle, so in this group, there is no necessity to evolve together. But, there is necessity to evolve together in gene in amino acid metabolism, by means of restriction of amino acid function.