
Lateral transfer of ribosomal RNA genes between different species observed in eukaryotes for first time

1. Overview

Scientist Akinori Yabuki and his colleagues in the Marine Biodiversity Research Program of the Institute of Biogeosciences (BioGeos), the Japan Agency for Marine-Earth Science and Technology (JAMSTEC; Asahiko Taira, President), have discovered that the microbial eukaryote^{*1} *Ciliophrys infusionum* has two types of ribosomal RNA^{*2} (rRNA) genes. The research has shown that one of the rRNA genes has come across (through a process of lateral transfer^{*3}) from a different species of eukaryote. To date, the rRNA genes of eukaryotes (including humans) have been presumed to be of only one type inherited from their ancestors and unlikely to undergo lateral transfer. Because of this characteristic, rRNA genes have been widely utilized as markers in environmental DNA analysis^{*4} to investigate diversity and distribution of microorganisms in the environment. Now that this research has confirmed lateral transfer of rRNA genes in eukaryotes, it is suggested that more specific analytical methods may be needed to evaluate diversity and distribution of microbial eukaryotes.

There are countless as-yet unidentified eukaryotes in the environment and their identification and analysis is important if we are to better understand early eukaryotic evolution. Environmental DNA analysis is a basic technique used in scientific investigations; these latest findings should contribute to the discovery of new methods and progress in future research.

The findings were published in the January 23, 2014 (JST) issue of *The ISME Journal*.

Title: Lateral transfer of eukaryotic ribosomal RNA genes: an emerging concern for molecular ecology of microbial eukaryotes

Authors: Akinori Yabuki,¹ Takashi Toyofuku,¹ Kiyotaka Takishita¹

1. JAMSTEC

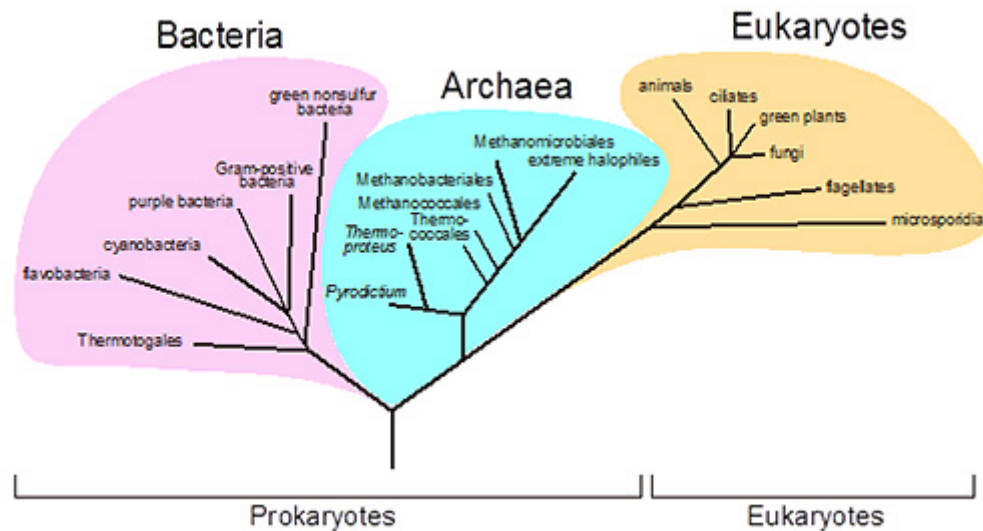
*1 Eukaryotes: Organisms, including animals, plants, fungi, and protists, that have an organelle called a nucleus inside their constituent cells.

Reference: All living things on Earth can be categorized into one of three domains*: Eukarya includes animals (including humans) and plants; Bacteria includes microorganisms (such as *Escherichia coli* and *Bacillus subtilis natto*); and Archaea includes many extremophiles (such as hyperthermophiles and extreme halophiles).

*: Domain

The highest taxonomic rank where the categorization is based on gene sequences

for RNA found in ribosomes (the organelles responsible for protein synthesis). All life on Earth can be divided into three domains: Eukarya, Bacteria, and Archaea.



*2 Ribosomal RNA: RNA found in the ribosome (the organelle responsible for protein synthesis in the cell). RNA stands for ribonucleic acid and is synthesized according to the information encoded in DNA (deoxyribonucleic acid).

*3 Lateral transfer of genes: Genes can be transferred vertically from one generation to the next, but are also known to transfer horizontally (or laterally), crossing from one species to another. This horizontal transfer is known as lateral gene transfer (or horizontal gene transmission). Laterally transferred genes contain phylogenetic information from the originating organism, not the organism into which the genes were transferred. For this reason, lateral transfer can become problematic for research that uses molecular phylogenetic analysis to identify an organism's lineage.

*4 Environmental DNA analysis: A method to estimate the biota in a particular environment by analyzing DNA directly extracted from mud, water, or other samples taken from the environment, rather than through observation or culture.

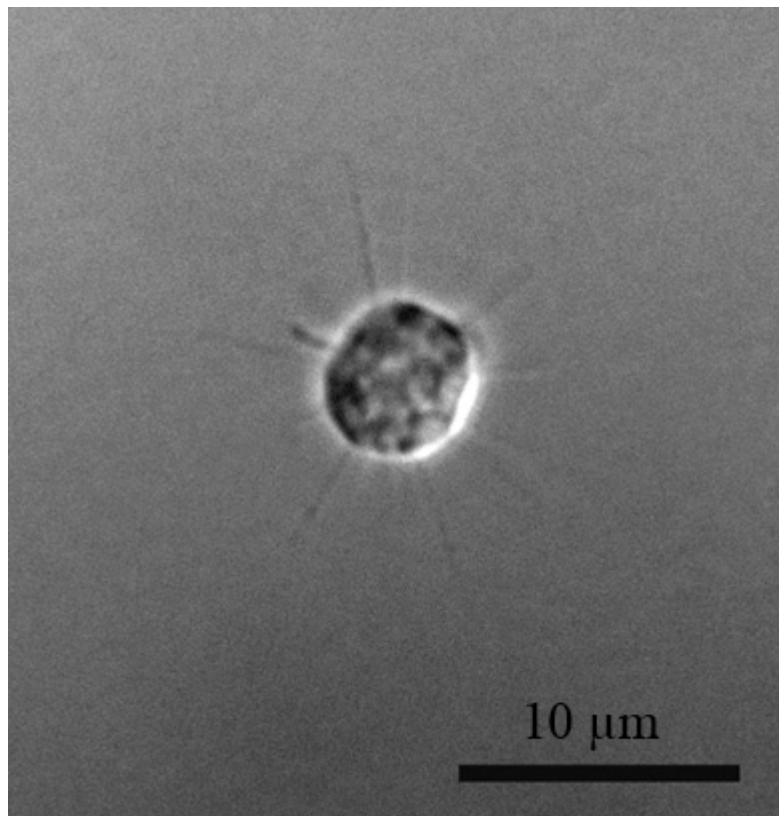


Figure 1. The single-celled eukaryote *Ciliophrys*, in which rRNA genes were identified as originating from lateral transfer. *Ciliophrys* is a member of stramenopiles, Ochrophyta, Dictyochophyceae; it preys on microbial organisms by entangling them in needle-like pseudopodia called axopodia. This species has vestigial chloroplasts (leucoplast) within the cell and has secondarily lost photosynthetic ability.

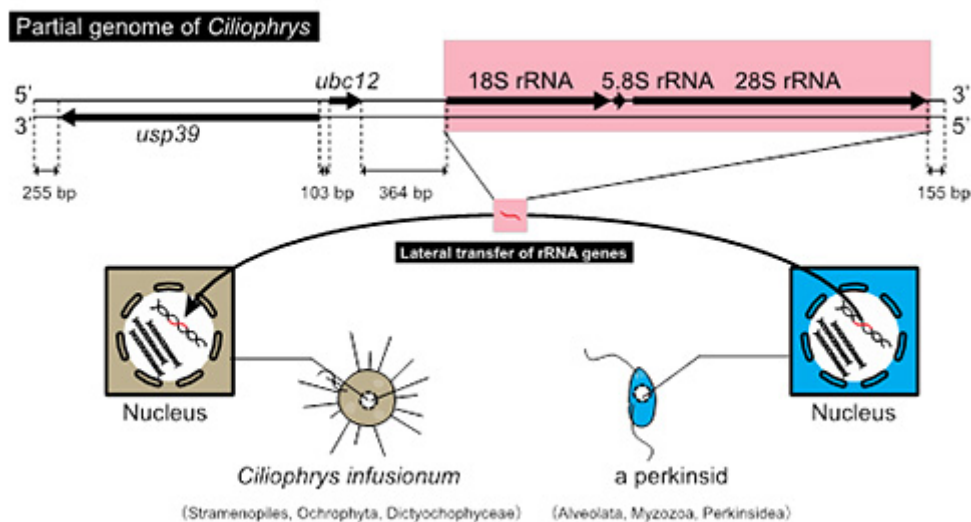


Figure 2. A schematic diagram showing lateral transfer of rRNA genes from a perkinsid species into *Ciliophrys*, as confirmed in the present study. Usually, rRNA genes are found in the genome as a set of three rRNA genes encoding 18S rRNA, 5.8S rRNA, and 28S rRNA. The partial genome sequenced in the present study suggests that the set of rRNA genes was transferred as a unit.

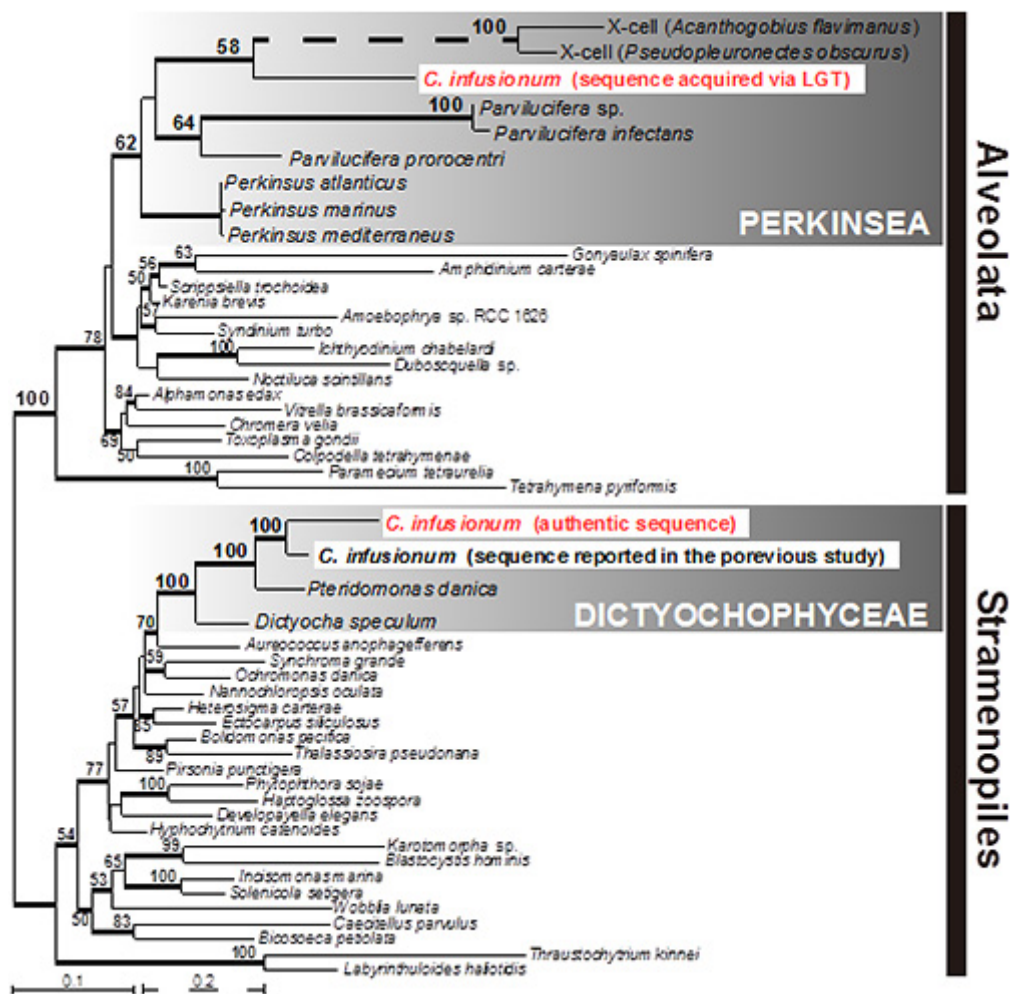


Figure 3. Molecular phylogenetic tree showing the source of the two types of 18S rRNA gene sequences identified in this study. The phylogenetic tree was constructed using a maximum likelihood method. The names shown in red in a white box are the two types of sequences identified and analyzed here. LGT; lateral gene transfer.

Contacts:

(For this study)

Akinori Yabuki, Scientist

Marine Biodiversity Research Program, Institute of Biogeosciences (BioGeos)

(For press release)

Kazushige Kikuchi, Manager Press Division, Public Relations Department