# Transcriptome analysis of *Tetrahymena thermophila*

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SUMMARY

Symbioses are widely found in nature. However, it is difficult to analyze how symbioses have been established, because symbioses in nature have already optimized their functions to maintain the sophisticated symbiotic relationship. To understand how symbiosis occurs, we are constructing an artificial symbiotic system between a ciliate, *Tetrahymena thermophila*, and a bacterium, *Escherichia coli*, in the laboratory. In the present study, we aimed to establish a transcriptome analysis method for *T. thermophila*, in order to understand the global changes in gene expression during development of the artificial symbiosis. We designed a custom high-density oligonucleotide microarray (Affymetrix GeneChip) for *T. thermophila*. Total RNA was isolated and purified from independently cultured *T. thermophila* cells. For GeneChip transcriptome analysis, standard methods for target sample preparation, hybridization, and scanned image analysis were carried out in accordance with the Affymetrix eukaryotic target preparation protocols. We confirmed specific hybridization between the target sample and *T. thermophila* probes. This result indicated that the present method would enable us to analyze changes in gene expression of *T. thermophila* during the development of the artificial symbiosis.