Non coding RNA Project


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The Ministry of Economy, Trade, and Industry (METI) launched "Functional RNA Project" in 2005. The project is headed by Dr. Kimitsuna Watanabe (Director, Biological Information Research Center). Recent studies have revealed that a large number of functional noncoding RNA molecules (RNA that does not code for proteins) are present in higher animals such as mammals. The purpose of this project is to develop techniques for predicting, analyzing, and measuring these functional noncoding RNA molecules, and to perform an analysis of their actual function.

The project encompasses the three groups of bioinformatics, assay tool development, and functional analysis. The project was undertaken by Japan Biological Informatics Consortium (JBIC). The participating members of bioinformatics group: Mizuho Information and Research Institute, Inc., Intec Web and Genome Informatics Corporation, and Mitsubishi Research Institute, Inc. AIST (Taishin Kin, Koji Tsuda, and Hisanori Kiryu), The University of Tokyo (Asai Laboratory), Keio University (Sakakibara Laboratory, Kanai Laboratory) and others are involved in the form of collaborative research with JBIC. Most researchers are assembled on the 7th floor (operations base for AIST-University of Tokyo Collaborative Research) of the same building as CBRC (Bio-IT Research Building) in Odaiba.

At present there are three research themes that we believe are the most important in the field of bioinformatics. The first theme is to develop a novel RNA sequence data analysis technique that will enable us to handle RNA secondary structure. That is because a sequence analysis technique of aligning RNA sequences in view of secondary structure, and comparing/classifying, then searching is important to find functional RNAs within a set of transcripts and genomic sequences. However, massive computational costs (both for memory and time) will be needed for the sequence comparison in view of secondary structures, so development of a new algorithm is critical. The second theme is to find functional RNAs by means of comparative genomics. There are already several software tools developed on comparative genomics for discovery of functional RNAs. While we use these tools for our analysis, we aim to devise our original methodology that fully exploits advantages of the techniques developed in the first theme to discover novel functional RNA molecules. The third theme is the development of a functional RNA database. Only a few years have elapsed since the concept of functional RNA began to receive attention. Although there are several RNA databases including widely known Rfam, a comprehensive and easy-to-use database has not been established, With the goal of providing an information infrastructure within the project, we will develop a database that covers the known functional RNA information, newly discovered functional RNA data, and interim analysis results.

RNA sequence data analysis software such as Scarna (RNA sequence alignment), Murlet (RNA sequence multiple alignment), RNAmine (RNA secondary structure motif extraction and clustering), PHMMTS (RNA structure alignment), and the like are under development by the project-participating members. In addition to these software tools and databases under development, a website has been launched that integrates information and data about functional RNA (http://www.ncrna.org).

Fig.1
Portal site for functional RNA (www.ncrna.org)

Fig.2
Scarna web server (www.scarna.org)

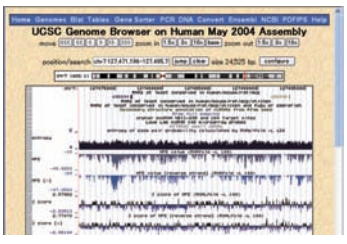

Fig.3
UCSC genome browser with functional RNA data