CDB SEMINAR

Speaker: **Yoshihide HAYASHIZAKI, M.D., Ph.D.**

<Project Director, Genome Exploration Research Group
RIKEN Genomic Science Center, Yokohama>

Title: “Functional RNA”

Date: Friday, January 21
Time: 10:00 -11:00
Place: IF Auditorium of Building C

Summary:

Through the FANTOM international consortium activity lead by GSC, we discovered a very large amount of unknown transcripts and half of them turned out to be non-coding RNA (“The RNAs Continent Theory”) by the analysis of 103,000 cDNAs, 10,000,000 CAGE-determined transcriptional starting sites and 2,500,000 transcriptional starting sites-termination sites determined by GSC and GIS technologies. At least 65% of genome is transcribed in hnRNA and number of transcripts being discovered is still now increasing. We have discovered mega RNAs spanning more than 500kb on the genome. The ncRNA, for which we could define a function, is constituted by structural RNAs and non-structural RNAs. We also showed that large parts of ncRNAs have sense-antisense (S/AS) function. Structural RNAs can fold in to higher-order structures having their own character, such as specific structure, like proteins, or enzyme activity. On the contrary, non-structural RNAs do not fold into such specific structures and constitute a major population of ncRNAs. We discovered that non-structural RNAi are related to regulation of gene expression. In fact, we discovered that at least 36,000 S/AS pairs are present in the transcriptome by analyzing the 103,000 FANTOM-3 cDNAs. These ncRNAs are involved in transcriptional and posttranscriptional regulation, which are very hot research areas and our findings are opening several new research fields. Short dsRNAs, one of the hottest recent research topics, directly regulate gene expression at chromatin level, such in case of Chromatin Based Gene Silencing (CBGS), promoter interference/enhancement at transcription level and RNAs at post-transcription level. In fact, several papers appeared recently in main journals regarding CBGS, RNAi and promoter interference/enhancement and finally “Functional RNA” has been chosen for the Nobel symposium in 2006 (Organizers: Y. Hayashizaki and C. Wahlestedt). The importance of “The RNA Continent theory” is also recognized during the FANTOM-3 research activity, showing that ncRNAs are functionally expressed to form S/AS pairs. We discovered the existence of transcripts antisense to a very large number of genes essential for life. Therefore, we should urgently establish a research system for comprehensively understanding functional RNA, based on our background and resources and by cooperating together between bradly-focused pivotal institutes (producing what we call “horizontal resources”), such as GSC, which shall produce the fundamental data, and specialized institutes (producing what we call “vertical resources”), for elucidating focused biological phenomena. Pivotal institutes, using systematic analyzing methods, and focused research teams, elucidating individual biological phenomena, should conduct the following research lines: 1) analysis of protein-RNA interaction and intracellular RNA localization for structural RNA and 2) identification of the functional mechanism of ncRNA and construction of a comprehensive analysis system for transcriptional regulation by S/AS in biological pathways. We have been finding atnisense transcripts for various genes, for which the analysis is now in progress, which regulates gene expression at pre, mid and post transcription level. Thus, we emphasize the importance to establish such systematic analytical system. CDB scientists are already researching various biological phenomena related to ncRNA. Therefore we would like to propose to the CDB to collaborate on such researches unifying own rich resource of knowledge and experiences, especially for the analysis of the Riboregulator Network at each developmental stage.

Host: **Masatoshi Takeichi** <Cell Adhesion and Tissue Patterning, CDB>
E-mail: takeichi@cdb.riken.jp Tel: 078-306-3116 (ext. 1321)
RIKEN Center for Developmental Biology http://www.cdb.riken.jp/