

Press Release

September 1st, 2005 (Eastern Time, USA)

The FANTOM Consortium for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute and Genome Science Laboratory, Discovery and Research Institute, RIKEN Wako Institute (Genome Network Core Group), announce the publishing of two milestone papers this week in the prestigious journal *Science*, which will transform our understanding of how the genes in mammals are controlled.

The past five years have seen the completion of several mammalian genome sequences, but these are of limited value unless we can decode the way that they are translated into functions required to create a mature animal. Only around 2% of the genome is translated into proteins (coding transcripts), the building blocks of the cells that make up our bodies. But which 2%, and how is it controlled?

The key intermediate is the transcriptome, which now has been subject to the most comprehensive characterization ever. The groundbreaking study has used new technology that accurately tags the beginning and end of each of over 20 million RNA messages (transcripts) created by genes, resulting in a powerful profile of the regulating control of genes. In addition, it has also shown that overlapping sense/antisense transcript pairs (both strands) are almost universal in the genome, and that S/AS pairs are especially abundant in imprinted loci, keeping with the putative role of non-coding RNA in the mechanism of gene silencing.

Since mammals only have slightly more conventional genes (around 22,000) than a simple worm, the results of the FANTOM Consortium study clearly indicate that while proteins comprise the essential components of our cells, the development of multicellular organisms like mammals is controlled by vast amounts of regulatory non-coding RNAs that until recently was not suspected to exist or be relevant to our biology. The findings

suggest that the difference between mouse and man may well lie in the control systems of these genes, and not in the structures of the proteins some of them code for

“We have provided the biomedical research community with the tools to understand the controls that are needed to make a mammal. We have deciphered the genome sequence not only for the code for making the parts (proteins) of a mammal, but also the code for making the right forms, in the right amounts, in the right place, at the right time.” states project leader Yoshihide Hyashizaki.

These studies have been carried out mainly on mice; the most widely used experimental mammalian species. Equivalent human data is not far behind, and RIKEN and many FANTOM members are actively involved in the next phase, the Genome Network consortium (<http://www.mext-life.jp/genome/english/index.html>), which aims to use these new tools to understand human development and disease. Associated with the publication of the Science papers, all of the information will be publicly released on Internet in a unique user-friendly format. (On the servers of DDBJ, National Institute of Genetics and RIKEN: <http://www.ddbj.nig.ac.jp/>, <http://fantom3.gsc.riken.jp/>, <http://www.ddbj.nig.ac.jp/whatsnew/050124-e.html>)