

— Keynote Address —

Comparative Genomics for Understanding Ourselves

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International Human Genome Sequencing Consortium including our Center has determined the draft sequence of the human genome, which revealed several interesting features of our genome including the existence of 30000 ~ 40000 genes and very large amount (~50%) of repetitive sequences. However, the information obtained through the human genome sequence itself is limited and various different types of approaches are required for further understanding.

One of the powerful approaches is “comparative genomics”. DNA is a common language to all the organisms, so that the information and knowledge of one organism could be easily compared with and transferred to the other. My group has been taking the comparative genomics approach by using several experimental organisms including yeast, fly and mouse. In yeast-human comparison, we identified a novel regulatory function of a highly conserved gene in amino acid metabolisms. *Drosophila*-human comparison successfully elucidated molecular mechanisms of circadian rhythms in mammals. As well, human-mouse comparison enabled us to identify highly conserved new genes, regulatory elements and other elements whose function is unknown. In addition, we started human-chimpanzee comparison to identify genes or genotypes that define the characteristic features of human such as the use of language and highly developed intelligence. I would like to report our recent progress in comparative genomics.