— 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 in-
cluding 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. Drosophia-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.