Genome-wide screenings for circadian clock genes in Drosophila

<u>Akira Matsumoto</u>

Research and Development Center for Higher Education, Kyushu University,

Fukuoka 810-8560, Japan

Circadian rhythms govern behavior, physiology and metabolism of living organisms. Recent studies have revealed the role of several genes in the clock mechanism both in *Drosophila* and mammals. The core molecular mechanism underlying circadian oscillation in *Drosophila* is comprised of two interlocked feedback loops: a *period (per)/ timeless (tim)* loop as a negative loop, and a *Clock (Clk)/cycle (cyc)* loop as a positive one. Although the framework of molecular mechanism of circadian oscillation is extensively elucidated, there are many issues unsolved concerning to the basic features of circadian rhythm.

To study how gene expression is globally regulated by the clock mechanism, we used a high-density oligonucleotide probe array (GeneChip) to profile gene expression patterns in *Drosophila* under light-dark and constant dark conditions. We found 712 genes showing a daily fluctuation in mRNA levels under light-dark conditions and among them expression of 115 genes was still cycling in constant darkness, i.e. under a free-running condition. Unexpectedly, expression of a large number of genes cycled only under constant darkness. We are now doing behavior screenings for core clock genes by RNAi method. I will report our preliminary results.

This project is the collaborate work with Hiroki Ueda (RIKEN CDB), Ryu Ueda, Kuniaki Takahashi (NIG), Kaoru Saigo (Univ. Tokyo) and Teiichi Tanimura (Kyushu Univ.).