OIST OKINAWA INSTITUTE OF SCIENCE AND TECHNOLOGY GRADUATE UNIVERSITY

OIST SEMINAR

Date: Thursday, March 8, 2014

Time: 11:00 – 12:300

Venue: OIST Campus Lab 1, Meeting Room C016 (Level C)

Speaker: Dr. Yumiko Yamasaki-Kato,

Affiliation: Biodiversity Group, Department of Natural History Science, Graduate School of Science, Hokkaido University

Title: "Analysis of the function of miR-124 during medaka neural development"

Abstract:

MicroRNAs (miRNAs) comprise a group of small noncoding RNA molecules (about 22 nucleotides) thought to have contributed to the evolution of vertebrate brain homogeneity as well as diversity. The miRNA miR-124 is well conserved between invertebrates and vertebrates and is expressed abundantly in the central nervous system (CNS).

For my doctoral dissertation, I studied the function of miR-124 in *Oryzias latipes* (medaka). In this research, I collaborated with Dr. Rie Kusakabe and Prof. Dr. Kunio Inoue of Kobe University, Japan. We identified five candidate genes for medaka miR-124. The five genes are unlinked on four different chromosomes and differ in nucleotide length. Their sequences suggest that they can generate functional miRNAs through conventional miRNA biogenesis by folding into stem-loop structures. By RT-PCR, we showed that the five genes were expressed at different levels and the possibility they have distinct spatiotemporal roles. Whole-mount in situ hybridization and northern blotting revealed that mature miR-124 is specifically expressed in the CNS and the eyes starting at 2 days post-fertilization. These results suggest that medaka miR-124 is related to neural differentiation. We also examined the sequences and expression of medaka *Polypyrimidine tract binding protein 1* (*Ptbp1*), a possible direct target of miR-124. The 3′UTR of medaka *Ptbp1* contains predicted binding motifs (target sites) for miR-124. A GFP reporter assay for the target sites or the entire 3′UTR showed that exogenous miR-124 silences PTBP1 expression in vivo. These results suggest that medaka miR-124 is involved in post-transcriptional regulation of target genes in neural development.

MiR-124 plays an important role in development of the CNS in medaka, as well as in other vertebrates. Further analysis will reveal that distinct spatiotemporal expression patterns of medaka miR-124 genes are strictly regulated and contribute to the functional diversity.

I would also like to talk about my future researches. I want to continue research on neural development and I hope to investigate gene regulatory networks, possibly using the teleost retina as a model system. I am especially interested in epigenetic regulatory systems including DNA methylation and chromatin organization that are required for normal spatiotemporal gene expression and control cell differentiation in neurogenesis.

Hosted by Developmental Neurobiology Unit (Masai Unit)