CDB SEMINAR

Date: Tuesday, December 9
Time: 13:00 P.M.~15:00 P.M.
Place: 6F Conference Room of Building C, CDB

<13:00~14:00>

Speaker: **Yasushi Nakagawa**

<Department of Neuroscience, Stem Cell Institute, University of Minnesota>

Title: **“A GENETIC APPROACH TO THE DEVELOPMENT OF SENSORY MAPS IN MAMMALIAN NEOCORTEX”**

Summary

The mammalian neocortex is essential for processing and ultimately perceiving sensory information. The adult neocortex has anatomically and physiologically distinct areas that serve three sensory modalities, vision, somatic sensation and hearing. Each primary sensory area receives its information via axons from a corresponding principal sensory nucleus of the dorsal thalamus. The aim of our research is to understand the mechanisms responsible for development of the unique features of the different cortical sensory areas. It is likely that this process is controlled by both intrinsic mechanisms involving patterning molecules and transcriptional regulation, and extrinsic mechanisms such as those mediated by the input from other parts of the brain. We are interested in the extrinsic mechanisms, particularly in the roles of thalamocortical projections in area differentiation and how they cooperate with the intrinsic mechanisms.

To begin such analyses, I established a line of mice in which Cre recombinase cassette was inserted in *ROR* gene, a member of the nuclear receptor family. These knock-in mice exhibit Cre-mediated recombination specifically in the three principal sensory nuclei of dorsal thalamus, where endogenous *ROR* is normally expressed at a high level. By crossing these mice with axon-targeted Cre reporters, we are analyzing the development of thalamocortical projections from *ROR* -expressing, dorsal thalamic neurons. We also plan to use the *ROR* *Cre* mice to selectively ablate some of the dorsal thalamic nuclei so that we can test the specific roles of thalamic input in area differentiation of the neocortex.

<14:00~15:00>

Speaker: **Masaru Nakamoto**

<Department of Neurosciences, Lerner Research Institute, The Cleveland Clinic Foundation>

Title: **“Eph receptors and ephrins in neural map development”**

Summary

Eph receptor tyrosine kinases and their ligands, ephrins, are predominantly expressed in the developing central nervous system with distinct but overlapping patterns. Whereas several members of the Eph and ephrin families have been implicated in specific axon pathfinding and target selection, the functional significance of partially-overlapped expression is not well-understood. In recent studies on the chicken olivocerebellar projection, we have found that different combinations of Eph receptors and ephrins are expressed in distinct domains of the inferior olive and the cerebellum, respectively. The domains defined by the Eph/ephrin expression correspond to olivocerebellar mapping domain. In vivo and in vitro axon guidance assays suggest that combinations of EphA receptors and ephrin-As constitute domain-specific positional information, and the spatially accurate receptor-ligand interaction is essential to guide inferior olive axons to their correct target domains in the cerebellum. Several models for the molecular mechanisms by which the Eph/ephrin interaction guide inferior olive axons to their correct cerebellar target domains will be discussed.

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