CDB SEMINAR

Speaker: Yoshinori Fujiyoshi

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Title: "Structure and function of channels analysed by cryo-electron microscopy"

Date:	**Thursday, March 18**
Time:	**17:00 -18:00**
Place:	**7th floor Conference Room of Building A,CDB**

Summary:

Cells regulate cell signaling by ion channels. Water movement through the membrane should therefore be strictly separated from the movement of ions. This means water channels must be highly specific for water to prevent any ions. The studies on function of a water channel, aquaporin-1, for the last decade put us puzzling questions. For answering these questions, structure of aquaporin-1 was analysed by electron crystallography. In our body, eleven water channels, aquaporin-0 to 10, were identified. Aquaporin-4 is the predominant water channel in brain and thus an important target for treatment of cerebral edema. The water channel is abundantly expressed in glial cells in the brain, particularly in glial end feet where it forms orthogonal arrays and in glial lamellae of the hypothalamus where it may play a role in osmo-, thermo- and glucose-sensing. Two-dimensional crystals were analysed. The results provide insights into the fast water conductance by narrow pore, and also suggest a structural role for aquaporine-4 in the adhesion of membrane layers in glial lamellae.

We are also interested in function of ion channels. The muscle-derived electric organ of the Torpedo electric ray is highly enriched in acetylcholine (ACh) receptor-containing membranes. The membranes are readily converted into tubular crystals. By imaging of the tubular crystals in thin films of amorphous ice structure of ACh receptor was analysed. The ACh receptor has a cation-selective pore, delineated by a ring of five subunits. In each subunit, four membrane-spanning segments, M1-M4 were predicted and the second membrane-spanning segment, M2, shapes the lumen of the pore and forms the gate of the channel. We also analysed structure of voltage sensitive Na+-channel as well as IP3 receptor by single particle method, while the resolutions are limited. I would like to introduce recent structural biology of membrane proteins by utilizing our cryo-electron microscope with helium cooled specimen stage.

Host: **Masatoshi Takeichi** **Cell Adhesion/Tissue Patterning ,CDB**
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