

# 生命科学セミナー

## Charm of the structure-function study of ion channels

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**KUIAS Main Building, 2F Seminar Room**  
(Kyoto University Campus map #77)

### **Abstract:**

Ion channels are membrane proteins that play fundamental physiological roles, including the regulation of excitability in neurons and muscles. Since the cloning of ion channel cDNAs, structure-function studies in heterologous expression systems have elucidated the functioning mechanisms, and recent advances in structural biology have greatly accelerated this progress. In this seminar, I will present two studies that illustrate the “charm” of ion channel research.

[ A novel ion-conducting pathway in an inherited GIRK mutant (J Physiol, 2022) ]

G protein-gated inwardly rectifying K<sup>+</sup> (GIRK) channels are critical regulators of membrane excitability in the brain, heart, and other organs. K<sup>+</sup> channels are highly selective for K<sup>+</sup> over Na<sup>+</sup>, a property conferred by the selectivity filter in the central pore. Mutations in and around the GIRK selectivity filter are associated with some inherited human diseases. It is widely assumed -without direct evidence- that the pathophysiology arises from impaired selectivity caused by deformation of the central permeation pathway. We showed that this is not necessarily the case: in some mutants, a distinct secondary ion-conducting route exhibiting abnormal ion selectivity is formed alongside the central pore.

[ An extracellular K<sup>+</sup>-gated Cl<sup>-</sup> channel, DmAlka (unpublished) ]

Extracellular K<sup>+</sup> strongly influences membrane excitability by setting the K<sup>+</sup> equilibrium potential, yet membrane proteins directly regulated by the binding of extracellular K<sup>+</sup> have not been described in animals. DmAlka, a Cys-loop receptor type anion channel expressed in the Drosophila nervous system, has been characterized as an extracellular pH-sensitive channel. We serendipitously discovered that DmAlka is directly regulated by extracellular K<sup>+</sup> within the physiological range, and mutational analysis identified a candidate K<sup>+</sup>-binding site consistent with direct gating.



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