第9回　埼玉大学脳科学セミナー

主催：埼玉大学脳科学融合研究センター

The nematode *C. elegans*: an ideal model system for the study of membrane traffic in the post-genomic era

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場 所:　大学会館 ２階 小集会室

本セミナー修了後に簡単な懇親会を予定しております
（参加費３００円、学生無料）

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セミナー要旨　**Abstract**

Membrane traffic is a fundamental cellular process not only for viability in eukaryotic cells, but also for development and homeostasis in multicellular organism. The genes involved in membrane traffic have been identified during the last decade or two, but their physiological roles remains largely unknown. *Caenorhabditis elegans* is the first multicellular organism whose complete genome sequence has been determined. Many of the genes that are homologous to known vertebrate genes which may participate in membrane traffic are conserved on the *C. elegans* genome. Towards reverse genetics approach for the genes of interest, we have developed an efficient gene knockout protocol for isolation of deletion mutants using TMP/UV method combined with PCR-based screening. We have systematically isolated deletion mutants for three main protein families; Rab GTPase, t-SNARE (syntaxin) and SM (Sec1/Munc18), which are generally known as essential factors for docking/fusion of membrane-bound organelles. Some of these mutations resulted in various severe phenotypes including embryonic or larval lethality, sterility and defective movements, whereas others appear superficially normal. In this talk, I will focus on the functional analyses of the SM family using combination of gene knockout and transgenic analysis to visualize membrane traffic pathways in living animals. Our results revealed that SM family members have specific functions in the secretory and the endocytic pathways, which regulate neurotransmitter release and cell integrity in *C. elegans*.