CDB SEMINAR

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16:30 - 17:30 C1F CDB Auditorium

Developmental biology meets single-molecule detection technologies; Measurement-based mathematical modeling of PAR protein localization in *C. elegans* embryos

Abstract

Genetic and molecular analyses have shown that asymmetric localization of PAR proteins is achieved by mutual inhibition and feedback controls. However, it remains largely unknown how the physical properties of polarity proteins are controlled in the pattern formation. Recently, we succeeded in detecting single molecules of a Ring protein PAR-2 fused with GFP in living embryos using total internal reflection fluorescent microscopy (TIRFM). PAR-2 formed oligomers, and larger oligomers accumulated in the posterior side of the embryo. The cortical localization of PAR-2 proteins is known to be regulated by PKC-3-dependent phosphorylation. By comparing dissociation rate constants between PAR-2 proteins in different oligomer sizes or in different phosphorylation states, we demonstrated that the phosphorylation promotes, but the oligomerization negatively regulates PAR-2's dissociation from the cortex. Furthermore, we constructed a mathematical model, in which all the physical parameters were determined by *in vivo* measurements using single-molecule detection technologies. In this model, we reproduced the asymmetric localization of PAR-2 proteins, indicating that the multiple components identified by our measurements were sufficient for asymmetric localization. Thus, the asymmetric localization of PAR-2 proteins is maintained by a molecular state control to diversify kinetic rates of PAR-2 proteins in living embryos.

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