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Self-Organization of the Phosphatidylinositol Lipids Signaling System for Random Cell Migration
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Phosphatidylinositol (PtdIns) lipids have been identified as key signaling mediators for random cell migration as well as chemoattractant-induced directional migration. However, how the PtdIns lipids are organized spatiotemporally to regulate cellular motility and polarity remains to be clarified. Here, we found that self-organized waves of PtdIns 3,4,5-trisphosphate [PtdIns(3,4,5)P3] are generated spontaneously on the membrane of Dictyostelium cells in the absence of a chemoattractant. Characteristic oscillatory dynamics within the PtdIns lipids signaling system were determined experimentally by observing the phenotypic variability of PtdIns lipid waves in single cells, which exhibited characteristics of a relaxation oscillator. The enzymes phosphatase and tensin homolog (PTEN) and phosphoinositide-3-kinase (PI3K), which are regulators for PtdIns lipid concentrations along the membrane, were essential for wave generation whereas functional actin cytoskeleton was not. Defects in these enzymes inhibited wave generation as well as actin-based polarization and cell migration. On the basis of these experimental results, we developed a reaction-diffusion model that reproduced the characteristic relaxation oscillation dynamics of the PtdIns lipid system, illustrating that a self-organization mechanism provides the basis for the PtdIns lipids signaling system to generate spontaneous spatiotemporal signals for random cell migration and that molecular noise derived from stochastic fluctuations within the signaling components gives rise to the variability of these spontaneous signals. PNAS 107 12399-12404

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The Combination of Pulsatile and Switch-Like Behaviors of p53 in Response to DNA Damage
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Upon DNA damage, p53 is stabilized and activated to induce diverse cellular outcomes including cell cycle arrest and apoptosis. The p53 dynamics can exhibit distinct modes, depending on cell and stress types. In an analog mode, high (low) levels of p53 lead to cell death (survival) in response to lethal (sublethal) DNA damage. By contrast, p53 levels exhibit a series of discrete pulses in a digital mode, wherein it is the number of p53 pulses that determines the cell fate [1]. Here, we explore whether both the modes of p53 are exploited in one cellular response. We propose a modular model for the cell fate decision between survival and death, which is governed by the p53 network. At low damage levels, p53 levels exhibit few pulses, and the cell returns to normal proliferation after DNA damage is fixed. For irreparable damage, the amount of p53 first displays four pulses and then switches to high levels, and the cell undergoes apoptosis. The negative feedback loop between p53 and Mdm2 and that between ATM and p53 via Wip1 are responsible for p53 oscillations, whereas the switching behavior occurs when the positive feedback loop between p53 and PTEN predominates over the negative feedback loops. Such a combination of pulsatile and switch-like behaviors of p53 may represent a flexible and reliable control mode, avoiding unnecessary cell death or promoting execution of apoptosis. This work also underscores that both the nature and strength of feedback loops determine p53 dynamics.
[1] X.-P. Zhang, F. Liu, Z. Cheng, and W. Wang (2009) Cell fate decision mediated by p53 pulses. Proc. Natl. Acad. Sci. USA. 106, 12245-12250.

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Time-Keeping in the Transcriptional Cascades of the Developing C. elegans Embryo
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Cell differentiation and cell proliferation are coordinated during animal development by mechanisms that remain largely unknown. We use the fact that the timespan of development in C. elegans can be varied significantly by changes in temperature and mutations to discern the nature of the coordination mechanism at play in this organism. We have measured time profiles of gene expression in key organogenesis pathways of C. elegans embryos that have grown under conditions and genetic backgrounds that significantly change the overall rate of development. We used the single molecule RNA fluorescence in situ hybridization technique recently developed by our group to obtain absolute RNA transcript numbers with single molecule sensitivity. The data allow us to determine the extent to which RNA dynamics remain locked to the cell cycle as lifespan is varied and infer the existence of coordinator processes from changes of apparent induction thresholds in transcriptional cascades.

PLATFORM O: Actin & Actin-binding Proteins

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Structural Polymorphism in F-Actin
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Actin plays a major role in many cellular processes including motility, cell division, endocytosis, and exocytosis. Actin has also maintained an exquisite degree of sequence conservation over large evolutionary distances for reasons that are not understood. Generating an atomic model of the actin filament (F-actin) has been driven by the desire to explain phenomena from muscle contraction to cytokinesis in mechanistic detail. To understand how key mobile elements of actin contribute to the intrinsic structural polymorphism of F-actin we carried out electron microscopic studies of the frozen-hydrated actin filaments. We show that frozen-hydrated actin filaments possess substantial structural polymorphism. We demonstrate at higher resolution (~ 10 Å) that within the actin filament subdomain 2 of actin (SD2) can undergo significant structural alterations from an ordered position to complete disorder, and that its dynamics is coupled with that of the C- and N-termini of actin molecule. Our observations reconcile the multiplicity of structural conformations of actin observed by x-ray crystallography with the multiplicity of conformations seen within F-actin. We link a number of disease-causing mutations in the human ACTA1 gene to the most structurally dynamic elements of actin. Since F-actin is structurally polymorphic it cannot be described using only one atomic model, and must be understood as an ensemble of different states.

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Multiple Actin Structures in Monomeric and Filamentous States
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One of the most abundant proteins in eukaryotes is actin, a ubiquitous protein that plays a role in cell dynamics like cell migration. The dynamics of actin filament treadmilling is regulated by two actin structural states: globular actin (G-actin) and filamentous actin (F-actin). Although recently it was reported that the structure of the two actins differ (Oda., et al, Fujii., et al), there is still much to resolve on the matter of their dynamic structures.
Here we observed the dynamics of the actin structural states under various conditions by using single-molecule FRET in combination with TIRF microscopy. We found that bothF-actin and G-actin have at least two distinct states, and that the population distribution of these states depends on the ionic conditions. Furthermore, these states were sensitive to actin binding proteins like myosin and actinin. We are currently investigating actin structural states by performing FRET measurements to observe various positions of actin in the presence of the actin binding proteins myosins.

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Observation of Individual Actin Filaments Reveals that ATP Hydrolysis is a Random Mechanism
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After their polymerization into a filament, actin monomers hydrolyze their ATP and release the resulting inorganic phosphate (Pi). This phenomenon is of primary importance for the filament's assembly dynamics, as well as for its interaction with various regulatory proteins. However, the long debated question of whether Pi release follows a random or a vectorial mechanism still awaits conclusive experimental data.
We have developed a novel experimental approach, combining microfluidics, optical tweezers and fluorescence microscopy, in order to manipulate and observe individual actin filaments in a controlled biochemical environment. Our data provides a direct measurement of the Pi profile in actin filaments, and clearly shows that Pi release occurs according to a random mechanism.
In addition, using the same experimental setup, we have monitored the Pi profile in filaments polymerized in presence of profilin, and we have measured the impact of profilin on the kinetics of filament disassembly. We show that profilin