Division of Biosciences

Department of Integrated Biosciences

Laboratory	Faculty	Introduction of research activities and laboratory	Key words	Projects or activities summer program students can participate
Signal Transduction Laboratory	Prof. Yoshikazu OYA Assoc. Prof. Kuninori SUZUKI	The budding yeast Saccharomyces cerevisiae is a very attractive model organism for studying the fundamental theories and concepts of eukaryotic cells. We applied the power of yeast genetics to understand many aspects of yeast cells. Our current research is mainly focused on (1) system biology based on cell imaging, (2) function of cell wall and cell wall integrity checkpoint, and (3) autophagy. (1) To understand biological system as the network of logical and informational process, one of the invaluable tools is genetics. Global analysis of the mutant phenotypes can provide relationships between knockout of the gene and function in the network. We developed CalMorph image analysis system useful to examine high-dimensional quantitative phenotypes under the fluorescent microscope. This method can be applied to identifying intracellular drug target, monitoring fermentation process during culture and studying biological diversity. Our ultimate goal is to place all yeast genes and their corresponding products on a functional signaling network based on phenotyping. (2) The cell wall is an essential cellular component in yeast. The cell wall is dynamic, because it undergoes remodeling during the cell cycle. We demonstrated that small rho type GTPase Rho1 is regulated by the progression of the cell cycle. We also found that there is a new cell cycle checkpoint mechanism called “cell wall integrity checkpoint” which functions to control cell cycle progression in response to cell wall perturbation. We are now studying such signaling mechanism as well as biosynthesis of the cell wall in yeast. (3) Autophagy is a major pathway of bulk degradation of cytoplasmic materials. In yeast, autophagy has been studied as a cellular response for	Budding yeast Saccharomyces cerevisiae; systems biology; imaging; cell cycle; autophagy	(1) Live imaging and biochemical analysis of autophagosome formation and its degradation (2) Cell biological analysis of membrane sources of autophagosomes (3) Chemical genetic analysis of yeast autophagy (4) Multivariate analysis of high-dimensional morphometric data to our understanding of the pharmacology of antifungal drugs. (5) High-Content, image-based profiling to identify drug target. (6) High-dimensional quantitative phenotyping of yeast haploinsufficient genes (7) Single-cell phenomics with morphological data to reveal biodiversity and intraspecies variation in yeast. (8) Genetic study of multiple functional domains of the yeast 1,3-β-glucan synthase subunit by quantitative phenotypic analysis of temperature-sensitive mutants. (9) Phenotypic robustness contributed by the cell wall by protecting the intracellular functional network from environmental conditions. (10) Application of image-based monitoring system for green algal Haematococcus pluvialis (Chlorophyceae) cells during culture

		survival during nutrient-limited conditions. During autophagy, cytoplasmic components are enclosed in a membrane compartment, called an autophagosome. We are now studying the mechanisms of autophagosome formation and its degradation. Moreover, we have a particular interest in physiological significance of autophagy.		