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	1) Budding yeast saccharomyces cerevisiae 2) Systems biology 3) Imaging 4) Cell cycle 5) Autophagy	(1) Multivariate analysis of high-dimensional morphometric data to our understanding of the pharmacology of antifungal drugs. (2) High-Content, image-based profiling to identify drug target. (3) Chemical genetic analysis of yeast cell cycle (4) High-dimensional quantitative phenotyping of yeast essential genes (5) Single-cell phenomics with morphological data to reveal biodiversity and intra- species variation in yeast. (6) Biochemical study of dual role of the late S-phase transcription factor Hcm1 in yeast cell cycle regulation (7) Genetic study of multiple functional domains of the yeast 1,3-β-glucan synthase subunit by quantitative phenotypic analysis of temperature-sensitive mutants. (8) Phenotypic robustness contributed by the cell wall by protecting the intracellular functional network from environmental conditions. (9) Application of image-based monitoring system for green algal Haematococcus pluvialis (Chlorophyceae) cells during culture

		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 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.		(10) Live imaging and biochemical analysis of autophagosome formation and its degradation (11) Chemical genetic analysis of yeast autophagy (12) Cell biological analysis of membrane sources of autophagosomes
Kawamura Laboratory	Prof. Shoji KAWAMURA	It is crucial to understand humans within an evolutionary framework. By using non-model organisms to explore genetic variation and its ecological correlates in wild populations, it is now possible to reevaluate the evolutionary significance of human genetic variation. The evolutionary diversity of sensory systems-the visual system in particular-is an excellent model case for addressing these questions because recent technical developments have enabled functional evaluation of the relevant genes. Bearing these issues in mind, we pursue the following ongoing and prospective research projects using an interdisciplinary approach that spans molecular biology (population DNA sequencing, gene expression analysis, in vitro functional assays), biochemistry, population/evolutionary genetics, and behavioral ecology.	1) Color vision 2) Genetic variation 3) Primates 4) Evolutionary study 5) Sensory ecology	Reconstruction of color opsins of New World monkeys from fecal samples. Monkeys living in Meso and South America are well known as having extensive color vision variation and are an excellent model to study evolutionary forces to maintain color vision variation in humans. The color vision variation in New World monkeys is due to allelic polymorphism of the single-locus L/M opsin gene on the X chromosome. We have conducted field research of New World monkeys (capuchin, spider, and howler monkeys) in Costa Rica to study interrelation of color vision with behaviors. We have collected fecal samples from these monkeys to extract their genomic DNA and analyze their L/M opsin gene. The purpose of this program is for students to experience fecal

		(1) The evolutionary origin and driving force of variation in human color vision. (2) New World monkeys as models for understanding the evolutionary significance of primate trichromatic color vision. (3) Fish as a model to study the evolutionary flexibility of color vision. (4) Coevolution of chemical sense and vision in primates.		DNA extraction, quantification of monkey DNA from the fecal DNA, isolation and genotyping of the L/M opsin gene by PCR and nucleotide sequencing, reconstitution of the opsin photopigment in vitro, and measurement of its absorption spectra. Through this procedure, we can evaluate how variable the L/M opsin gene and color vision is within and between populations and species of these monkeys. This is the essential information to which we correlate behavioral variation and from which we elucidate evolutionary forces behind.
Nakayama Laboratory	Assoc.Prof. Kazuhiro NAKAYAMA	Our project focused on role of genetic adaptation for local environments in shaping the ethnic variety of diseases susceptibilities in East Asians. We recently reported evidence for positive natural selection events in Mongolians, one of the representative nomadic group in East Asia, using high density genome wide single nucleotide polymorphism (SNP) data (Nakayama K et al. Mol Biol Evol 2017 34:1936-46.). SNP that showed signature of selection in Mongolians would contribute to evolution of metabolic traits in Mongolians. We also identified the TRIB2 as a gene influencing visceral fat accumulation in modern East Asians and moreover, discovered signatures of positive natural selection related with adaptation to cold environments in ancestors of East Asians during the last glacial maximum (Nakayama K et al. Hum Genet 2013 132:201-17; Nakayama K and Iwamoto S J Physiol Anthropol 2017 36:16.).	1) Human 2) Genome variation 3) Evolution 4) Adaptation	We are planning to assess functional and phenotypic consequences of the variants under selection using medical genetic approaches, including in silico functional prediction, in vitro functional assays, and the association analysis with health checkup cohorts. The student can learn about DNA extraction and genotyping of focal SNPs in human DNA samples. Additionally, the student may learn about the principal of evolutionary genetic analyses using focal and genome-wide SNP genotype data.