

## Laboratory of Molecular Genetics

Professor: Satoshi Harashima, Associate Professor: Yoshinobu Kaneko,  
Assistant Professor: Minetaka Sugiyama

URL:

<http://www.bio.eng.osaka-u.ac.jp/mg/biomgadm/index.html>

E-mail: [harashima@bio.eng.osaka-u.ac.jp](mailto:harashima@bio.eng.osaka-u.ac.jp)

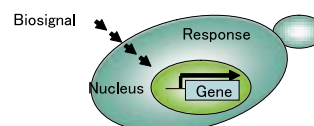


The main research interest of our laboratory is elucidating the basic mechanisms of gene regulation and genome function in eukaryotic organisms and their applications to molecular breeding. To achieve this aim, a simple eukaryotic microorganism, "*Saccharomyces cerevisiae*", was selected as a model organism because it is possible to perform precise genetic analysis with this organism and a sophisticated host-vector system has been developed. In recent years, *Saccharomyces* has attracted much interest as a model organism for the elucidation of basic cellular mechanisms, such as growth control and transcriptional regulation, in eukaryotes. The importance of *Saccharomyces* in the brewing and fermentation industries has also conferred on this organism a significant role as an experimental subject for research. Based on these facts, we are pursuing several research topics under the following four main research project headings. Furthermore, this laboratory also contributes to the activities of the Yeast Genetic Resource Center, under the [auspices of the] National BioResource Project, [supported][nominated] by MEXT as a COE (Center Of Excellence).

## Signal transduction and Regulation of Gene Expression in Yeast

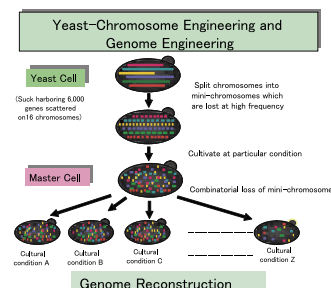
One of the main research topics in modern biosciences is the elucidation of signal transduction mechanisms. We have been interested in cellular responses to a variety of biological signals such as inorganic phosphate (Pi), lactic acid, oxygen and temperature. Recently, we have solved one of the fundamental issues regarding the Pi signal transduction system, i.e., whether intracellular or extracellular phosphate is an intrinsic signal, by demonstrating that the expression of target genes is strongly correlated with levels of intracellular orthophosphate and polyphosphate. However, the most fundamental issue, i.e., how cells sense phosphate availability and transduce the phosphate signal, is yet to be solved. We are striving to form a complete picture of this system in order to contribute to the understanding of the precise mechanism of eukaryotic signal transduction (1, 2).

Signal Transduction and Regulation of Gene Expression in Yeast



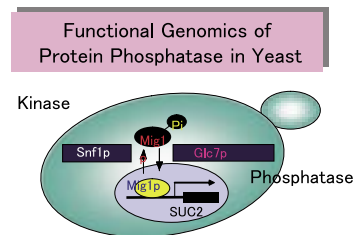
## Yeast Chromosome and Genome Engineering

Chromosome and genome engineering should be one of the fundamental technologies in bioscience and biotechnology in 21<sup>st</sup> century. We have developed a simple yet innovative method to split chromosomes in *Saccharomyces cerevisiae*. Chromosome splitting technology provides an efficient tool with which to engineer the yeast genome, using techniques such as genome reconstruction and [large-scale][a large scale of] deletion (3, 4, 5).



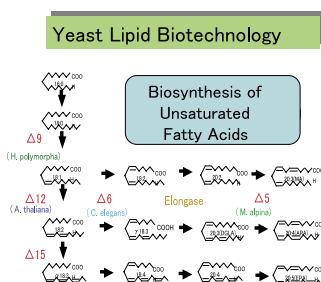
## Functional Genomics of Protein Phosphatases in Yeast

Protein phosphorylation/dephosphorylation plays an important role in regulating many cellular processes such as signal transduction, cell cycle progression and gene expression. In *Saccharomyces cerevisiae*, the nucleotide sequence of the entire genome predicts 117 protein kinase (PKase) and 32 protein phosphatase (PPase) genes out of a total of approximately 6,000 genes. Uncovering the role of the entire suite of PPases in a single-celled model eukaryote would contribute to understanding their physiological roles in higher eukaryotes. We are currently focusing our efforts on clarifying the role of each of the PPases in *S. cerevisiae* by means of a functional genomic approach.



## Yeast Lipid Biotechnology

Fatty acids (FAs), especially polyunsaturated fatty acids (PUFAs), are important in the human diet and as pharmaceuticals. Microorganisms are a promising source, serving as a “cell factory” to produce a variety of PUFAs. However, the biotechnology needed to employ microorganisms as a cell factory to produce PUFAs in an efficient and controlled manner has not yet been established. This is mainly due to the lack of understanding regarding the regulatory mechanism involved in the biosynthesis of PUFAs. We are using the methylotrophic yeast, *Hansenula polymorpha*, in our research to address this issue since, unlike *S. cerevisiae*, this yeast is able to produce PUFAs and it is possible to perform genetic analysis on it (6, 7).



## References (main papers in 2004 - 2007)

- (1) Intracellular phosphate serves as a signal for the regulation of the PHO pathway in *Saccharomyces cerevisiae* Choowong Auesukaree, Tomoyuki Homma, Hidehito Tochio, Masahiro Shirakawa, Yoshinobu Kaneko, Satoshi Harashima. *J Biol Chem.* 279(17):17289-17294 (2004).
- (2) Plc1p, Arg82p, and Kcs1p, enzymes involved in inositol pyrophosphate synthesis, are essential for phosphate regulation and polyphosphate accumulation in *Saccharomyces cerevisiae*. Choowong Auesukaree, Hidehito Tochio, Masahiro Shirakawa, Yoshinobu Kaneko, Satoshi Harashima *J Biol Chem.* 280(26):25127-25133 (2005).
- (3) PCR-mediated repeated chromosome splitting in *Saccharomyces cerevisiae*. Minetaka Sugiyama, Shigehito Ikushima, Toshimasa Nakazawa, Yoshinobu Kaneko Satoshi Harashima. *Biotechniques* 38(6):909-914 (2005).
- (4) Chromosome XII context is important for rDNA function in yeast. Yeon-Hee Kim, Daisuke Ishikawa, Ho Phu Ha, Minetake Sugiyama, Yoshinobu Kaneko, Satoshi Harashima. *Nucleic Acids Res.* 34(10):2914-2924 (2006).
- (5) Chromosome shuffling technique for selected chromosomal segments in *Saccharomyces cerevisiae*. Minetaka Sugiyama, Eishi Yamamoto, Yukio Mukai, Yoshinobu Kaneko, Masafumi Nishizawa, Satoshi Harashima. *Appl. Microbiol. Biotech.* 72(5):947-952 (2006).
- (6) Identification and Characterization of a Very Long-Chain Fatty Acid Elongase Gene in the Methylotrophic Yeast, *Hansenula polymorpha*. Phatthanon Prasitchoke, Yoshinobu Kaneko, Takeshi Bamba, Eiichiro Fukusaki, Akio Kobayashi, Satoshi Harashima *Gene* 391(1-2):16-25 (2006).
- (7) Functional analysis of verylong-chainfattyacidelongase gene, *HpELO2*, in the methylotrophic yeast *Hansenula polymorpha*. Phatthanon Prasitchoke, Yoshinobu Kaneko, Minetaka Sugiyama, Takeshi Bamba, Eiichiro Fukusaki, Akio Kobayashi, Satoshi Harashima *Appl. Microbiol. Biotech.* 76(2): 417-427 (2007).