

F301 The studies of *Schizosaccharomyces pombe* mutants defective
in the division of the cell cycle

Seong Chul Kim* and Hyong Bai Kim
Division of Molecular Biology, Graduate School of Biotechnology,
Korea University, Seoul 136-701, Korea

Fission yeast *S. pombe* is a rod-shaped cell that divides by medial cleavage using an actin based contractile ring and the septum. In order to understand the mechanism of cytokinesis, we have screened for temperature-sensitive *cdc* mutants which show abnormal cell division. One of the mutants (named as #17) is the longer than the wild type and cannot finish the cytokinesis at restricted temperature(37°C). The mutant 17 was shown scattered nuclei in the cytoplasm. We have cloned the gene from the mutant 17 using the functional complementation effect at the restricted temperature(37°C). The newly cloned gene has an open reading frame of 2090 bps containing 2 introns. The deduced amino acid sequence predicts a protein of 76 kDa containing 689 amino acids. We are trying to find out the role of the gene in septum formation.

F302 Molecular Characterization of the *soo1-1* Mutant Allele
Which Confers Osmofragility by Impairing Cell Wall
 β -1,3-Glucan Biosynthesis in *Saccharomyces cerevisiae*

Jae-Joon Lee*, Dong-Won Lee, and Hee-Moon Park
Department of Microbiology, Chungnam National University

Our previous study showed that the mutation in the *SOO1/aCOP* gene of *Saccharomyces cerevisiae* conferred temperature sensitive(ts) osmofragility by impairing cell wall β -1,3-glucan biosynthesis. To characterize the mutation at molecular level, the *soo1-1* mutant allele were cloned and characterized. Complementation test and nucleotide sequencing located two mutations at the N-terminal region of the *soo1-1*; one deletion at position 45(G) and the other G to A base substitution at 681. The deletion causes a frame shift and incomplete termination by the stop codon at 76. However, complementation test with the various N-terminal deletion constructs of the *SOO1* confirmed synthesis of an active truncated Soolp using a ATG codon at 421. These results indicate that the ts phenotype of the *soo1-1* mutation may be due to the change of Gly²²⁷ to Asp and that Gly²²⁷ may be crucial for translocation of protein(s) involved in β -1,3-glucan biosynthesis to plasma membrane via COPI vesicle in *S. cerevisiae*.