7th International
Molecular Biology and Biotechnology
Congress
25-27 April 2018, www.molbiotech.gen.tr

Role of *Schizosaccharomyces pombe git1* gene in oxidative stress response

Sedef Akcaalan[1], Bedia Palabiyik[2]

[1]Department of Molecular Biology and Genetics, Faculty of Science, Konya, Necmettin Erbakan University, Turkey
[2]Department of Molecular Biology and Genetics, Faculty of Science, Istanbul University, İstanbul, Turkey
sakcaalan@konya.edu.tr

Abstract

Glucose is the preferred energy and carbon source for many organisms. Glucose sensing and signal transduction in yeast is generally accomplished through a system of heterotrimeric G-protein and G protein-coupled cell surface receptors. Signal transduction pathway to cAMP/protein kinase is activated with glucose sensing. In this pathway, *Git1* is a C2 domain protein that is directly linked to adenylate cyclase and it is one of the 6 proteins required for the activation of adenylate cyclase. The 3' end of *git1* gene contains ''Mammalian uncoordinated homology 13, domain 2.'' It plays role membrane trafficking, exocytosis, vesicle secretion. This study aims to find out whether the *git1* gene, which is one of the genes involved in glucose signaling, and the 3' end of git1 gene, are related to oxidative stress response. In this study, *Schizosaccharomyces pombe* wild type (972h-) and git1- (*git1Δ*) mutant with *Escherichia coli DH5α* were used. Genomic DNA of S. pombe 972h- was used as a template to obtain *git1* and 3' deletion *git1* genes. These genes were cloned into plasmid pSGP572 containing the GFP reporter gene in the cloning site. The resulting recombinant vectors were transfected into super-efficient *E. coli DH5α* and then isolated. These isolated vectors were transformed into the *S. pombe git1Δ* mutant. Cell morphologies of transformants in the selective media were stained DAPI and then examined under confocal microscope. Transformants carrying recombinant plasmids were confirmed by GFP luminescence detected in a confocal microscope. There was no statistically significant difference in superoxide dismutase and catalase enzyme activities in H2O2 induced oxidative stress conditions in S. pombe recombinants and *S. pombe git1Δ* mutant. These results make think that cells probably select the different pathway alternatives in the stress response.

Keywords: *Schizosaccharomyces pombe*, *git1* gene, oxidative stress, glucose metabolism.