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A Novel Protein, Psp1, Essential for G_1/S Cell Cycle Progression of *Schizosaccharomyces pombe* Is Phosphorylated by Cdc2-Cdc13 upon Entry into G_0-Like Stationary Phase and Dis2 Dephosphorylates It.

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A novel gene, *psp1*$^+$, complementing a temperature-sensitive mutant defective in G_1 to S phase cell cycle progression has been isolated and is shown to be an essential gene for cell viability. However, overexpression of this gene in the actively growing cell showed inhibition of cell growth and DNA content analysis revealed multiple copy of DNA in the cell indicating the blockage of the proper DNA replication process. Psp1 protein exists in two different molecular weight form *in vivo*. The low molecular weight form is dominant in the actively growing cells and it became phosphorylated to a high molecular weight form upon entry into the stationary phase. Cdc2/Cdc13 complex phosphorylates the GST-Psp1 fusion protein *in vitro* and serine residue at the position 333 in the C-terminal region is absolutely required for phosphorylation by Cdc2/Cdc13. Meanwhile, a phosphatase Dis2 of *S. pombe* dephosphorylated the Psp1 *in vitro*. Western analysis and yeast two hybrid analysis confirmed that Cdc2/Cdc13 and Dis2 bound to Psp1. We suggest that this novel protein Psp1 is required as a dephosphorylated form during the progression of active cell cycle and is phosphorylated by mitotic Cdc2/Cdc13 complex when its function is not required for growth or upon deprivation of nutrient. A *S. pombe* phosphatase, Dis2, could be one of the elements that triggers activation of Psp1 by dephosphorylating Psp1 upon initiation of active growth cell cycle. This work was supported in part by the grants N80880, N81310, HS1030, HS1640 from Ministry of Science and Technology of Korea.

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A novel GATA type transcription factor involved in regulation of sexual development of *Aspergillus nidulans*

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Several mutants which never undergo sexual development(NSD) of *Aspergillus nidulans* have been isolated and characterized. A gene(*ncdA*) that complements *nsdD19* mutant allele was cloned and analyzed. Sequence analysis revealed that a putative zinc finger DNA binding domain was encoded by C-terminus of the gene. The zinc finger domain was similar to that of GATA factor but had two major differences. The number of amino acid in the central loop was 18 while that in GATA factor is 17, and the conserved leucin residue which is important for recognizing the target sequence was substituted by glutamic acid. This zinc finger was almost identical to the the WC gene product of *Neurospora crassa*. Several ORF deletion mutants were generated and revealed to have a significant defect in sexual development. The ORF of the gene was fused downstream the *niiA* promoter of *A. nidulans* and expressed in the wild type strain. Being induced with nitrate, the transformants developed a dramatically increased the number of cleistothecia. Expression of the gene was repressed by ammonium indicating that the gene may be responsible for the N source dependent sexual development. These results suggest that the *ncdA* gene encodes a putative transcription factor that has a zinc finger DNA binding domain and positively regulates the sexual development.