F021

Involvement of *CaKNS1* in *Candida albicans* Morphogenesis

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Previously we have reported the role of the dual-specificity LAMMER kinase in yeast morphogenesis by identifying that *Schizosaccharomyces pombe* LAMMER kinas homolog, Lkh1p, is a negative regulator of filamentous growth and flocculation. Recently we also found the requirement of Kns1p for the butanol-induced haploid filamentous growth in *Saccharomyces cerevisae*. Based on these results, we tried to reveal the involvement of Kns1p in differentiation of the opportunistic human pathogen, *Candida albicans* We cloned the *CaKNS1* and constructed the single- and double-disruptant of the *CaKNS1*. Interestingly, the *CaKNS1* disruption showed significant alterations in hyphae and colony morphology in gene-dosage dependent manner on various culture conditions In addition, the disruptants showed higher flocculation activity but lower level of chlamydospore-production than the wild type. Our results demonstrate that the *CaKNS1* plays a role in *C. albicans* morphogensis including filamentous growth like in other yeasts, *S. cerevisiae* and *S. pombe*

F022

ppGpp is Responsible for Boosting SigB Transcription, Osmo-adaptation and Diffrentiation In *Streptomyces Coelicolor* A3(2)

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SigB, A sigma factor which is responsible for osmo-adaptation and erecting aerial hypae is activated by alamone, ppGpp in *Streptomyces coelicolor* We disrupted RelA, measured ppGpp level by HPLC and confirmed abolishing of ppGpp peaks in RelA mutant We examined SigB transcription level via S1 mapping, the transcription level was lower than WT cell under osmotic stress condition RelA deletion mutant showed osmo-sensitivity and can not sporulation, resulting in bold phenotype These phenomena caused by insufficient SigB transcription and provide an important clue to understand the relationship between osmo-regulation and sigma competetion role of ppGpp in actinomycetes

F023

Stable Expression of GFP in the Phytopatogenic Fungus *Ustilago maydis* Isolated in Korea by REMI

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Ustilago maydis was transformed unstably using recombinant plasmid containing a hygromycin B phosphotransferase gene(*hph*) under controled *U maydis* glyceraldehyde-3-phosphate dehydrogenase(gap) promoter and that the plasmid werw integrated chromosomally in the transformant Here we roport a stable transformation of the fungus to hygromycin B resistance, using a recombinant green fluorescent protein (GFP) gene fused with *hph* gene. Transformants expressed GFP in culture and had the same general appearance as the wild type and GFP observed in all fungal structure An increase in the transformation efficiency using restriction-enzyme-mediated-integration(REMI)was also demonstrated

F024

Identification of *PRX1* of *Candida albicans*

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In the opportunistic fungal pathogen *Candida albicans*, a thiol-specific antioxidant (TSA1) has recently been characterized to function as a thioredoxin peroxidase, which scavenges H_2O_2 We have discovered another putative antioxidant enzyme named PRX1 by Blast search through the Candida Genome Database (Stanford Genome Technology Center) Amino acid sequence alignments between *C albicans* PRX1 and TSA1 showed 28% of homology, C albicans PRX1 and *S cerevisiae* PRX1 showed 31%. Peroxiredoxins (Prxs) have been classified in two groups depending on the presence of either one (1-Cys Prx) or two (2-Cys Prx) conserved cysteine residues *C. albicans* PRX1 has only one cysteine residue at the 69th amino acid, which may be essential for the antioxidant activity as a thioredoxin peroxidase Under reducing conditions when denatured with DTT, recombinant Prx1p showed two bands that corresponded to the molecular size of monomers while under nonreducing conditions Prx1p rendered one band, the molecular size of a dimer The substrate of Prx1p was examined and turned out to be H_2O_2 To examine the localization of Prx1p, antibody against Prx1p is under construction