F041

The *smtA* Gene Encoding a Putative SAM Methyl Transferase are Necessary for Progression of Both Sexual and Asexual Development of *Aspergillus nidulans*

Hyo-Jeong Kim[1*], Jee- Hyun Kim[1], and Dong-Min Han[2]
[1]*Institute of Basic Natural Science, Wonkwang University,* [2]*Division of Life Science, Wonkwang University*

The *smtA*(*S*-adenoslymethionin *M*ethyl *T*ransferase) gene was identified as a multi-copy suppressor of various mutations such as *sndE80, silC188, silD6, silE181* and *silF174*, which overcame the inhibitory effect of stresses on sexual development. The gene is predicted to encode a putative methyl transferase carrying an S-adenosylmethionin binding domain. The *smtA* ORF consists of 353 amino acids and is disrupted by 9 introns. The null mutant showed defects both in sexual and asexual developments. Conidiation and cleistothecia maturation were delayed and the amounts were reduced. The *smtA* gene was expressed in high level during vegetative growth and maintained only upto the early stages of asexual and sexual development The *smtA* mRNA level was largely reduced in *veA* or *fluG* null mutant indicating that the *smtA* gene expression may by controlled by those genes. The veA null mutation was epistatic to smtA mull mutantion. These results together suggest that SmtA play some role in progression of both sexual and asexual development downstream of VeA and FluG.

[Supported by grants from KISTEP]

F042

Identification of Amino Acid Residues Critical for Binding of a 7mer Peptide to TiO_2 Nanoparticles

Min Hee Seo[1,*], Jonh Ho Lee[1], Min Soo Kim[1], Heekwon Chae[2], and Heejoon Myung[1]
[1]*Department of Bioscience and Biotechnology,* [2]*Department of Chemistry, Hankuk University of Foreign Studies*

We have isolated peptides specifically binding to TiO_2 nanoparticles using phage dispaly peptide libraries and biopanning procedure A 7mer, C-7-Cmer, and 12mer peptide libraries were screened. The target particles were either 7 nm, 15 nm, or 25 nm TiO_2 More than 20 independent clones were selected The binding was confirmed by electron microscopy analysis The binding was shown to be specific by dose-dependency tests After cross-binding experiments, the bindings were not shown to be particle size-specific. To identify the nature of the binding between a selected peptide and nanoparticles, an alanine scanning mutagenesis was done for the peptide The putative role of amino acids responsible for binding are discussed

F043

The *sndA*, a Suppressor Gene of *nsdD*, Encodes a Zn(II)2Cys6 Protein That Negatively Regulates Sexual Development of *Aspergillus nidulans*

Jee-Hyun Kim*, Hye-Ryun Kim, and Dong-Min Han
Division of Life Science, Wonkwang University

The *Aspergillus nidulans nsdD* gene encodes a GATA-type transcription factor that is required for sexual development. To further understand the NsdD-mediated regulatory cascade, we isolated various suppressors of *nsdD* (SND) that restored cleistothecia development in the absence of *nsdD* function. Two mutant alleles(*sndA16* and *sndA88*) were identified in *sndA*, one of five complementation groups(*sndA-E*). They were all recessive to wild type allele and located on linkage group II. The *sndA* gene, which has an ORF with 693 bp and disrupted by an intron, is predicted to encode a putative transcription factor carrying a GAL4-like Zn(II)2Cys6 binuclear cluster DNA-binding domain. ORF deleted mutant developed a largely increased amount of cleistothecia, even in the presence of environmental stresses such as high osmolarity, visible light or acetate as sole C source. When the *sndA* gene was over expressed, cleistothecia were not formed These results suggested that SndA is a negative regulator of sexual development. The sndA gene was expressed throughout the life cycle and not significantly affected by stresses. The gene expression was negatively regulated by *nsdD* or *veA*, the positive regulators of sexual development

F044

The 5'-end Nucleotide Sequences of the Porcine Reproductive and Respiratory Syndrome Virus Are Essential for RNA Replication: Discovery of Novel 5'-end Nucleotide Sequence Acquisition

Yu-Jeong Choi, Sang-Im Yun, Jeong-Min Kim, Byung-Hak Song, and Young-Min Lee*
Department of Microbiology, College of Medicine and Medical Research Institute, Chungbuk National University

Porcine reproductive and respiratory syndrome virus (PRRSV) belongs to the family *Arteriviridae* in the order *Nidovirales* together with equine arteritis virus, simian hemorrhagic fever virus, and the lactate dehydrogenase-elevating virus of mice Like the other arteriviruses, PRRSV is a small-enveloped virus with a positive-sense, single-stranded RNA genome of ≈15 kb in length The genome has a cap structure at its 5' end and a poly (A) tail at its 3' end We have recently developed an efficient reverse genetics system for PRRSV by construction of an infectious bacterial artificial chromosome Using our system, the viral cap structure and poly (A) tail are shown to be essential for replication Serial mutations deleted up to seven nucleotides at the PRRSV 5' end in genomic RNAs show a gradually decrease in their replicability, while mutations deleted more than nine nucleotides completely abolish their replicability. Various pseudo-revertants are isolated and acquisition of novel 5' sequences composed of mostly A and T bases with various sizes appears to be responsible for restoring their replicability Thus, this study provides new insight into functional elements in the PRRSV 5' end during RNA replication