S3-3

Differential Expression of Developmental Genes in *Streptomyces griseus*

Jangyul Kwak
Biological Resource Center, Korea Research Institute of Bioscience and Biotechnology

Streptomyces is a gram-positive bacterium that has been intensively studied for secondary metabolite production. *Streptomyces* is also an attractive host because it undergoes a complex cycle of morphological differentiation. To understand the morphological events during sporulation of *Streptomyces griseus*, we characterized a group of nonsporulating mutants by genetic complementation experiments with the genomic DNA fragments from the wild-type strain. Further analyses of genetic mapping and DNA sequence determination revealed that the mutations were located at two regulatory genes, *bldA* and *adpA* required for aerial mycelium formation and streptomycin production. S1 nuclease protection assays and western hybridization analyses demonstrated that both subgroups of mutants aberrantly accumulated two key developmental factors, *eshA* and *ftsZ*. The mutants did not accumulate the *eshA* transcript and protein during sporulation, which is required for growth of sporogenic hypha and confinement of septation and spore. *ftsZ* is expressed predominantly from a single promoter during vegetative growth and the level of transcripts from the major sporulation-specific promoters increased just prior to septation. The sporulation-specific transcripts of *ftsZ* were expressed much earlier and more abundantly in the nonsporulating mutants. The aberrant expression of two developmental genes in the nonsporulating mutants is consistent with the phenotypic defects of accelerated septation and spore maturation at the pre-existing vegetative filaments. To test whether *eshA* is regulated by *adpA*, the key transcription activator during sporulation, we carried out gel mobility shift assays using the recombinant AdpA. The AdpA bound toe the upstream regulatory region of *eshA* in a concentration-dependent manner. This result demonstrated that *eshA* is another member of the *adpA* regulon.