

**F324**      The gene encoding 60S ribosomal protein L3 of *Aspergillus nidulans* is sexual developmentally expressed.

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Through the expressed sequence tags (ESTs) the genes specifically expressed in early sexual developmental stage in *Aspergillus nidulans*, we isolated a clone having an EST, esd0123, which is homologous to the gene for *Saccharomyces cerevisiae* ribosomal protein L3. The whole genomic DNA for the clone esd0123 was obtained by colony hybridization from a genomic library of *A. nidulans* and sequenced. There was an ORF containing 393 amino acids and 5 introns. The amino acid sequence showed more than 70% of identities to the 60S ribosomal protein L3 of *Schizosaccharomyces pombe* and other eukaryotic organisms including human. Northern analysis revealed that the transcription for L3 protein sustained in vegetative growth, asexual and sexual developmental stage at a basal level. However the transcript level was gradually increased from initiation of induction of sexual development. To characterize the cellular function of L3 protein, we are constructing the over-expression or deletion mutant.

**F325**      Isolation and Characterization of the gene *npgA* in *Aspergillus nidulans*

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The *npgA* gene has been known that it plays an important role in constructing cell wall structure or depositing pigment. To study the biological function of *npgA* gene we isolated and sequenced the nucleotide of the DNA fragment that was able to complement *npgA1* mutation from the genomic library of *Aspergillus nidulans*. Sequence data of the full-length *npgA* showed that there was an open reading frame (ORF) possibly encoding 344 amino acid polypeptide. The amino acid sequence showed no significant similarity to other polypeptide that had been reported to date except the amphipatic protein surfactin of *Bacillus subtilis* that was shown about 40% similarity. The sequence analysis revealed that the gene *npgA* was linked to the gene *bimA* on the chromosome 1. The 269th codon (TTA) for leucine of wild type ORF was replaced by termination codon (TGA) in *npgA1* mutant. Northern blot analysis using total RNAs showed that the transcript of *npgA* was identified to be about 1.5 Kb long. The transcript of *npgA* gene was expressed through all life cycle. The deletion mutant of *npgA* neither grew well nor showed pigmentation throughout the whole life cycle suggesting that the full length of NpgAp was required for normal growth and pigmentation.