F314 **The Priming Activity of Human HBV Polymerase is affected by Heat Shock Protein 90kDa(HSP90)**

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Human HBV polymerase (N-terminaly FLAG epitope fusion protein) was expressed in Sf-9 (*Spodoptera furugiperda*-9) cell line using recombinant baculovirus (vFPolE) which contains HBV pol ORF and epsilon stem loop region. The purified HBV polymerase was active in protein priming and this priming activity was blocked by HSP90 antibody. Although ATP is energy source of p23 protein which supplies ATpase activity to HSP90, increasement of ATP does not affected priming activity of human HBV polymerase. When HSP90 was immunoprecipitated by HSP90 antibody from Sf-9 cells which were infected by vFPolE, HBV polymerase fused with FLAG epitope was immunostained by M2 monoclonal antibody. Above results indicates that human HBV polymerase is complexed with HSP90 and affected by this protein like as Duck HBV polymerase.

F315 Molecular Cloning of the *nahB* Gene Encoding *cis*-1,2-Dihydro-1,2-dihydroxynaphthalene Dehydrogenase from *Pseudomonas fluorescens*

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The *nahB* which encodes *cis*-1,2-dihydro-1,2-dihydroxynaphthalene dehydrogenease is gene for the conversion of naphthalene to salicylate. The *Sal* I - *Sal* I fragment(3.0kb) from chromosomal DNA of *Pseudomonas fluoresces* was cloned into pUC19 vector, resulting recombinant plasmid, pNH3. Restriction endonuclease mapping of the pNH was carried out with *Apa* I, *EcoR* I, *Hind*III, *Kpn* I, *Pst* I, *Sac* I, *Sal* I, and *Sph* I. The nucleotide sequence of the pNH3 revealed that 3.0kb fragment contained three ORFs(open reading frame). One was complete ORF(*nahB*) and the others were two truncated ORFs(*nahA* and *nahF*). A complete *nahB* of 780 bp contains 260 amino acids corresponding to molecular weight 29kDa. The amino acid sequence of the *nahB* from *Pseudomonas fluorescens* SME11 showed a high level of homology with corresponding genes from other *Pseudomonas* strains.