10^{-8} - 6.6 x 10^{-8}, respectively) efficiently, compared with HIV-1 RT (8.4 x 10^{-5} - 8.0 x 10^{-4} and 4.3 x 10^{-5} - 7.5 x 10^{-4}, respectively). The higher efficiency of misinsertion by HBV polymerase at purine:pyrimidine and pyrimidine:purine mispairs was achieved by the lower Km for the dNTP being misinserted. The data suggest that HBV polymerase is error-prone depending on the template, and HBV genetic variability may be related to the ability of HBV polymerase to form purine:pyrimidine or pyrimidine:purine mismatches during DNA replication

F318

Role of PhoU, a Negative Regulator of Pho-regulon, in Polyamine-dependent Transcriptional Expression of *paiAB* Operon of *E. coli*: *phoU*$^+$ is Required for Transcriptional Expression of *paiAB*

Myung Hoon Choi and Jong Ho Lee*
Department of Biological Science, Sung Kyun Kwan University

In an attempt to elucidate the role of PA in the PA-dependent transcriptional regulation of *paiAB* locating 29.3 min. of *E. coli* chromosome, we have isolated a mutant (tentatively named *parE*) defective in putrescine-dependent expression of *paiA::lacZ*. The *parE* was mapped both genetically and physically at 84.1-84.2 min (3,915 kb - 3,921 kb) in *E. coli* chromosome. The 5.92 kb *Hin*dIII/*Pst*I fragment of the genomic DNA bearing whole *pstSCAB-phoU* operon complemented the *parE*. The expression of the PhoU protein from P*lac* complemented the *parE*. The *parE* mutant showed constitutive expression of *phoA* encoding bacterial alkaline phosphatase. Based upon the results, it was concluded that the negative regulator gene of the phosphate regulon, *phoU*, is identical to *parE*, and is required for the PA-dependent transcriptional expression of *paiA*. Sequence analysis of the *paiA* promoter upstream region revealed presence of two well-conserved PhoB-box centered at -76 bp and -57 bp, respectively. These results demonstrate that PA plays an important role in the phosphate-mediated global transcriptional regulation of gene expression.

F319

Regulation of Polyamine-dependent Transcription of *paiAB* Operon of *E. coli*: ArcA is Required for Transcriptional Expression of *paiAB*

Mun Su Rhee*, Wook Seo, Kui Joo Lee and Jong Ho Lee
Department of Biological Science,Sung Kyun Kwan University, Suwon 440-746

In an effort to uncover physiological role of polyamine (PA), our group has recently identified a novel operon in *Escherichi coli*, *paiAB* mapped at 29.3 mim., whose expression is totally dependent on PA with an extent of induction as high as 105-fold. The PA-dependent expressions of *paiAB* under aerobic conditions are about 105-fold higher than under anaerobic conditions. A mutation in the regulator gene (arcA) of the two component Arc-system, controlling the transcriptional expression of a group of genes involved in aerobic respiratory metabolism, was found to enhance the PA-dependent *paiAB* expression about 50% compared to an isogenic *arcA*$^+$. Sequence analysis of *paiAB* promoter upstream region revealed the presence of one perfect ArcA$^-$ binding site overlapping -35 bp region. Electrophoretic mobility shift analysis, using purified ArcA protein and *paiAB* promoter DNA, showed direct binding of ArcA.