T3-015

The Genetic Regulation of The Chromosomal yefM-yoeB_{Spn} Toxin-Antitoxin Locus of Streptococcus pneumoniae

Chan W.T.¹, S.K. Khoo², C. Nieto³, M. Espinosa³, J.A. Harikrishna¹, C.C. Yeo²

¹Department of Genetics, Faculty of Science, University Malaya ²Department of Biotechnology, Malaysia University of Science and Technology ³Centro de Investigaciones Biológicas, CSIC, Madrid

Toxin-antitoxin (TA) systems encoded on prokaryotic chromosomes have been found to have effects on genome stability, gene regulation, growth control and programmed cell death [Magnuson (2007) J. Bacteriol. 189: 6089 – 6092]. At least 3 TA loci have been identified in the chromosome of *Streptococcus pneumoniae*. One of these loci, designated *yefM-yoeB*_{Spn}, is homologous to the *yefM-yoeB* TA genes of *E. coli*. Overexpression of the YoeB_{Spn} toxin led to cell growth arrest, which could be reversed by expression of its cognate antitoxin YefM_{Spn} in both *S. pneumoniae* and *E. coli*. This indicated that *yefM-yoeB*_{Spn} is a functional TA system, [Nieto *et al.* (2007) J. Bacteriol. 189:1266-1278].

In the present study, we demonstrated using reverse-transcriptase PCR of total RNA of S. pneumoniae that yefM-yoeBspn were organized in a single operon, which is a norm for TA systems. Experiments using lacZ transcriptional fusions in E. coli DH5á showed that the yefM-yoeB_{Spn} genes were co-transcribed from two Σ^{70} -type promoters upstream of the yefM_{spn} reading frame, designated yefMp1 and yefMp2. Transcriptional fusion results also indicate that in the presence of the yefM_{Spn} reading frame, the promoter activity is increased by up to 3.7-fold. This indicated that the YefM_{Spn} antitoxin may possibly function as a transcriptional activator unlike other antitoxins which have been reported to act as transcriptional repressors. However when both the YefM_{Spn} antitoxin and the YoeB_{Spn} toxin were co-expressed, the YefM_{Spn}-mediated activation was negated. Gel shift assays indicate both YefM_{Spn} and YefM-YoeB_{Spn} complex bind to palindrome 2 (44 bp), which is centered 62 bp upstream of yefMspn and overlapped the yefMp1 and yefMp2 promoters whereas no binding was observed for palindrome 1 (46 bp), which is centered 196 bp upstream of the yefM_{Spn} start codon. How binding of YefM_{Spn} to palindrome 2 activates transcription from the yefMp1 and yefMp2 promoters is unknown.