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SLT/SLT-IIe (O139) protein

Catalog Number: bs-0994P
AA Seq: Purified native protein
Predicted MW: 35
Activity: Yes
Endotoxin: Not analyzed
Form: Lyophilized or Liquid
Storage: 10 mM TBS (pH=7.4).
Stored at -70°C or -20°C. Avoid repeated freeze/thaw cycles.

Background: Shiga-like toxin type II (SLT-II) and Shiga-like toxin type II variant (SLT-IIv) are cytotoxins produced by certain strains of Escherichia coli. Nucleotide sequence analyses had revealed that the structural genes for the A subunit and B subunit of SLT-II or SLT-IIv are arranged in an operon. Primer extension and S1 nuclease protection analyses identified a promoter for the slt-II operon 118 bases upstream of the slt-IIA gene. The slt-IIv promoter was demonstrated to be identical to the slt-II promoter. The slt-II and slt-IIv promoters differed significantly from the previously characterized Shiga toxin (stx) and Shiga-like toxin type 1 (slt-I) promoters. The transcriptional efficiencies of the stx and slt-II promoters were compared in fusions to the chloramphenicol acetyltransferase gene, and constitutive expression of the slt-II promoter was found to be equivalent to derepressed expression of the stx promoter. In contrast to the stx and slt-I promoters, the slt-II and slt-IIv promoters did not contain sequences for binding of the Fur repressor protein, and SLT-II production was not determined by iron levels in the media in various E. coli strains with wild-type or mutant ferric uptake regulation (fur) alleles. Northern (RNA) blot analysis demonstrated a single mRNA transcript for the slt-II operon, and further analysis of the slt-II operon by primer extension did not reveal an independent promoter for the B subunit gene. A putative rho-independent transcription terminator was identified 274 bases downstream of slt-IIB. These data indicated that the slt-II and slt-IIv operons differ from the stx/slt-I operon in regulation of their transcription by iron. Whether these regulatory differences enable the type I and type II groups of Shiga-like toxins to perform different roles in the pathogenesis of infectious diseases remains to be established.