F317 Isolation of the *Vibrio vulnificus* DNA sequences which complement the phenotype of *Escherichia coli* defective in starvation sigma factor

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As an effort on the identification of the genes required for starvation-survival of *V. vulnificus*, the library was prepared of *V. vulnificus* genomic DNA partially digested by *Sau*3AI. Several clones expressing high activity of β-galactosidase were isolated from the transformants of *rpoS*-defective *E. coli* cell containing *rpoS*-dependent promoter, *bolA*::*lacZ* fusion. One of the *rpoS*-complementing plasmids, pSK22 includes a small sized, 403bp, DNA insert. The deduced polypeptide sequence of the putative ORF is composed of 56aa residues of which size (about 6kDa) was confirmed by SDS-PAGE of IPTG-induced cell extract, and does not show any significant similarity with the known bacterial proteins. In addition to induction of *bolA* promoter by pSK22, another *rpoS*-dependent promoter, *katE* is also induced more than 25-folds by the presence of this plasmid in *E. coli* cell. We have constructed a series of plasmids including the different lengths of the coding region. The effect of these deleted plasmids on the expression of *rpoS*-dependent promoters is under the investigation. We discuss the possible role of this short DAN sequence in ecological and physiological cycle of *V. vulnificus* in nature.

F318 Molecular Analysis of the aroB, a Gene Encoding DHQ Synthase in Corynebacterium glutamicum

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The aroB gene encoding dehydroquinate synthase of Corynebacterium glutamicum encoding dehydroquinate synthase has been cloned by complementation of the auxotrophic mutant of Escherichia coli with the genomic DNA library. The recombinant plasmid containing 1.4 kb fragment complemented the DHQ synthase-deficient mutant of E. coli. The nucleotide sequence analysis of the subcloned DNA has been determined. The sequence contained an open reading frame of 360 codons, from which a protein with a molecular weight of about 38 kDa could be predicted. Alignment of different prokaryotic and eukaryotic aroB gene products reveals an overall identity ranging from 32 to 56%.