

Streptomyces contain a 7.0 kDa cold shock like protein

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The major protein synthesized in *Escherichia coli* following a shift of exponentially growing cells from 37 to 10°C is a 7.4 kDa hydrophilic protein, CS7.4 (1). Recent studies indicate that CS7.4 may be a positive transcriptional regulator for genes belonging to the cold shock regulon (2, 3). Remarkably, CS7.4 has extensive sequence similarity to the DNA binding domain of a family of eucaryotic nucleic acid binding proteins, the Y box transcription factors (4). It has been proposed that the common DNA recognition motif, the cold shock domain (CSD), present in these prokaryotic and eucaryotic proteins is of ancient origin and widespread (5).

We report here the amino acid sequence of a 7.0 kDa protein from the gram positive bacterium *Streptomyces clavuligerus* that closely resembles that of the *E. coli* CS7.4 protein. During a study of the thioredoxin system of *S. clavuligerus* we noticed that thioredoxin copurified with another low molecular weight protein with an apparent molecular mass of 8–10 kDa, as judged by SDS polyacrylamide electrophoresis. The latter protein was subsequently designated SC 7.0. To isolate the gene encoding SC 7.0, an amino terminal sequence of 40 residues of that protein was made by Edman degradation and used to construct a mixed degenerate oligodeoxynucleotide probe for screening a bacteriophage λ genomic library of *S. clavuligerus* (6). An ORF of 66 codons was found. The amino terminal sequence deduced from that ORF completely matched that found by protein microsequencing. Figure 1 shows the amino acid sequence of SC 7.0. The calculated size of the protein is 7.008 kDa. The *S. clavuligerus* SC 7.0 amino acid sequence has a striking resemblance to the *E. coli* CS 7.4 amino acid sequence with which it has been aligned in Figure 1. The two proteins share 56% sequence identity and more than 80% sequence similarity. This finding suggests they have a common biological function. Also, the fact that CSP 7.4 and SC 7.0 occur in two distantly related gram negative and gram positive bacteria, respectively, strengthens the view that the cold shock domain is a widely distributed and highly conserved protein recognition motif.

At the time of submission of this note we learned that the *Bacillus subtilis* cold shock protein, CSPB, has been isolated (7). The authors state that CSPB is a 7.36 kDa protein and shares 60% amino acid sequence identity with *E. coli* CS 7.4.

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	10	20	30	
CSP7.4	MSGKMTGIVKWFNADKGF	GFITPDDGSKDVFVHF		
	:	:	:	:
SC 7.0	MA---TGTVKWFNAEKGF	FIAQDGGGPDVVFVHY		
		10	20	30
	40	50	60	70
CSP7.4	SAIQNDGYKSLDEGQKVS	FFTIESGAKGPAAGNV	TSL	
	:	:	:	:
SC 7.0	SAINATGFRSLEENQV	VNFDVTHGE-GPQAE	NVSPA	
	40	50	60	

Figure 1. Comparison of the amino acid sequences of *E. coli* CS 7.4 (1) and *S. clavuligerus* SC 7.0 proteins. Double dots indicate identity, single dots indicate conservative changes.

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