F338 Expression of *cspH*, encoding a member of major cold shock protein CspA family in *Salmonella typhimurium* UK-1.

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In *E.coli*, cold shock proteins(Csp family) contaning two cold-box domains(homologous to Y-box in eukaryotes: it has nucleotide binding property) at its amino acid sequence have been well known about induction conditions(at cold(10-25℃), stationary phase, starvation, etc) and functions (RNA chaperone, etc). Csp family known in *E.coli* is 9 proteins from CspA to CspI. But, in *Salmonella typhimurium*, scarcely has Csp family been known except *cspA* and *cspB*. The *cspH*, one of the Csp family, has not been known about an expression condition and its functions in both *E.coli* and *S.typhimurium*. In this study, we analyzed the promoter sequence of *cspH* between *E.coli* and *S.typhimurium*, and found the very different sequence composition. After the sequence analysis, we investigated the patterns of expression of its gene in *S.typhimurium* with Northern hybridization, translational promoter-*lacZ* fusion (pRS414), etc. And then, we found that like *E.coli* CspA, CspH is induced after temperature downshift(approximately 15℃) only in log phase(not induced in stationary phase), and expressed during growth under non-stress condition. We also found the transcriptional start site of *cspH* by primer extension analysis. Extraordinary, the untranslated region(UTR) of its gene is very short unlike cold shock genes of *E.coli*. Judging from our experiments, We suggest that the CspH may be required not only for adaptation at cold temperature but also efficient growth in early log phase. We also demonstrate that because of very short UTR, *cspH* in S.typhimurium may be regulated by transcriptional level.

F339 The *snpA* gene, a suppressor of *npgA1*, encodes a translation termination factor, RF1, of *Aspergillus nidulans*

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The *snpA* gene, originally identified as a suppressor of *npgA1* mutation which is defective in the arrangement of outer layer of cell wall and thus eventually results in the lack of pigments in hyphae, conidia and ascospores, has been known to be involved in differentiation since a temperature sensitive allele, *snpA6*, caused pleiotrophic phenotypes in growth and differentiation at high temperature. We cloned the gene from chromosome specific library III by complementation assay. The full complementing activity was retained in 2.5 kb EcoRV fragment. Nucleotide sequence analysis revealed that the gene encoded a translation termination factor, RF1. It showed a high similarity to that of *Podospora anserina*, higher than 80% in part. Mutation phenotypes of *snpA6* showed also great similarity to those in RF1 genes of other fungi, *Saccharomyces cerevisiae* and *P. anserina*., which were identified as omni-potent suppressor and caused also pleiotrophic phenotypes related to differentiation, respectively.