FUNCTION, REGULATION AND APPLICATION OF THE BACTERIAL STARVATION RESPONSE

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Non-spore forming bacteria respond to starvation by synthesizing unique proteins that make them markedly resistant to several stresses. Exactly how these proteins enhance cellular resistance is unknown, but many are concerned with prevention of macromolecular damage and affecting their repair. The metabolic shift in starving *E. coli* is caused by increased concentration of an alternate sigma factor, sigma S (coded by the *rpoS* gene), resulting in increased expression of the genes transcribed by $E\sigma^S$(1). The *rpo*S-*lac*Z transcriptional and certain translational fusions exhibit increased expression during starvation, leading to the conclusion that both transcriptional and translational controls contribute positively to increase in *rpo*S levels (2). However, direct quantification of rpoS mRNA and its translational efficiency in different growth phases showed that there is a maked decrease in sigma S synthesis during starvation (3). Sigma S is highly unstable in nutrient-proficient cells, being cleaved specifically by the ClpXP protease. A Stretch of some twenty amino acids in about the middle of the sigma factor is apparently the target site for this protease. In starved cells the sigma factor becomes resistant to the protease (4).

Glucose-limited chemostat experiments showed that with decreasing growth rate, there was a progressive increase in sigma S stability accompanied by decreased synthesis. The sigma factor attained the greatest stability and cellular concentration at a growth rate of 0.15 h^{-1} (4.6 h generation time), and exhibited lower levels of these parameters in stationary phase cells. Thus, increase in sigma S resulted solely from its increased stability, despite decreased synthesis, and the translational fusions had indicated, not translational control, but posttranslational processing of RpoS-LacZ hybrid proteins that contained the sigma S target site for the ClpXP protease. Use of starvation promoters permits expression of desired biochemical activity independent of rapid growth. This approach has permitted us to reduce nutrient requirement and biomass formation by over a hundred-fold in trichloroethylene degradation (5,6)

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