

E339 RpoS Regulated Aerobiosis and Anaerobiosis in Virulent *Salmonella typhimurium*

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Salmonella, as well as many other bacterial pathogens, encounter a wide variety of physiological stresses during their life cycle. These include ultraviolet light, starvation, shifts between aerobic and anaerobic conditions, heat shock, oxidative stress, and fluctuations in external pH. Many of the defense mechanisms that *Salmonella/E.coli* use to protect themselves from environmental perturbations have been studied in some detail at the biochemical, genetic and molecular levels. Recently, we found an anaerobic-inducible gene (*aniA1::MudJ*) using the P22 mediated MudJ(*lacZ*, Km) operon fusion technique. The *aniA1-lacZ* was only expressed by anaerobic condition. In addition, LacZ activity of this mutant in pH5.8 was showed 5 times higher than in pH7.7. Also, *aniA1-lacZ* on RpoS negative background was expressed in aerobic condition. This result suggested that *rpoS* was negatively regulator for *aniA1* in aerobic condition. Therefore, *rpoS* was suggested important putative sigma factor for switching mechanism between aerobiosis and anaerobiosis.

E340 Catalase and Catalase-peroxidase from *Streptomyces seoulensis*

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In the course of differentiation, *S. seoulensis* expressed one substrate mycelium-specific catalase and one aerial mycelium-specific catalase. Two types of catalase-peroxidase were detected during the surface culture: one was active in substrate mycelium, the other one was active in the sporulation stage. However, in the stage of the formation of aerial mycelium both types of catalase-peroxidase were present. Genomic southern analysis revealed that *S. seoulensis* contained one homologue of *catC* gene of *S. coelicolor*. On the other hand, the homologues of *catA* and *catB* encoding substrate mycelium-specific catalase and aerial mycelium-specific catalase were not detected. Approximately 2.4 kb DNA fragment containing the homologue of the *catC* gene of *S. coelicolor* A3(2) M145, which encodes catalase-peroxidase was isolated from λ EMBL3 genomic library of *S. seoulensis* using a DNA fragment PCR-amplified *catC* gene of *S. coelicolor*. The result of BLAST search showed that cloned sequence have the highest homology with *catGII* encoding catalase-peroxidase from *Mycobacterium tuberculosis*.