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Crosstalk between Oxidative Stress Response and Metal Homeostasis in *Streptomyces coelicolor*

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Streptomyces coelicolor serves as a good model system to study physiological and morphological differentiation. It is a Gram-positive bacterium that undergoes fungus like morphological differentiation and produces a variety of secondary metabolites including antibiotics. Its linear chromosome of 8,667,507 bp is predicted to encode 7846 proteins (Bentley *et al*., 2002). It devotes more than 12% of its genes (> 900 gene products) as transcriptional regulators. The presence of over 60 sigma factors reflects the complexity of its gene regulation.

The list of regulators that control genes for oxidative defense system includes σ^R/RsrA (sigma/anti-sigma), σ^B/RsbA/RsbV (sigma/anti-sigma/anti-anti sigma), OxyR (positive regulator of alkylhydroperoxide reductase system), CatR (Fur-type repressor of catalase A), Nur (Ni-responsive regulator), and OhrR (repressor of organic peroxide reductase). Among these, redox sensitive modulation of activity has been observed in RsrA, CatR, and OxyR (Kang *et al*., 1999; Hahn *et al*., 2000; Hahn *et al*., 2002).

It contains four members of Fur family regulators. FurA controls a catalase peroxidase (CatC), CatR controls catalase A in response to peroxide stress, Nur controls Ni SOD and Fe SOD in response to nickel, and Zur controls zinc homeostasis. Except Zur all three Fur family regulators control the level of enzymes that remove reactive oxygen species. Upon zinc depletion, Zur loses its repressor activity for zinc uptake system and some ribosomal protein genes. Replacement of zinc containing ribosomal proteins with zinc less paralogues is thought to be an efficient mechanism to maintain zinc homeostasis in the cell. Interestingly, the synthesis of a zinc less ribosomal protein is also controlled by σ^R/RsrA system, suggesting a connection between zinc and oxidative defense system. Role of these Fur family regulators in the physiology of *S. coelicolor* will be discussed.

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