Genome-wide Reconstruction of OxyR and SoxRS Transcriptional Regulatory Networks under Oxidative Stress in Escherichia coli K-12 MG1655

Three transcription factors (TFs), OxyR, SoxR, and SoxS, play a critical role in transcriptional regulation of the defense system for oxidative stress in bacteria. However, their full genome-wide regulatory potential is unknown. Here, we perform a genome-scale reconstruction of the OxyR, SoxR, and SoxS regulons in Escherichia coli K-12 MG1655. Integrative data analysis reveals that a total of 68 genes in 51 transcription units (TUs) belong to these regulons. Among them, 48 genes showed more than 2-fold changes in expression level under single-TF-knockout conditions. This reconstruction expands the genome-wide roles of these factors to include direct activation of genes related to amino acid biosynthesis (methionine and aromatic amino acids), cell wall synthesis (lipid A biosynthesis and peptidoglycan growth), and divalent metal ion transport (Mn\(^{2+}\), Zn\(^{2+}\), and Mg\(^{2+}\)). Investigating the co-regulation of these genes with other stress-response TFs reveals that they are independently regulated by stress-specific TFs.

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