Chapter 8
Sensory Transduction Network of *E. coli*

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Abstract  The genome of *Escherichia coli* K12 encodes at least 6 classes of sensor proteins: 30 histidine protein kinases, 5 methyl-accepting chemotaxis proteins, 23 membrane components of the sugar:phosphotransferase system (PTS), 29 proteins with diacylumbyle cyclase and/or c-di-GMP-specific phosphodiesterase activity and two predicted serine/threonine protein kinases. The full signal transduction network additionally includes 32 response regulators, numerous chemotaxis proteins, PTS components, adenylyl cyclase, CRP, and uncharacterized c-di-GMP-responsive components. Bacterial response to environmental signals can occur on several levels: the level of individual genes and proteins (changes in gene expression, post-translational regulation), the whole-cell level (chemotaxis), and the multicellular level (biofilm formation). All signal transduction systems are energy-dependent but their energy expenditure is miniscule compared to that of the processes they

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regulate. A better understanding of the signal transduction mechanisms and integration of these mechanisms into the metabolic pathway model of the E. coli cell will remain major challenges for systems biology.

8.1 Introduction

For many years, Escherichia coli K12 served as a favorite model organism for studying principles and mechanisms of bacterial signal transduction. As a result, the current understanding of the signal transduction machinery in E. coli, albeit obviously incomplete, is probably as good as that for any organism in the prokaryotic or eukaryotic world. The availability of complete genome sequences of three strains of E. coli K12 (Blattner et al. 1997, Hayashi et al. 2006, Durfee et al. 2008) and their pathogenic counterparts (Hayashi et al. 2001, Perna et al. 2001, Welch et al. 2002, Johnson et al. 2007) made it possible to enumerate all (known) components of the signal transduction machinery encoded in each E. coli genome. This, in turn, allowed identification, at least in terms of sequence, of those signal transduction proteins whose biological functions are still unknown and remain to be experimentally characterized. In many respects, E. coli K12 proved to be a very convenient model: its signal transduction machinery is far more complex than that of its relatives who are obligate pathogens, such as Haemophilus influenzae or Legionella pneumophila. On the other hand, E. coli encodes far fewer signal transduction proteins than its free-living relatives (and opportunistic pathogens), such as Pseudomonas aeruginosa, Shewanella oneidensis, or Vibrio cholerae, not to mention the enormous expansion of signaling systems in the genomes of such model organisms as Anabaena PCC7120, Myxococcus xanthus, or Streptomyces coelicolor (Galperin 2005). Thus, signal transduction in E. coli is an experimentally tractable system that is responsible for much of the progress in understanding the principles and mechanisms of prokaryotic signal transduction.

The difficult task of a systematic description of the bacterial signal transduction machinery has been greatly simplified by the availability of specialized public databases, such as the Microbial Signal Transduction database (MiST, http://genomics.orl.gov/mist) at the Oak Ridge National Laboratory in Tennessee (Ulrich and Zhulin 2007) and the Kyoto Encyclopedia of Genes and Genomes (KEGG, http://www.genome.ad.jp/kegg/) at the Kyoto University in Japan (Kanehisa et al. 2008). The web pages of these databases dedicated to E. coli K12 (http://genomics.orl.gov/mist/view_organism.php?organism_id=99, and http://www.genome.ad.jp/dbget-bin/get_pathway?org_name=eco&mapno=02020, respectively) provide a bird’s eye view of the composition and properties of signaling proteins encoded in the E. coli genome. In addition, the author maintains tables of Signal Transduction Census and Response Regulator Census at the web sites http://www.ncbi.nlm.nih.gov/Complete_Genomes/SignalCensus.html and http://www.ncbi.nlm.nih.gov/Complete_Genomes/RRcensus.html, respectively. These web sites provide an easy way to access up-to-date information on signal transduction mechanisms in E. coli and related bacteria.