Transcription regulation by FFRPs in Pseudomonas aeruginosa

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The gram-negative eubacterium *Pseudomonas aeruginosa* is an opportunistic pathogen, and at the same, possesses a high ability to resist antibiotics and disinfectants, in addition causes outbreaks of serious epidemics even inside hospitals. Many pathogens are parasitic and able to survive only inside their hosts. However, *P. aeruginosa* is fairly ubiquitous, adapting to various ecological niches from water and soil to plant and animal tissues. It is believed that this remarkable adaptability originates in its efficient gene-regulatory mechanism, although details remain unknown. Using its efficient transcription regulation, *P. aeruginosa* even responds to signal to from other bacteria of the same species, similarity to intercellular communications inside eukaryotes (i.e. the quorum sensing).

In general, feast/famine regulatory proteins (FFRPs) regulate transcription of genes thereby controlling metabolism, growth and environmental adaptation of organism. Thus, although no direct evidence is established, it is possible that FFRPs directly regulate pathogenic functions of *P. aeruginosa*.

We have identified eight FFRPs by analyzing the genome sequence of *Pseudomonas aeruginosa* PAO1. The number of FFRPs is the largest among eubacteria so far examined. The fact may well indicate the importance of these proteins. In order to study gene regulation by these FFRPs, we constructed the overproduction system of these FFRPs in *P. aeruginosa* PAO1 and searched genes regulated by these FFRPs using GeneChip *Pseudomonas aeruginosa* Genome Array (Affymetrix, Inc.). We found that some genes associated with quorum sensing were regulated by FFRPs. In this symposium, we discuss how FFRPs regulate the production of pyocyanin that is quorum sensing-regulated virulence factor,