

BACTERIAL PATHOGENESIS

Fis: global but specific

The nucleoid-associated protein Fis has an important role in the transcriptional control of *Salmonella* motility and virulence, according to a report from the research groups of Charles Dorman and Jay Hinton that has been published in the latest issue of *Microbiology*.

It has been known for many years that the effects of Fis, the factor for inversion stimulation — despite its name — are not restricted to DNA inversion. Results from many previous analyses have shown that this small DNA-binding and -bending protein not only influences DNA topology but also modulates the expression of a wide range of genes. In this latest work, Kelly *et al.* combined a microarray analysis with more specific assays to analyse the range of influence of Fis on gene expression in *Salmonella enterica* serovar Typhimurium.

In the microarray work, Fis-regulated genes were identified by comparing gene expression in a wild-type strain and a Fis-knockout mutant. This transcription profiling revealed that the most strongly Fis-activated genes were those located within the *Salmonella* chromosomal pathogenicity islands (SPI-1–5), particularly SPI-2, which encodes a type III secretion system (T3SS) required for survival within macrophages, and the motility and flagellar genes, also a T3SS. As the third *Salmonella* T3SS, which is required for invasion of epithelial cells, is located in SPI-1, these results

show that Fis regulates all three TTSSs. More detailed analysis of the effects on representative flagellar and SPI-2 genes using transcription fusion and mobility shift assays showed that Fis affects these genes directly by binding to the promoter regions.

Among the most strongly Fis-repressed genes were genes involved in metabolism and transport, many of which are required for colonization of the gut. The authors propose the attractive hypothesis that the positive and negative regulatory effects of Fis — in concert with other regulators — allow the coordination of *Salmonella* motility and metabolism with virulence.

Previous work had indicated that Fis was involved in the regulation of virulence genes in *Escherichia coli*, *Shigella flexneri* and *S. typhimurium*. The analysis of Kelly *et al.* has given us a more detailed picture of the effects of Fis on *S. typhimurium* gene expression. Their results confirm that Fis is a global regulator with wide-ranging effects on gene expression, but have revealed that it acts mainly on specific gene sets.

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References and links

ORIGINAL RESEARCH PAPER Kelly, A. *et al.* A global role for Fis in the transcriptional control of metabolism and type III secretion in *Salmonella enterica* serovar Typhimurium. *Microbiology* **150** 2037–2053 (2004)

FURTHER READING

Dorman, C. J. & Deighan, P. Regulation of gene expression by histone-like proteins in bacteria. *Curr. Opin. Genet. Dev.* **13**, 179–184 (2003)

IN BRIEF

FUNGAL GENETIC ANALYSIS

Genome-wide single-nucleotide polymorphism map for *Candida albicans*

Forche, A. *et al. Eukaryot. Cell* **3**, 705–714 (2004)

A SNP map that covers the entire genome has been developed for *Candida albicans* strain SC5314 using the genome sequence. The SNP markers are evenly spread on chromosomes 1, 2, 4, 5 and 6 but chromosomes 3 and 7 are mainly homozygous. The SNP microarray that has been built should enable analysis of strategies, such as mitotic recombination, that this opportunistic pathogen uses to thrive in human hosts.

PARASITOLOGY

Transient cross-reactive immune responses can orchestrate antigenic variation in malaria

Recker, M. *et al. Nature* **429**, 555–558 (2004)

A new model has revealed why individuals with a strong cross-reactive immune response to *Plasmodium falciparum* are likely to succumb to chronic infection. Recker *et al.* developed a model to predict how the variation of *P. falciparum* antigens might affect host immune responses. The model proposes that transient host responses to variant antigens coordinate the production of dominant antigenic variants.

BACTERIAL PHYSIOLOGY

The type II protein secretion system of *Legionella pneumophila* promotes growth at low temperatures

Soderberg, M. A. *et al. J. Bacteriol.* **186**, 3712–3720 (2004)

Legionella pneumophila causes Legionnaires diseases and is widespread in water supplies. Pili enable attachment to host cells and intracellular growth requires type II secretion. Both of these processes require PilD, a pre-pilin peptidase. *pilD* is transcriptionally upregulated as the temperature decreases. Inactivating type II secretion genes (rather than pili genes) dramatically reduced growth at low temperatures. This shows that *L. pneumophila* has cold-adaptation mechanisms (rather than cold-shock responses) for growth below 20°C and that secretion has a role in this process.

VIRUSES AND CANCER

Selection pressure-driven evolution of the Epstein–Barr virus-encoded oncogene LMP1 in virus isolates from southeast Asia

Burrows, J. M. *et al. J. Virol.* **78**, 7131–7137 (2004)

Epstein–Barr virus is associated with nasopharyngeal carcinoma (NPC) and latent membrane antigen 1 (LMP1) is an NPC-associated EBV oncogene. LMP1 genes from multiple geographical clinical isolates were sequenced, and phylogenetics revealed that LMP1 was divergent, with distinct lineages that occurred in different locations. Selective pressure could drive LMP1 evolution so that virus genetics could impact on NPC malignancy.

