IN BRIEF

BIOFILMS

Rhizobium common *nod* genes are required for biofilm formation

Fujishige, N. A. *et al. Mol. Microbiol.* 16 Dec 2007
(doi 10.1111/j.1365-2958.2007.06044.x)

Bacterial nucleotide-binding oligomerization domain (Nod) factors (NFs) have a key role in stimulating the formation of nitrogen-fixing nodules by rhizobial bacteria on plants. According to a paper just published in *Molecular Microbiology*, NFs also have a role in biofilm formation by rhizobial bacteria. Building on a previous study that linked the *nod* genes of rhizobia to biofilm formation, Fujishige *et al.* analysed biofilm formation by *Sinorhizobium meliloti nod*-gene mutants; those mutated in genes encoding NF failed to form biofilms *in vitro* or on plants. The plant hormone luteolin, which activates *nod* genes during nodule formation, was not required for biofilm formation. Treatment with chitinase, which degrades NF, completely dispersed biofilms, which led the authors to propose a role for NF in cell–cell adhesion.

COMPUTATIONAL BIOLOGY

A predictive model for transcriptional control of physiology in a free living cell

Bonneau, R. *et al. Cell* **131**, 1354–1365 (2007)

Extracting meaningful information about microbial metabolism and gene regulation from genome sequences, to engineer new solutions to biotechnological and medical problems, is often confounded by a lack of information on the basic biology of sequenced microorganisms. A team led by Nitin Baliga integrated the results of multiple microarray and proteomics experiments (carried out under a range of environmental conditions) with information on protein-structure predictions and insights from gene knockouts to produce a network model for the prediction of cellular responses in the poorly characterized halophile *Halobacterium salinarum* NRC-1. The resulting model recapitulates known metabolic processes for ~80% of the genes and its validity was established by predicting transcriptional responses to stimuli and then confirming these data experimentally. This showcases the power of systems approaches for rapidly analysing the biology of sequenced microorganisms.

STRUCTURAL BIOLOGY

Structural insights into the enzymatic mechanism of the pathogenic MAPK phosphothreonine lyase

Zhu, Y. *et al. Mol. Cell* **28**, 899–913 (2007)

Type three secretion systems (T3SSs) are used by pathogenic bacteria to deliver effectors directly into host cells. Some T3SS effectors, including OspF (*Shigella* spp.), SpvC (*Salmonella* spp.) and HopA1 (*Pseudomonas syringae*), irreversibly inactivate plant and animal host mitogen-activated protein kinase (MAPK) pathways to downregulate host innate immune responses. MAPKs are activated by dual phosphorylation of a threonine-variable-tyrosine (T-X-Y) motif (present in an activation loop) to yield pT-X-pY. Using mass spectrometry, Zhu *et al.* now reveal that OspF and SpvC are phosphothreonine lyases. Analysis of a crystal structure of the complex formed by SpvC with a phosphopeptide substrate, together with kinetic studies to determine the catalytic activity of SpvC mutants, enabled them to propose an acid/base mechanism for a β-elimination reaction that is catalysed by SpvC. This lyase function is proposed to be extremely similar to that of lantibiotic synthetase, so this research might have implications for the design of antibiotics.