# IN BRIEF

## BACTERIAL PATHOGENESIS

### GMP completes the cycle

Cyclic nucleotides are important second messengers, and for many (such as cyclic di-GMP) their roles in a diverse range of bacterial developmental processes and functions, including virulence, are well known. By contrast, the role of cyclic GMP (cGMP) as a bacterial signalling molecule is largely unknown. Ryan and colleagues screened transposon mutants of *Xanthomonas campestris* and identified two strains with reduced cGMP synthesis, both of which had defects in *XC_0250*, a gene encoding a guanylyl cyclase that converts GTP to cGMP. Compared with the wild-type strain, an *XC_0250* deletion mutant showed reduced biofilm formation and virulence in plants, which was reflected by altered transcription of genes known to be involved in these processes. Deletion of *XC_0249*, a gene with a putative cyclic-mononucleotide-binding domain and a diguanylyl cyclase domain, had similar phenotypic and transcriptional effects. On the basis of further structural and functional data, the authors propose a model that directly links cyclic mononucleotide and dinucleotide signalling, in which cGMP induces XC_0249-mediated cyclic di-GMP synthesis.

**ORIGINAL RESEARCH PAPER** An, S. *et al.* A cyclic GMP-dependent signalling pathway regulates bacterial phytopathogenesis. *EMBO J.* http://dx.doi.org/10.1038/emboj.2013.165 (2013)

## SYMBIOSIS

### Friend or food?

The soil-dwelling amoeba *Dictyostelium discoideum* lives in close association with bacterial symbionts. It can carry, seed and later harvest the bacterium *Pseudomonas fluorescens* in a process described as farming. However, farming amoebae carry both food and non-food strains, and the function of the non-food strains was unclear. *D. discoideum* clone QS161 carries two strains of *P. fluorescens*. Liquid chromatography–mass spectrometry analysis of culture extracts of the food and non-food strains revealed that the inedible strain produces two beneficial secondary metabolites: the antifungal pyrrolnitrin and a new compound called chromene. Both metabolites stimulated *D. discoideum* QS161 spore production, a process that depends on successful symbiosis. Genome sequencing identified a premature stop codon in the *gacA* gene of the food strain. This mutation inactivates the two-component GacA–GacS system, which normally upregulates the production of antimicrobials such as pyrrolnitrin. Thus, the mutation converts the beneficial but inedible symbiont into a food source.

**ORIGINAL RESEARCH PAPER** Stallforth, P. *et al.* A bacterial symbiont is converted from an inedible producer of beneficial molecules into food by a single mutation in the *gacA* gene. *Proc. Natl Acad. Sci. USA* http://dx.doi.org/10.1073/pnas.1308199110 (2013)

## BACTERIAL PATHOGENESIS

### InlB uses SIRT2 to go nuclear

*Listeria monocytogenes* was known to induce histone H3 deacetylation in infected epithelial cells, but the underlying mechanisms were unclear. A new study shows that *L. monocytogenes* infection leads to the deacetylation of H3 lysine 18 (H3K18) and that this modification depends on nuclear translocation of the host histone deacetylase SIRT2. Mutant *L. monocytogenes* lacking the surface protein internalin B (InlB) did not induce SIRT2 translocation or H3K18 deacetylation. Importantly, *inlB*-null *L. monocytogenes* also produced fewer colony-forming units than wild-type bacteria in mice, indicating that histone deacetylation is central for virulence.

**ORIGINAL RESEARCH PAPER** Eskandarian, H. A. *et al.* A role for SIRT2-dependent histone H3K18 deacetylation in bacterial infection. *Science* **341**, 6145 (2013)