RESEARCH HIGHLIGHTS

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 diquanylyl 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 <u>http://dx.doi.org/10.1073/pnas.1308199110</u> (2013)

BACTERIAL PATHOGENESIS

InIB 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 (InIB) did not induce SIRT2 translocation or H3K18 deacetylation. Importantly, *inIB*-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.* Arole for SIRT2-dependent histone H3K18 deacetylation in bacterial infection. *Science* **341**, 6145 (2013)