IN BRIEF

BACTERIAL GENETICS

Regulated secretion of a protease activates intercellular signaling during fruiting body formation in *M. xanthus*.

Rolbetzki, A. *et al. Dev. Cell* **15**, 627–634 (2008)

Starved *Myxococcus xanthus* cells aggregate to form fruiting bodies that contain spores. The C-signal protein p17 coordinates aggregation and sporulation, and during starvation its precursor p25 accumulates in the outer membrane of *M. xanthus* cells. Rolbetzki *et al.* identified serine proteases that might be able to cleave p25 and knocked out five protease genes that were upregulated in starving cells. *popC* mutants failed to form fruiting bodies during starvation, and assays with purified proteins proved that PopC cleaves p25. PopC is present in the cytoplasm of vegetative cells but is secreted and then rapidly degraded in starving cells; the authors propose that selective secretion of PopC results in the formation of active p17 only in starving cells.

BACTERIAL PHYSIOLOGY

2-alkyl-4-hydroxymethylfuran-3-carboxylic acids, antibiotic inducers discovered by *Streptomyces coelicolor* genome mining

Corre, C. *et al. Proc. Natl Acad. Sci. USA* 27 Oct 2008 (doi 10.1073/pnas.0805530105)

The main class of signalling molecules in streptomycetes is γ-butyrolactones (GBLs), of which the best-studied is A-factor. A homologue of the A-factor synthase is present next to the methylenomycin synthesis operon, but previous work had shown that methylenomycin production was unlikely to be induced by lactones. Comparative metabolic profiling was used to identify a novel family of five small molecules that were collectively named methylenomycin furans (MMFs), were assembled by the *mmfL*, *mmfH* and *mmfP* genes and induced the production of methylenomycin in *Streptomyces coelicolor*. The authors propose that MMFs and GBLs might be derived from the same precursor and that MMFs could be produced by other streptomycetes.

ANTIBIOTICS

The RNA polymerase 'switch region' is a target for inhibitors

Mukhopadhyay, J. *et al. Cell* **135**, 295–307 (2008)

An inhibitor of Gram-negative virulence protein secretion

Felise, H. B. *et al. Cell Host Microbe* **4**, 325–336 (2008)

Two new papers report advances in the search for new antibiotics. Mukhopadhyay *et al.* report in *Cell* that myxopyronin, corallopyronin and ripostatin bind to the switch region of the bacterial RNA polymerase (RNAP), thereby inhibiting transcription. These antibiotics do not have cross-resistance with rifamycins that also target RNAP (because they bind to a different part of the enzyme) and bind to residues that are conserved among Gram-positive and Gram-negative bacteria, so could form a class of new broad-range drugs. Felise *et al.* used a high-throughput screen to identify a small molecule, 2-amino-5-arylidene thiazolidinone, that inhibits the type II and III secretion systems of animal and plant pathogenic bacteria without inhibiting growth. Inhibiting secretion of bacterial virulence factors is an attractive therapeutic approach that might reduce the emergence of resistance because it does not reduce bacterial fitness.

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