IN BRIEF

PARASITE BIOLOGY

Shedding light on *Toxoplasma* invasion

To date, genome engineering in *Toxoplasma gondii* has proved difficult owing to inefficient gene targeting. The observation of a mild phenotype in a knockdown experiment always leads to some uncertainty about whether the gene of interest is essential. Now, Andenmatten *et al.* have used a gene swap approach based on the conditional dimerizable Cre recombinase (DiCre) system to dissect *T. gondii* gliding motility and host cell invasion. Replacing components of the actin–myosin invasion complex with the gene encoding YFP allowed easy identification and analysis of reliable knockouts. Surprisingly, genes encoding two components of the invasion complex, myosin A (MyoA) and micronemal protein 2 (MIC2), which previously had been described as essential, were dispensable in the gene swap experiments. The isolation of viable *MyoA* and *MIC2* knockout clones suggests the existence of a novel, as-yet-uncharacterized invasion mechanism in *T. gondii*.

ORIGINAL RESEARCH PAPER Andenmatten, N. *et al.* Conditional genome engineering in *Toxoplasma gondii* uncovers alternative invasion mechanisms. *Nature Methods* **10**, 125–127 (2013)

MARINE MICROBIOLOGY

A day in the life of a microplankton community

Planktonic microorganisms must adapt quickly to environmental fluctuations such as nutrient depletion or light changes, but it is difficult to follow how discrete plankton communities respond to such challenges *in situ*. Ottesen *et al.* followed one plankton population along the Californian coast for 2 days using a robotic sampler attached to a free-drifting float. Repeated sampling combined with whole-genome transcriptome analysis revealed synchronous, distinct gene expression changes, particularly for genes involved in growth and nutrient acquisition pathways. Photosynthesis genes showed a 24-hour expression cycle, whereas heterotrophic substrate metabolism genes exhibited more temporally variable fluctuations. Across species, the changes observed in metabolic genes were remarkably similar, probably owing to general changes in nutrient availability. The detection of such robust expression patterns indicates that there is a well-regulated, rapid response to environmental cues and possibly even interspecies coordination in plankton communities.

ORIGINAL RESEARCH PAPER Ottesen, E. A. *et al.* Pattern and synchrony of gene expression among sympatric marine microbial populations. *Proc. Natl Acad. Sci. USA* 23 Jan 2013 (doi:10.1073/pnas.1222099110)

ANTIMICROBIALS

Aminoglycosides flip the switch on resistance

Enzymatic drug modification is the most common type of aminoglycoside resistance, but the molecular mechanisms involved in inducing resistance are not yet clear. A new study by Jia *et al.* identified a regulatory region in the leader RNA of the transcripts encoding aminoglycoside acetyl transferase and aminoglycoside adenyl transferase, which confer resistance to aminoglycoside antibiotics. They found that aminoglycosides bind to this regulatory region, mediating a conformational change that unmasks the ribosome-binding site to initiate enzyme translation. This is the first description of such a small-molecule-binding regulatory RNA, also called a riboswitch, in the context of antibiotic resistance. The aminoglycoside riboswitch is highly conserved across resistant pathogens and can be found on R plasmids responsible for multidrug resistance, thus enabling a rapid induction of resistance and even spread to other cells.

ORIGINAL RESEARCH PAPER Jia, X. *et al.* Riboswitch control of aminoglycoside antibiotic resistance. *Cell* **152**, 68–81 (2013)