

IN BRIEF

BACTERIAL ECOLOGY**Cheaters take advantage**

Microbial cooperation includes various behaviours, such as nutrient acquisition. However, little is known about the costs and benefits of cooperation in relation to microbial growth. A recent study by Sexton and Schuster investigated the effects of nutrient limitation on the production of the siderophore pyoverdine (PVD), one of the main models for bacterial cooperation in *Pseudomonas aeruginosa*. By using a genome-scale metabolic *in silico* model, the authors showed that the production of PVD has a fitness cost only when its metabolic building blocks — carbon and nitrogen — are limited, as under these conditions it competes with biomass synthesis. Moreover, by testing microbial growth in continuous culture chemostats, they showed that bacteria that do not produce PVD (cheaters) had a large fitness advantage over bacteria that do produce it (cooperators), and that they spread with high frequency when carbon sources (but not other nutrients, such as phosphorus) were limited.

ORIGINAL ARTICLE Sexton, J. D. & Schuster, M. Nutrient limitation determines the fitness of cheaters in bacterial siderophore cooperation. *Nat. Commun.* **8**, 230 (2017)

PARASITE DEVELOPMENT**RBP10 is key for parasite development in the blood**

During its life cycle, *Trypanosoma brucei* multiplies in the blood of infected individuals as the bloodstream form and in the midgut of Tsetse flies as the procyclic form. Changes in mRNA and protein levels accompany these developmental transitions. Mugo and Clayton now show that the RNA-binding protein RBP10 promotes the development of the bloodstream form of *T. brucei* and functions as an on–off regulatory switch. The authors showed that the depletion of RBP10 from bloodstream forms promoted their conversion into procyclic forms, whereas its expression had the opposite effect. In addition, they found that RBP10 bound to procyclic-specific mRNAs that contained an UAUUUUUU motif in the 3' UTR and targeted them for translational repression and degradation. Target mRNAs included a major procyclic surface protein, metabolic enzymes, kinases and stage-specific RNA-binding proteins, which suggests that RBP10 may control a post-transcriptional regulatory cascade.

ORIGINAL ARTICLE Mugo, E. & Clayton, C. Expression of the RNA-binding protein RBP10 promotes the bloodstream-form differentiation state in *Trypanosoma brucei*. *PLoS Pathog.* **13**, e1006560 (2017)

ARCHAEOLOGICAL GENETICS**Structural insights into archaeal chromatin**

Most archaea have small basic proteins that are likely to share a common evolutionary ancestor with eukaryotic histones. A recent study by Mattioli, Bhattacharyya *et al.* reported the 4 Å crystal structure of an archaeal histone–DNA complex. The authors reported that the DNA is wrapped around an extended polymer composed of three histone homodimers forming a quasi-continuous superhelix ramp that resembled the geometry of eukaryotic nucleosomes. In addition, mutagenesis experiments that targeted histone polymerization indicated that this assembly is important for the regulation of gene expression. Despite the structural similarities shown by archaeal histone–DNA complexes and eukaryotic nucleosomes, archaea were shown to form a greater variety of complexes with a different number of histone homodimers.

ORIGINAL ARTICLE Mattioli, F., Bhattacharyya, S. *et al.* Structure of histone-based chromatin in Archaea. *Science* **357**, 609–612 (2017)