Nature Reviews Microbiology | AOP, published online 9 February 2015

IN BRIEF

MICROBIOME

Secret behind commensal resilience revealed

Predominant members of the human gut microbiota show temporal stability despite exposure to the host inflammatory response, but the mechanisms involved are poorly understood. Cullen *et al.* show that the dominant gut phyla are resistant to inflammation-associated antimicrobial peptides (AMPs), and that in the common gut commensal *Bacteroides thetaiotaomicron*, resistance is mediated by a lipopolysaccharide (LPS) modification. The authors found that the bacterial phosphatase LpxF — which catalyses the removal of the 4′-phosphate group from the lipid A moiety of LPS — increases resistance to AMPs by reducing AMP-dependent membrane disruption. In mice that were colonized with representatives of the human gut microbiota, wild-type *B. thetaiotaomicron* was temporally stable following infection with the enteropathogen *Citrobacter rodentium*, whereas a *B. thetaiotaomicron lpxF*-null mutant was rapidly and specifically depleted. These data highlight the importance of LpxF activity for the persistence of *B. thetaiotaomicron* following pathogen-triggered inflammation. As LpxF orthologues are widespread, this may be a common strategy used by gut commensals to resist host inflammation.

ORIGINAL RESEARCH PAPER Cullen, T. W. *et al.* Antimicrobial peptide resistance mediates resilience of prominent gut commensals during inflammation. *Science* http://dx.doi.org/10.1126/science.1260580 (2015)

BACTERIAL PHYSIOLOGY

Riboswitch control is key to ZTP mystery

De novo purine biosynthesis in bacteria relies on an adequate supply of the tetrahydrofolate (THF) derivative 10f-THF. The purine biosynthetic intermediate ZTP (5-aminoimidazole-4-carboxamide riboside 5′-triphosphate) has been proposed to function as a sensor of 10f-THF deficiency, but the mechanism involved is unclear. A new study now shows that a widespread class of riboswitches bind to ZTP and its precursor ZMP (5-aminoimidazole-4-carboxamide ribonucleotide) with nanomolar affinity. Kim *et al.* show that the binding of the Z-nucleotides to these riboswitches — which are associated with genes involved in purine biosynthesis and central carbon metabolism — triggers the expression of downstream genes to maintain the cellular pool of 10f-THF. Biochemical data indicate that ZTP and ZMP accumulate and are sensed by the riboswitches when 10f-THF is deficient, which activates a gene expression programme to restore the levels of 10f-THF.

ORIGINAL RESEARCH PAPER Kim, P. B. *et al.* An ancient riboswitch class in bacteria regulates purine biosynthesis and one-carbon metabolism. *Mol. Cell* **57**, 317–328 (2015)

MICROBIOME

A dysbiotic enteric virome

The two main forms of human inflammatory bowel disease (IBD) — ulcerative colitis (UC) and Crohn's disease (CD) — are associated with enteric bacterial dysbiosis, and new data now reveal that the gut virome is also perturbed in these diseases. Metagenomic sequencing was used to analyse the DNA of virus-like particles from faecal samples obtained from controls and from patients with CD and UC. The abundance of *Caudovirales* bacteriophages was increased in both CD and UC, with distinct phages co-occuring with each disease type. Importantly, these changes were not correlated with changes in bacterial abundance, which indicates that the enteric virome may have a direct role in intestinal inflammation.

ORIGINAL RESEARCH PAPER Norman, J. M. *et al.* Disease-specific alterations in the enteric virome in inflammatory bowel disease. *Cell* http://dx.doi.org/10.1016/j.cell.2015.01.002 (2015)