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IN BRIEF

MICROBIOME

Good for the gut, good for the brain

Using a mouse model, Benakis *et al.* describe a gut–brain axis of ischaemic stroke, in which the commensal gut microbiota confers a neuroprotective effect by modulating immune cells in the small intestine: bacterial priming of dendritic cells results in an expansion of regulatory T cells, which secrete interleukin-10 (IL-10) to suppress the differentiation of γδ T cells into IL-17$^+$ γδ T cells. Although this modulation of immune cells by the microbiota occurs in the gut, its effects are relayed to the brain, owing to the migration of IL-17$^+$ γδ T cells from the gut to the meninges following ischaemic stroke, which upregulates cytokine genes that contribute to brain injury through the promotion of neutrophil infiltration. Dysbiosis of the microbiota induced by antibiotic treatment or faecal transplant resulted in an imbalance in this gut–brain axis that was responsible for a more than two-fold increase in the volume of necrotic tissue.

ORIGINAL ARTICLE Benakis, C. *et al.* Commensal microbiota affects ischemic stroke outcome by regulating intestinal γδ T cells. *Nat. Med.* http://dx.doi.org/10.1038/nm.4068 (2016)

SYNTHETIC BIOLOGY

Genomes just got smaller

What is the smallest possible genome that can sustain a viable bacterial cell? Venter and colleagues now report a synthetic genome ('JCVI-syn3.0') that is smaller than any known genome of an autonomously replicating cell and yet can support robust growth when transplanted into *Mycoplasma capricolum* cells. The 531 kb genome owes its design to a refinement of the *Mycoplasma mycoides* genome that was guided by transposon mutagenesis screens that identified non-essential genes. The 438 protein-coding genes and 35 RNA-coding genes of JCVI-syn3.0 include those with predicted functions in gene expression (195 genes), the cell membrane (84 genes), metabolism (81 genes), and genome preservation and cell division (36 genes), in addition to 79 genes for which a function could not be predicted. Although not all of the genes were essential for viability, further minimization prevented robust growth, which would preclude the use of cells with genomes smaller than JCVI-syn3.0 as an experimental model.

ORIGINAL ARTICLE Hutchison, C. A. *et al.* Design and synthesis of a minimal bacterial genome. *Science* **351**, aad6253 (2016)

VIRAL EVOLUTION

More of the world's a phage

More than 1,000 genomes of DNA phages have been identified in metagenomic datasets. By contrast, very little is known about RNA phages, with only 19 complete genome sequences available and only 2 families described: leviviruses (which have single-stranded RNA genomes) and cystoviruses (which have double-stranded RNA genomes). Wang and colleagues reasoned that genomes of RNA phages might be present in metatranscriptomic datasets and detectable by alignment methods. Indeed, such an approach enabled the assembly of partial genomes for 138 leviviruses and 5 cystoviruses, which represented an estimated 111 novel levivirus species and 3 novel cystovirus species. The expansion of the known diversity of RNA phages was further marked by the identification of novel host species and communities, including the first non-proteobacterium host (a Gram-positive bacterium) and microbial communities that inhabit invertebrates or sulfur springs.

ORIGINAL ARTICLE Krishnamurthy, S. R. *et al.* Hyperexpansion of RNA bacteriophage diversity. *PLoS Biol.* **14**, e1002409 (2016)