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IN BRIEF

MICROBIOME

Early life dysbiosis increases asthma risk

Mouse models have pointed to a role for dysbiosis of the gut microbiota during early life in the aetiology of asthma. Arrieta *et al.* surveyed 319 children from a 3-year longitudinal study and found that a similar phenomenon occurs in humans. 16S rRNA profiling of stool samples from 3-month and 1-year time points showed that an increased risk of asthma was associated with a reduced abundance of four bacterial genera — *Lachnospira*, *Veillonella*, *Faecalibacterium* and *Rothia* — during the first 100 days of life. Using a mouse model of asthma, inoculation of germ-free animals with one of the human dysbiotic stool samples confirmed that the severity of the inflammatory response could be significantly weakened by supplementation with these four genera. Finally, metabolic measurements of the dysbiotic stools revealed functional changes in the microbiome, including a decrease in the concentrations of LPS and acetate compared with healthy stools, although how these functional changes might relate to asthma is not known.

ORIGINAL RESEARCH PAPER Arrieta, M.-C. *et al.* Early infancy microbial and metabolic alterations affect risk of childhood asthma. *Sci. Transl Med.* **7**, 307ra152 (2015)

VIRAL EVOLUTION

Waking a sleeping giant

The discovery of giant viruses has recast ideas on what constitutes a virus. Although diverse in many respects, all giant viruses have an extremely large virion (up to 1.5 µm) and genome (up to 2.8 Mb). Legendre *et al.* recently described a giant virus, Pithovirus sibericum, in 30,000-year-old permafrost, and now isolate a second giant virus, Mollivirus sibericum, from the same ancient sample. Despite its epoch-long freeze, M. sibericum remains infectious. Electron microscopy revealed a 0.6 µm spherical virion that releases its DNA through a 200 nm apex; viral DNA migrates to the host nucleus, but the virion factory is perinuclear. The 0.65 Mb genome does not seem to share recent ancestry with any other sequenced virus but, intriguingly, has acquired a large number of genes from other giant viruses and its amoeba host by horizontal transfer. More intriguing still is the detection of host ribosomal proteins within virions, which has not been seen in other viruses.

ORIGINAL RESEARCH PAPER Legendre, M. *et al.* In-depth study of *Mollivirus sibericum*, a new 30,000-y-old giant virus infecting *Acanthamoeba*. *Proc. Natl Acad. Sci. USA* **112**, E5327–E5335 (2015)

TECHNIQUES & APPLICATIONS

Cpf1 makes for a CRISPR cut

The CRISPR–Cas protein Cas9 — together with its companion CRISPR RNA (crRNA) and *trans*-activating crRNA (tracrRNA) — has been developed as a tool for genome engineering, owing to its readily programmable ability to cleave any desired DNA sequence. Now, Zetsche *et al.* establish a previously uncharacterized CRISPR–Cas protein, Cpf1, as a novel tool with several advantages over Cas9. First, whereas Cas9 generates cleavage products with blunt ends, Cpf1 makes staggered cuts, resulting in a 5′ overhang that improves the precision of DNA insertions. Second, unlike Cas9, Cpf1 cuts at a distal site, which preserves the seed region — essential for target recognition — for future editing. Third, the T-rich protospacer-adjustment motif (PAM; a secondary recognition site) makes Cpf1 better suited to editing AT-rich DNA than Cas9, which has a G-rich PAM. Last, Cpf1 may be easier to deliver to cells, as it is smaller and does not require a tracrRNA.

ORIGINAL RESEARCH PAPER Zetsche, B. *et al.* Cpf1 is a single RNA-guided endonuclease of a class 2 CRISPR–Cas system. *Cell* http://dx.doi.org/10.1016/j.cell.2015.09.038 (2015)