IN BRIEF

MICROBIOME

Expanding diversity of the human microbiome

The diversity of the human microbiome is underexplored, as exemplified by a recent study that recovered thousands of new species. Segata and colleagues used a large-scale metagenomic-assembly approach to reconstruct bacterial and archaeal genomes from publicly available databases and newly obtained samples that span multiple populations, body sites, ages and lifestyles. The authors reconstructed more than 150,000 genomes and obtained 4,930 species-level genome bins (SGBs). They found that 3,796 of the SGBs (77%) did not contain genomes from sequenced isolates or publicly available metagenomic assemblies, thus greatly expanding the diversity of the human microbiome. They also report that non-Westernized populations harbour a large fraction of the newly discovered species. This new genome set provides a resource for future studies to further explore the phylogenetic and functional diversity of the human microbiome.

ORIGINAL ARTICLE Pasolli, E. et al. Extensive unexplored human microbiome diversity revealed by over 150,000 genomes from metagenomes spanning age, geography, and lifestyle. *Cell* https://doi.org/10.1016/j.cell.2019.01.001 (2019)

BACTERIAL SECRETION

The effector repertoire of *Legionella*

Legionella pneumophila is an opportunistic bacterial pathogen that uses the Dot–Icm type IV secretion system (T4SS) to translocate effector proteins into host cells, which promote survival and replication of the pathogen. Buchrieser and colleagues analysed 80 *Legionella* strains belonging to 58 *Legionella* species and subspecies and report that the pan-genus pool of putative T4SS effectors comprises >18,000 proteins. In addition, the authors identified >200 eukaryotic-like proteins and 137 eukaryotic domains in the genomes of *Legionella* spp., including Rho-GTPase and Rab-GTPase domains, which were shown to be T4SS-secreted. Moreover, the repertoire of these proteins varied in different species, and the data suggest that these genes were mostly acquired through independent gene-gain events. The acquired genes might modulate specific eukaryotic host functions to promote intracellular survival and replication and may have led to the emergence of human *Legionella* pathogens.

ORIGINAL ARTICLE Gomez-Valero, L. et al. More than 18,000 effectors in the *Legionella* genus genome provide multiple, independent combinations for replication in human cells. *Proc. Natl Acad. Sci. USA* https://doi.org/10.1073/pnas.1808016116 (2019)

VIRAL INFECTION

Promoting persistence

Many plant viruses are transmitted by insect vectors, such as leafhoppers. Viral infections of the vectors are non-lethal and cause limited damage to ensure viral persistence and efficient spread. In this study, Chen, Zheng et al. show that infection of leafhoppers with the reovirus rice gall dwarf virus induces apoptosis to promote viral replication and transmission by the insect vector. Fibrillar structures composed of viral non-structural protein Pns11 interacted with voltage-dependent anion channels on the outer membrane of mitochondria, which lead to the induction of apoptosis. Moreover, expression levels of apoptosis-related genes increased and then decreased during the latent period, with viral transcript levels also increasing rapidly and then remaining stable. The findings suggest that the virus-induced apoptotic response is modulated to prevent pathology in the vector.

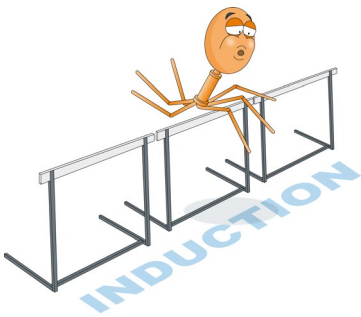
ORIGINAL ARTICLE Chen, Q., Zheng, L. et al. Fibrillar structures induced by a plant reovirus target mitochondria to activate typical apoptotic response and promote viral infection in insect vectors. *PLOS Pathog.* https://doi.org/10.1371/journal.ppat.1007510 (2019)

PHAGE BIOLOGY

Phage induction in different contexts

During the lysogenic cycle of temperate phages, the phage genome can be integrated into the bacterial chromosome as a prophage. Lytic production of phage particles is induced under stress conditions, such as DNA damage. Phages encode various virulence factors, such as Shiga toxins of enterohaemorrhagic *Escherichia coli* (EHEC). Moreover, prophages are also prevalent in bacteria associated with the human gut microbiome. Two studies now address the mechanism of phage induction in the context of a gut symbiont and EHEC infection.

In the first study, Oh et al. investigated the biological role of the prophage of the beneficial gut symbiont *Lactobacillus reuteri*. They recovered less wild-type *L. reuteri* from the caecum, colon and faeces of mice than *L. reuteri* in which prophages were deleted, which suggests that prophages are induced during gastrointestinal transit and reduce the fitness of *L. reuteri*. Next, the authors showed that fructose — an abundant sugar in the Western diet — increased *L. reuteri* phage production in vitro and in vivo. Dietary fructose activated the Ack



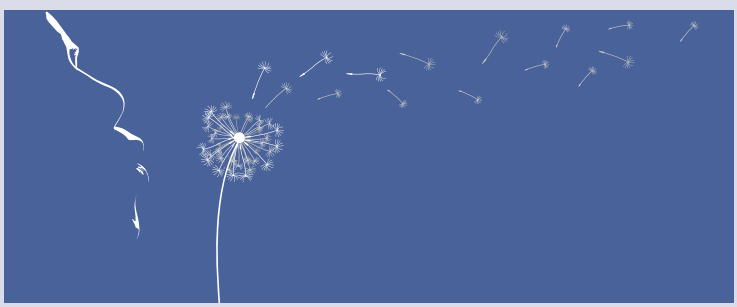
Credit: Philip Patenall/Springer Nature Limited

BACTERIAL EVOLUTION

Disarming to disseminate

Acinetobacter baumannii infections are a major health-care concern owing to the increased prevalence of multidrug resistance (MDR). Transmissible plasmids have an important role in the emergence and dissemination of MDR, with large conjugative plasmids (LCPs) carrying up to 13 antibiotic resistance cassettes. The spread of LCPs is cell–cell contact dependent, yet most *A. baumannii* strains constitutively express a type VI secretion system (T6SS), a molecular machine that is chromosomally encoded and kills non-sister bacterial competitors by injecting toxins into them in a contact-dependent fashion. This poses a challenge to the spread of conjugative plasmids as donors and recipients may kill each other. Now, Feldman and colleagues show that silencing T6SS is essential for plasmid conjugation and the dissemination of MDR in *A. baumannii*.

First, the authors observed that LCPs of *A. baumannii* origin repress T6SS in the unrelated *Acinetobacter baylyi* and *Acinetobacter nosocomailis*,



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