Nature Reviews Microbiology | Published online 7 Nov 2016

IN BRIEF

VIRAL INFECTION

Rabies virus causes stress

Exposure of cells to different types of stress, including heat shock and oxidative stress, leads to the accumulation of translationally stalled mRNAs in cytoplasmic structures known as stress granules. Nikolic *et al.* report that rabies virus induces the assembly of dynamic stress granules. These virus-induced structures are distinct from other stress granules and localize close to cytoplasmic inclusions bodies, in which viral transcription and replication take place. In addition, viral mRNAs, but not genomic RNA, are selectively transported into stress granules from inclusion bodies. Finally, infection-initiated stress granule assembly was dependent on protein kinase R (PKR, which mediates translation inhibition following viral infection), and depletion of PKR increased viral replication and decreased the induction of type I interferon genes, which suggests that the PKR-dependent formation of stress granules restricts viral replication.

ORIGINAL ARTICLE Nikolic, J. *et al.* Rabies virus infection induces the formation of stress granules closely connected to the viral factories. *PLoS Pathog.* **12**, e1005942 (2016)

MICROBIOME

Complexity at the sub-genus level

Bacteroidetes is one of the most abundant phyla in the gut, and studies have suggested that *Prevotella* spp. are associated with a high-fibre diet, whereas *Bacteroides* spp. are associated with the consumption of animal fat and a protein-rich diet. De Filippis *et al.* used oligotyping of 16S rRNA sequencing data to analyse differences in populations of *Prevotella* spp. and *Bacteroides* spp. in faecal samples from omnivores and non-omnivores. The authors identified 24 and 51 oligotypes for *Prevotella* spp. and *Bacteroides* spp., respectively. However, different oligotypes in these genera had a differential relative abundance in both groups. The heterogeneity in these genera and the correlation to dietary components and the metabolome suggest that the association of genera in the Bacteroidetes with a specific diet may oversimplify diet-dependent microbiota–host associations, and that diversity at the sub-genus level may need to be taken into account in diet-based intervention studies.

ORIGINAL ARTICLE De Filippis, F. *et al.* Unusual sub-genus associations of faecal *Prevotella* and *Bacteroides* with specific dietary patterns. *Microbiome* **4**, 57 (2016)

FUNGAL BIOLOGY

A key regulator of secondary metabolites

Fungi are a rich sources of secondary metabolites that are relevant to human health, including antibiotics and fungal toxins. However, our understanding of the regulation of secondary metabolite biosynthetic gene clusters is limited. Oakley *et al.* carried out a genetic screen in *Aspergillus nidulans* and discovered a previously uncharacterized gene that is predicted to encode a zinc-finger transcription factor. This transcription factor was shown to function as a negative regulator of important secondary metabolite biosynthetic gene clusters and they thus termed the gene multicluster regulator A (*mcrA*). Deletion of *mcrA* led to the identification of two secondary metabolites and the finding that *A. nidulans* produces the antibiotic, felinone A. Thus, deletion of *mcrA* homologues in fungi is a promising tool for the discovery of novel compounds.

ORIGINAL ARTICLE Oakley, C. E. *et al.* Discovery of McrA, a master regulator of *Aspergillus* secondary metabolism. *Mol. Microbiol.* http://dx.doi.org/10.1111/mmi.13562 (2016)