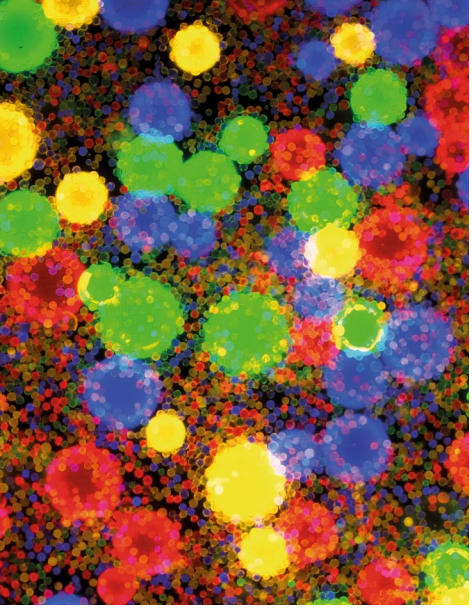

Artificial food particles. Courtesy of M. L. Patnode, Washington University School of Medicine St. Louis, USA.

metabolism of specific carbohydrate structures.

The authors then used multi-taxon insertion sequencing of four *Bacteroides* spp. to further define pathways required for the responses to fibres. Indeed, mutants that had defects in the same polysaccharide utilization loci identified in the proteomics datasets lost the capacity for the fibre-specific increases in abundance. Interestingly, some of the *Bacteroides* strains competed for the same fibre component, whereas others deferred to their neighbours.

Finally, the authors constructed artificial food particles that functioned as biosensors of microbial fibre digestion in vivo. Particles coated with different fibre polysaccharides were fed to mice colonized with combinations of *Bacteroides* spp. Indeed, beads recovered from the faeces had less polysaccharide on their surface in a manner that was dependent on community composition.

In summary, responses of the gut microbiota to fibre are specific to both the fibre components and the species present. The new biosensors are a promising tool to characterize the nutrient processing capacities of microbial communities and develop next-generation microbiota-directed foods.

Ursula Hofer

ORIGINAL ARTICLE Patnode, M. L. et al. Interspecies competition impacts targeted manipulation of human gut bacteria by fiber-derived glycans. *Cell* **179**, 1–15 (2019)
RELATED ARTICLE Kolodziejczyk, A. A., Zheng, D. & Elinav, E. Diet–microbiota interactions and personalized nutrition. *Nat. Rev. Microbiol.* https://doi.org/10.1038/s41579-019-0256-8 (2019)

germ-free mice had lower levels of HDAC3. The authors showed that the deacetylase was recruited to histones in a diurnally rhythmic manner. Moreover, IECs in which HDAC3 had been depleted showed increased target gene expression and exhibited dampened diurnal expression rhythms. In addition, the recruitment of HDAC3 was dependent on the microbiota, as the expression of target genes was higher in IECs from germ-free mice than in those from wild-type mice. Thus, the microbiota is required for the recruitment of HDAC3 to chromatin, where it functions as a co-repressor owing to its deacetylase activity.

Interestingly, mutant IECs also showed decreased expression of some genes involved in lipid absorption, including *Cd36* (encoding a fatty acid transporter), which is in agreement with the observed lower uptake of lipids into these cells. Moreover, mice lacking HDAC3 in IECs seemed to be protected from high-fat-diet-induced obesity, and depletion of the microbiota in wild-type mice led to the same phenotype (lowered body weight and body fat percentages). On the basis of these results, the authors proposed that epithelial HDAC3 is required for the microbiota to promote diet-induced obesity.

Finally, the finding that the expression of some of the genes involved in lipid absorption was decreased when HDAC3 was absent indicated that the enzyme can also affect gene expression through a nonconventional mechanism. Indeed, the authors showed that HDAC3 functions as a co-activator for oestrogen-related receptor-α, which leads to the rhythmic transcription of *Cd36*, in a manner dependent on the microbiota. Thus, the data support the notion that the microbiota promotes *Cd36* expression and lipid absorption through HDAC3.

In sum, the study identifies HDAC3 as a key factor that integrates microbial and circadian cues to regulate diurnal metabolic rhythms.

Andrea Du Toit

ORIGINAL ARTICLE Kuang, Z. et al. The intestinal microbiota programs diurnal rhythms in host metabolism through histone deacetylase 3. *Science* **365**, 1428–1434 (2019)

IN BRIEF

MICROBIOME

Providing resistance to rotavirus

Rotavirus is a contagious enteric pathogen and the leading cause of diarrhoea in infants and children. After ingestion, rotavirus infects the intestinal epithelium, which is colonized by diverse members of the gut microbiota. Shi et al. report that gut segmented filamentous bacteria (SFB) prevent and cure rotavirus infection in immunodeficient mice. The authors unintentionally developed a mouse breeding colony that was highly resistant to rotavirus infection and hypothesized that the gut microbiota conferred resistance. Accordingly, resistance was transferred by co-housing and faecal microbiota transplantation. The authors used filtration, heating, antibiotics and limiting dilution to identify SFB as the protective component of the microbiota. Protection was independent of previously observed rotavirus-restricting immunological factors. Instead, SFB caused changes in host gene expression and enhanced gut epithelial turnover, and SFB-containing faeces reduced rotavirus infectivity in vitro, suggesting that SFB could be used to combat rotavirus infections.

ORIGINAL ARTICLE Shi, Z. et al. Segmented filamentous bacteria prevent and cure rotavirus infection. *Cell* https://doi.org/10.1016/j.cell.2019.09.028 (2019)

FUNGAL PATHOGENESIS

A probiotic for candidiasis?

Non-*albicans Candida* (NAC) species infections are of increasing concern owing to rises in complications associated with antifungal resistance, necessitating novel approaches for combating these fungal pathogens. Now, Kunyeit et al. report probiotic yeasts that inhibit virulence of several NAC species, including multidrug-resistant *Candida auris*, an important emerging pathogen. The authors tested the ability of two food-derived yeasts — *Saccharomyces cerevisiae* (strain KTP) and *Issatchenkia occidentalis* (strain ApC) — to inhibit traits such as adhesion, filamentation and biofilm formation in several NAC species. Probiotic treatment prevented adhesion to abiotic surfaces and cultured gut epithelial cells, and inhibited the formation of mixed-culture biofilms as well as biofilms of NAC species and *Candida albicans* in vitro. Furthermore, experiments in *Caenorhabditis elegans* suggest that exposure to the probiotic yeasts attenuates NAC species infection in vivo, highlighting a potential new strategy to prevent or treat candidiasis.

ORIGINAL ARTICLE Kunyeit, L. et al. Probiotic yeasts inhibit virulence of non-*albicans Candida* species. *mBio* https://doi.org/10.1128/mBio.02307-19 (2019)

ENVIRONMENTAL MICROBIOLOGY

Distinct drivers of functional diversity

Soil microbiomes have a central role in biogeochemical cycles, so it is important to understand the impact of global change on community function. Zhang et al. found that the functional diversity of core and accessory genes (genes required for living in a specific environment) are governed by distinct processes. The authors performed a longitudinal 5 year nitrogen and water addition experiment in the Eurasian steppe and surveyed the microbial gene diversity using metagenomics. Rises in nitrogen led to an increase in the abundance of ammonia-oxidizing bacteria, which in turn increased the relative abundance of core genes. Water addition stimulated microbial respiration such that carbon sources became limited, leading to a decrease in the diversity of accessory community genes. These findings highlight that the functional diversity of soil microbiomes is affected differently by distinct environmental change processes.

ORIGINAL ARTICLE Zhang, X. et al. Distinct drivers of core and accessory components of soil microbial community functional diversity under environmental changes. *mSystems* https://doi.org/10.1128/mSystems.00374-19 (2019)