An apple a day helps Bacteroides to stay

Previous studies have shown that the gut microbiota can have a role in protection from obesity, in particular certain Bacteroides spp. However, the relationship is complex and involves interactions between different members of the microbiota and dietary components such as fibre. It has been difficult to determine the underlying mechanisms, molecules and pathways and thus to target them specifically. In a new study, Gordon and colleagues use germ-free mice, colonized with defined consortia of gut bacteria, and artificial food particles coated with different fibres to better understand these interactions.

The authors colonized germ-free mice with bacteria isolated from a lean donor and fed them a human diet high in fat and low in fruits and vegetables supplemented with 34 different fibres, including fibres from apples, citrus, peas and other plants. The different fibres had specific effects on the composition of the gut bacterial community; for example, fibre from pea skins increased the abundance of Bacteroides thetaiotaomicron, whereas fibres from orange peels increased Bacteroides cellulosilyticus.

The next step was to identify the bioactive fibre components and how they were used by community members. Biochemical analyses showed that the fibres contained complex mixtures of different molecular components. The authors used proteomic analysis to demonstrate that Bacteroides spp. responding to different types of fibres upregulated enzymes encoded in polysaccharide utilization loci linked to...

IN BRIEF

MICROBIOME

Providing resistance to rotavirus

Rotavirus is a contagious enteric pathogen and the leading cause of diarrhea 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.


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, Kuneiet 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 Issatchenka orientalis (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.


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.