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# IN BRIEF

## ANTIMICROBIALS

### Breaking ground for new antibiotics

Antimicrobial drug discovery has focused on bacteria growing in cultures, but now, Brady and colleagues have developed a culture-independent natural product discovery platform. Using a metagenome-based approach, they analysed >2,000 soil samples from diverse environments and reported the discovery of novel antibiotics, termed malacidins. Malacidins exhibit potent antibacterial activity against Gram-positive pathogens that are resistant to clinically used antibiotics such as vancomycin, and this activity was calcium-dependent. Moreover, malacidins did not select for resistance under laboratory conditions, and cutaneous wounds infected with methicillin-resistant *Staphylococcus aureus* were efficiently treated with a novel malacidin in a rat model. In sum, metagenome-driven discovery platforms could lead to the identification of previously uncharacterized antibiotics.

**ORIGINAL ARTICLE** Hover, B. M. et al. Culture-independent discovery of the malacidins as calcium-dependent antibiotics with activity against multidrug-resistant Gram-positive pathogens. *Nat. Microbiol.* https://doi.org/10.1038/s41564-018-0110-1 (2018)

## VIRAL INFECTION

### CRISPR–Cas enhances HGT by transduction

The major mechanisms of horizontal gene transfer (HGT) in bacteria are natural transformation, conjugation and transduction (phage-mediated transfer of bacterial DNA). In addition to a role in phage resistance, CRISPR–Cas systems have been shown to inhibit conjugation and transformation, whereas their role in transduction is not well understood. Watson et al. show that in *Pectobacterium atrosepticum*, phage-mediated transduction of plasmids, chromosomal loci and genomic islands can be limited by CRISPR–Cas interference. However, owing to the infrequency of spacers acquired during transduction compared with spacers from phages, they hypothesized that the canonical role of CRISPR–Cas in phage resistance would enhance HGT by increasing the survival of transductants. Indeed, spacer acquisition from phages enabled CRISPR–Cas to protect bacteria from infection and increased the generation of transductants. Finally, bacteria acquired a chromosomal CRISPR–Cas system through transduction.

**ORIGINAL ARTICLE** Watson, B. N. J. et al. CRISPR-Cas-mediated phage resistance enhances horizontal gene transfer by transduction. *mBio* **9**, e02406-17 (2018)

## MICROBIOME

### Principles of microbiota engraftment

Faecal microbiota transplantation (FMT) has proved to be an effective treatment strategy for recurrent infections with *Clostridium difficile*. The success of FMT requires donor bacteria to engraft in the gut of the patient, but the factors that promote engraftment of individual strains has remained elusive. Alm and colleagues used high-resolution deep shotgun metagenomics sequencing to profile the faecal microbiota of patients with recurrent *C. difficile* after FMT. They also developed Strain Finder, which infers the genotypes and frequencies of strains in complex metagenomics samples, and combined it with machine learning to quantitatively model bacterial engraftment in humans. They report that the most important factors in their model are bacterial abundances, bacterial taxonomy and the amount of elapsed time since the FMT. They validated their findings for metabolic syndrome, which suggests that the models of engraftment apply to other conditions.

**ORIGINAL ARTICLE** Smillie, C. S. *et al.* Strain tracking reveals the determinants of bacterial engraftment in the human gut following fecal microbiota transplantation. *Cell Host Microbe* **23**, 229–240.e5 (2018)