IN BRIEF

MICROBIAL ECOLOGY

Setting a trap

In natural ecosystems, non-pathogenic bacteria are consumed by bacterivorous nematodes, but microorganisms have evolved defence strategies against their predators. Here, Wang *et al.* show that bacteria isolated from cow dung induce the formation of predatory structures in the fungus *Arthrobotrys oligospora* to promote the capture and elimination of nematodes. Bacteria increase the production and secretion of urea by upregulating the expression of arginase, which converts arginine into urea and ornithine; secreted urea is taken up by the fungus via the urea transporter and catabolized to ammonia. Importantly, ammonia functions as a signalling molecule that promotes a lifestyle switch in *A. oligospora* from the saprophytic to the predacious stage, inducing the fungus to form trap structures and kill nematodes. These findings further our understanding of the complex predator–prey interactions in microbial communities.

ORIGINAL RESEARCH PAPER Wang, X. *et al.* Bacteria can mobilize nematode-trapping fungi to kill nematodes. *Nature Commun.* http://dx.doi.org/10.1038/ncomms6776 (2014)

TECHNIQUES & APPLICATIONS

Capturing bacterial chromosome conformation

Although chromosome organization in microorganisms has been investigated in single species, similar analyses of whole genomes in complex environmental microbial communities have been limited. Marbouty *et al.* developed a metagenomic chromosome conformation capture approach (termed meta3C) for the characterization of the average organization of individual genomes in mixed microbial communities. This approach, which is based on measuring the frequency with which two chromosomal segments come in contact, was tested on an artificial mixture of bacterial species and an environmental sample of unknown composition; the authors identified genomic regions that could be matched to a specific species and revealed the three-dimensional structure of the genomes in the mixed populations. Thus, meta3C has the potential to be used for the analysis of chromosome organization in environmental microbial communities.

ORIGINAL RESEARCH PAPER Marbouty, M. *et al.* Metagenomic chromosome conformation capture (meta3C) unveils the diversity of chromosome organization in microorganisms. *eLife* **3**, e03318 (2014)

VIRAL INFECTION

Filling the canyon

Enterovirus D68 (EV-D68) is a poorly characterized member of the *Enterovirus* genus that is responsible for recent outbreaks of respiratory illness worldwide, yet no antiviral treatment is available. Liu *et al.* solved the crystal structure of EV-D68 and showed that the capsid canyon — a deep surface depression that is the site of host receptor binding — is shallower and narrower than that of other enteroviruses. Similarly to other enteroviruses, the EV-D68 canyon is occupied by a pocket factor, a fatty acid that stabilizes the virus by preventing viral uncoating during transmission. The authors showed that pleconaril — an antiviral compound originally designed to inhibit rhinoviruses by binding to and stabilizing the capsid canyon — replaces the pocket factor of EV-D68 and fills the capsid canyon, probably blocking receptor binding and preventing viral uncoating. These data establish pleconaril as a possible drug candidate to treat EV-D68 infections.

ORIGINAL RESEARCH PAPER Liu, Y. *et al.* Structure and inhibition of EV-D68, a virus that causes respiratory illness in children. *Science* **347**, 71–74 (2014)