



suggests that DNA uptake by the pathogen is required for killing.

The authors could not find any evidence that the DNA contains a toxic locus; however, they observed that *N. elongata* and *N. gonorrhoeae* DNA are methylated differently. Thus, they tested whether this difference in methylation pattern determines the toxicity of the DNA for the pathogen. Indeed, DNA from several commensal *Neisseria* species, which are also methylated differently than *N. gonorrhoeae* DNA, reduces pathogen viability, whereas *N. elongata* DNA modified

and undergoes sexual reproduction leading to the production of oocysts, which are shed in faeces and then sporulate to produce infectious parasites. Previous work has shown *T. gondii* scavenges fatty acids and, furthermore, one particular fatty acid found in the diet, linoleic acid, has been shown to influence sexual development in fungi. Therefore, the authors set out to test the role of linoleic acid in the sexual development of *T. gondii*. In cat intestinal organoids, *T. gondii* formed merozoites, a pre-sexual stage, macrogametes and, finally, oocysts only in the presence of linoleic acid but not when the control fatty acid oleic acid was added.

Interestingly, cats lack intestinal delta-6-desaturase, which is the first enzyme in the pathway that metabolizes linoleic acid to arachidonic acid. Consequently, cats have much higher levels of linoleic acids than other animals, including mice and humans. The authors thus speculated that this fatty acid is a signal for the parasite to induce sexual development. Indeed, when they treated the mouse intestinal cells with linoleic acid and SC-26196, an inhibitor

to mimic the *N. gonorrhoeae* methylation pattern is reduced in toxicity. A DNA fragment with an *Escherichia coli* methylation signature kills the pathogen, but not if it carries the *N. gonorrhoeae* methylation signature. The authors also showed that the killing mechanism involves homologous recombination of the incoming commensal DNA with the pathogen genome. Finally, the authors found that DNA from commensal *Neisseria* species also kills the pathogen *Neisseria meningitidis*.

In sum, the findings suggest that commensal *Neisseria* species antagonize pathogenic *Neisseria* species through their DNA, by a mechanism based on genetic competence and DNA methylation state. The study also suggests that DNA, modified appropriately, may be useful as a preventative against *N. gonorrhoeae* infection.

Andrea Du Toit

ORIGINAL ARTICLE Kim, W. J. et al. Commensal *Neisseria* kill *Neisseria gonorrhoeae* through a DNA-dependent mechanism. *Cell Host Microbe* **26**, 228–239.e8 (2019)

of delta-6-desaturase, the parasites initiated sexual development. Furthermore, mice receiving high levels of linoleic acid together with the inhibitor also became permissive to sexual development of *T. gondii* and shed similar numbers of oocysts in their faeces as cats. Although mouse-derived oocysts were not as stable as cat-derived ones, they could sporulate and were able to infect recipient mice and form cysts in their brains.

In summary, the study identifies linoleic acid, which accumulates in the cat gut due to absent metabolic conversion of this fatty acid, as a determinant of species-specific sexual reproduction of *T. gondii*. These findings can be used to study sexual parasite development in mice, which is an easier model than cats, and they might also lead to interventions that prevent the development of infectious parasites in cats and thus transmission of *T. gondii*.

Ursula Hofer

ORIGINAL ARTICLE Martorelli Di Genova, B. et al. Intestinal delta-6-desaturase activity determines host range of *Toxoplasma* sexual reproduction. *PLOS Biol.* **17**, e3000364 (2019)

IN BRIEF

ARCHAEOLOGICAL GENOMICS

Getting your chromosomes organized

The three-dimensional organization of chromatin has an important role in genome functions. In bacteria and eukaryotes, structural maintenance of chromosomes (SMC) protein complexes such as condensin mediate higher-order chromosome organization. However, many archaea do not have condensin, and the establishment and maintenance of archaeal chromosome conformation was not well understood. Takemata, Samson and Bell used chromosome conformation capture to investigate the spatial organization of the chromosomes of *Sulfolobus* species. They found that the chromosomes are organized into two compartments with higher and lower gene expression activities — the A compartment and B compartment, respectively. This non-random chromosome organization was established by coalescin, a novel *Sulfolobus*-encoded SMC protein. Coalescin is enriched in the B compartment and binds to less active genes, thus maintaining the compartmentalization of the archaeal chromosome.

ORIGINAL ARTICLE Takemata, N., Samson, R. Y. & Bell, S. D. Physical and functional compartmentalization of archaeal chromosomes. *Cell* **179**, 165–179.e18 (2019)

MICROBIOME

Establishing the gut microbiota after birth

Following birth, newborn babies are rapidly colonized by microorganisms, and Shao et al. further corroborate that the mode of delivery is a crucial factor that shapes the gut microbiota during the neonatal period, with effects that persist into infancy. Metagenomic analysis of faecal samples from babies delivered vaginally were enriched with commensals (*Bifidobacterium*, *Escherichia*, *Bacteroides* and *Parabacteroides* species), whereas the gut microbiota of babies delivered by caesarean section were depleted of these commensal species and were dominated by opportunistic pathogens associated with the hospital environment (including *Enterococcus*, *Enterobacter* and *Klebsiella* species). Finally, large-scale culturing and whole-genome sequencing of opportunistic pathogens found in the faecal samples identified virulence factors and clinically relevant antimicrobial resistance genes, which suggests that opportunistic pathogen carriage is a risk factor for opportunistic infections.

ORIGINAL ARTICLE Shao, Y. et al. Stunted microbiota and opportunistic pathogen colonization in caesarean-section birth. *Nature* <https://doi.org/10.1038/s41586-019-1560-1> (2019)

MICROBIAL ECOLOGY

Core leaf taxa of biofuel crops

Perennial grasses have potential in the production of biofuels, and modulating plant microbiomes may enhance plant growth and productivity, and resilience to environmental stresses. However, our knowledge of the phyllosphere microbiome is limited, in particular for agricultural crops. In this study, Shade and colleagues investigated the assembly and seasonal dynamics of bacterial and archaeal microbiomes of the leaf surfaces and the associated soils of switchgrass and miscanthus across the two growing seasons in 2016 and 2017. They identified core leaf taxa for each crop and season based on abundance and occupancy, including several Proteobacteria (*Methylobacterium* spp., *Sphingomonas* spp. and *Pseudomonas* spp.) and Bacteroidetes (*Hymenobacter* spp.). Further analysis enabled them to identify seasonal trends of the core leaf taxa (that is, early, mid, and late season groups), which might be linked to plant development.

ORIGINAL ARTICLE Grady, K. L. et al. Assembly and seasonality of core phyllosphere microbiota on perennial biofuel crops. *Nat. Commun.* **10**, 4135 (2019)