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IN BRIEF

MICROBIOME

Getting organized early in life

In adults, distinct microbial communities inhabit different body sites and exert site-specific metabolic functions. However, when and how microbial community structure and function are established in early life have remained elusive. Chu *et al.* carried out a large population-based cohort study of maternal–infant pairs to determine the composition and metabolic function of the early neonatal microbiota and up to 6 weeks after delivery across several body sites (including stool, oral gingiva, nares, the skin and vagina). The neonatal microbiota was sparsely populated and predominantly comprised taxa of the maternal skin and vaginal microbiota. By 6 weeks, each body niche was enriched for taxa that were characteristic of their adult counterparts, which indicates a common maturation process. In addition, the microbial community function had expanded and diversified. Finally, although patterns of microbial composition in neonates were influenced by mode of delivery at birth, these differences were not present in the infants at 6 weeks of age, which suggests that the maturation of the infant microbiota is mainly driven by body site and not by mode of delivery.

ORIGINAL ARTICLE Chu, D. N. *et al.* Maturation of the infant microbiome community structure and function across multiple body sites and in relation to mode of delivery. *Nat. Med.* http://dx.doi.org/10.1038/nm.4272 (2017)

PARASITE EVOLUTION

Adding a piece to the puzzle

Genome-based studies increase our understanding of parasite evolution and host adaptation, but there was a lack of genetic information for *Plasmodium malariae* and two *Plasmodium ovale* species, which can cause human malaria but are found less often than other species. Rutledge *et al.* assembled a reference genome of *P. malariae* from clinically isolated parasites and they manually curated two draft genomes for both species of *P. ovale*; phylogenetic analysis provided insights into the evolution of the *Plasmodium* genus and species differentiation. Investigating host-specific adaptations, they report that *P. malariae* expresses a family of surface proteins that have structural similarities to a protein in *Plasmodium falciparum* that is essential for erythrocyte invasion. The newly available genomes will enable further studies of these *Plasmodium* species and the development of new diagnostic tools.

ORIGINAL ARTICLE Rutledge, G. G. *et al. Plasmodium malariae* and *P. ovale* genomes provide insights into malaria parasite evolution. *Nature* http://dx.doi.org/10.1038/nature21038 (2017)

BACTERIAL PATHOGENESIS

A deadly chain of events

Tuberculosis is characterized by the formation of granulomas. These macrophage-rich structures are formed to restrict the growth of *Mycobacterium tuberculosis*; however, macrophage necrosis in granulomas can facilitate pathogen growth. In this study, Mahamed *et al.* tracked infection outcomes in primary human macrophages *in vitro* using time-lapse microscopy and found that *M. tuberculosis* induced macrophage death dependent on the number of internalized bacteria. Phagocytosis of large bacterial aggregates was more cytotoxic than several small aggregates. Macrophage death did not result in bacterial clearance and, instead, *M. tuberculosis* grew faster in dead cells. Moreover, the internalization of dead infected cells resulted in a cell death cascade that fuelled bacterial infection and growth.

ORIGINAL ARTICLE Mahamed, D. *et al.* Intracellular growth of *Mycobacterium tuberculosis* after macrophage cell death leads to serial killing of host cells. *eLife* http://dx.doi.org/10.7554/eLife.22028 (2017)