in vitro revealed that the highest fold change in growth and the appearance of later stages of asexual development (a 48-hour cycle, with only the initial hours in the circulation) occurred at earlier culture times for the dry season samples than for wet season samples. Thus, either dry season *P. falciparum* completes asexual development more rapidly or they circulate in the blood for longer than wet season parasites.

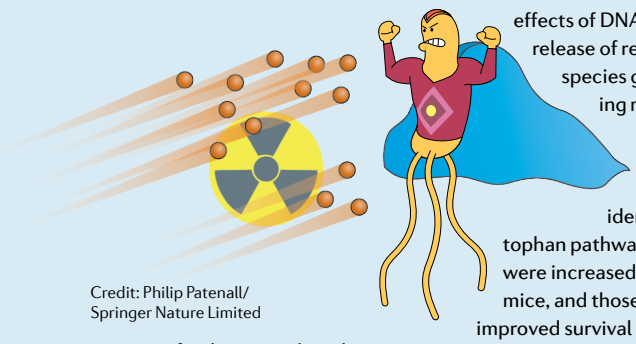
To distinguish between these possibilities, the authors determined the developmental stage of parasites in blood samples from different seasons, using the RNA-seq data and imaging of blood smears. The transcription profile of circulating parasites from dry season samples matched that of later stages of infection, and later parasite developmental stages were present in blood smears from dry season samples whereas only earlier stages were present in wet season samples. Thus, *P. falciparum* seems to remain in the circulation for longer at the end of the dry season than in the wet season.

What are the physiological consequences of this difference in circulation time? Using a microsphiltration system that models splenic clearance, the authors found that there was greater retention (that is, clearance) of infected RBCs (iRBCs) from dry season samples than from wet season malaria samples. Mathematical modelling suggested that changes in iRBC–endothelial cell adhesion alone could explain differences in parasitaemia progression, through the effect of splenic clearance on circulating parasites. However, the RNA-seq data did not show a significant difference in the expression of parasite-encoded adhesion molecules between dry and wet season samples.

In sum, this study suggests that persistence of *P. falciparum* through the dry season involves reduced iRBC adhesion and increased splenic clearance, thereby maintaining parasitaemia below a threshold above which clinical symptoms occur or an immune response is triggered.

Grant Otto

ORIGINAL ARTICLE Andrade, C. M. et al. Increased circulation time of *Plasmodium falciparum* underlies persistent asymptomatic infection in the dry season. *Nat. Med.* https://doi.org/10.1038/s41591-020-1084-0 (2020)



Credit: Philip Patenall/ Springer Nature Limited

severity of radiation-induced syndromes. The presence of Lachnospiraceae and Enterococcaceae was associated with the restoration of haematopoiesis and gastrointestinal repair, which is indicative of how radiation-induced damage might be alleviated. Moreover, these two bacterial taxa were also more abundant in patients undergoing radiotherapy who showed fewer adverse effects, which is in agreement with the notion that the distinct microbiota protects against radiation-induced injury.

Next, the authors showed that the production of short-chain fatty acids, specifically propionate, contributes to radioprotection by mitigating the effects of DNA damage and the release of reactive oxygen species generated by ionizing radiation. In addition, using an untargeted metabolomics approach they identified two tryptophan pathway metabolites that were increased in elite-survivor mice, and those significantly improved survival following radiation in vivo.

In sum, this study shows that Lachnospiraceae and Enterococcaceae, and specific bacterial metabolites, have a role in protecting their hosts from radiation-induced injury by promoting haematopoiesis and attenuating gastrointestinal damage. The identified bacterial metabolites might provide a possible treatment option to reduce the damage induced by radiation in patients.

Andrea Du Toit

ORIGINAL ARTICLE Guo, H. et al. Multi-omics analyses of radiation survivors identify radioprotective microbes and metabolites. *Science* **370**, eaay9097 (2020)

IN BRIEF

VIRAL INFECTION

Viral diversity in acute infection

The diversity of virus populations during acute infection and, in particular, the number of genotypes initiating an infection, is unclear. Gelbart et al. developed an ultra-deep sequencing approach termed AccuNGS to sequence acute infection samples from 43 patients infected with the DNA virus cytomegalovirus (CMV) or the RNA viruses human immunodeficiency virus 1 (HIV-1) or respiratory syncytial virus (RSV). Diversity was lower for CMV than for HIV-1 or RSV, probably owing to lower mutation rates in DNA viruses than in RNA viruses. Using a haplotype-inference approach they developed, the authors found strong evidence for the presence of multiple haplotypes in the most diverse samples, suggesting that multiple founder viruses initiated these infections. Host hyper-editing of viral genomes represented another source of diversity in samples. The two approaches used in this study could aid in characterizing pathogen evolution during infection from clinical samples.

ORIGINAL ARTICLE Gelbart, M. et al. Drivers of within-host genetic diversity in acute infections of viruses. *PLoS Pathog.* **16**, e1009029 (2020)

BACTERIAL GENETICS

A function for retrons

Retrons are bacterial genomic elements encoding a reverse transcriptase and a non-coding RNA (ncRNA). Despite their discovery more than three decades ago, the function of retrons remains unknown. Millman et al. found that many retrons are in close proximity in the genome to known phage-defence systems, suggesting that they are also involved in defence against phage infection. Retrons form a cassette that includes a reverse transcriptase, ncRNA and one or two genes encoding proteins that might function as effectors. Introduction of retrons and their effectors into an *Escherichia coli* strain lacking retrons provided defence against infection by various phages, by growth arrest or cell death. The authors showed that the defence mechanism of one retron involved sensing phage-mediated inactivation of the phage DNA-degrading RecBCD complex, which activated retron effectors and led to abortive infection.

ORIGINAL ARTICLE Millman, A. et al. Bacterial retrons function in anti-phage defense. *Cell* https://doi.org/10.1016/j.cell.2020.09.065 (2020)

CLINICAL MICROBIOLOGY

Towards a chlamydia vaccine

Chlamydia is the most common sexually transmitted bacterial infection in humans but is often asymptomatic. Left untreated, chlamydia infection can lead to serious complications, such as infertility, and thus vaccine development is a priority. Morrison et al. studied *Chlamydia muridarum* infection in mice, isolating a mutant *C. muridarum* strain (termed GIAM-1) that shows substantially reduced infection of the genital tract compared with that of the wild type. However, GIAM-1 efficiently infected the gastrointestinal tract, which induced robust humoral immunity against *C. muridarum*. Importantly, gastrointestinal tract infection with GIAM-1 protected mice against subsequent genital tract infection with wild-type *C. muridarum*. These results suggest that by manipulating tissue-tropism to obtain immunogenic bacterial strains that do not infect the genital tract, a live-attenuated vaccine for the human pathogen *Chlamydia trachomatis* might be obtainable.

ORIGINAL ARTICLE Morrison, S. G. et al. A genital infection-attenuated *Chlamydia muridarum* mutant infects the gastrointestinal tract and protects against genital tract challenge. *mBio* **11**, e02770-20 (2020)