IN BRIEF

■ BACTERIAL GENOMICS

The Bronze Age: a time before bubonic plague

Yersinia pestis, the causative agent of plague, is thought to have arisen from the less virulent enteric bacterium Yersinia pseudotuberculosis between 2.600 and 28.000 years ago. Until now, Y. pestis had not been recovered from human remains older than 1,500 years. Now, a report identifies Y. pestis in the teeth of 7 (out of 101) Eurasian individuals dating from 2,800 to 5,000 years ago. Notably, the Y. pestis genomes from these Bronze Age individuals all lacked ymt, the gene encoding a phospholipase that is essential for bacterial survival in the flea vector, which is responsible for transmission of bubonic plaque. Furthermore, the ancient Y. pestis genomes encoded the Pla protein, which is essential for deep tissue invasion, but they lacked an isoleucine-to-threonine mutation that is essential for developing bubonic plague. These data suggest that a less pathogenic Y. pestis was already endemic in humans before it acquired genetic changes that enabled bacterial survival in the flea vector and deep tissue invasion, which gave rise to more virulent strains responsible for pandemic bubonic plaque.

ORIGINAL RESEARCH PAPER Rasmussen, S. *et al.* Early divergent strains of *Yersinia pestis* in Eurasia 5,000 years ago. *Cell* **163**, 571–582 (2015)

→ VIRAL INFECTION

Highly flexible influenza polymerase

Influenza viruses rely on an RNA-dependent RNA polymerase, sometimes known as FluPol (comprising PB1, PB2 and P3 subunits), that both transcribes and replicates the viral RNA genome. Transcription initiation occurs by cap-snatching and depends on a viral RNA (vRNA) promoter; all currently available FluPol structures reflect this transcription pre-initiation state, with vRNA bound to FluPol. Now, Hengrung et al. report a new FluPol structure without vRNA. This structure reveals a novel 'closed' conformation in which the central PB1 subunit (which houses the polymerase active site) is capped on one end by PB2 and clamped between the two globular domains of P3. Notably, the cap-binding domain of PB2 is occluded in this closed state, suggesting that binding of the vRNA is responsible for substantial conformational changes that induce the transition of FluPol to the 'opened' transcription pre-initiation state.

ORIGINAL RESEARCH PAPER Hengrung, N. et al. Crystal structure of the RNA-dependent RNA polymerase from influenza C virus. Nature http://dx.doi.org/10.1038/nature15525 (2015)

■ MICROBIOME

Commensal bacterium prevents wasting

One common consequence of infection and inflammation is wasting of skeletal muscle and fat tissue. Now, a new study shows that gut colonization with the O21:H+ commensal strain of *Escherichia coli* can prevent wasting in a mouse model of intestinal inflammation or in mice infected with *Salmonella enterica* subsp. *enterica* serovar Typhimurium or *Burkholderia thailandensis*. Protection mediated by *E. coli* O21:H+ required bacterial translocation to the white adipose tissue (WAT) following infection or intestinal inflammation. In the WAT, *E. coli* O21:H+ induced high levels of insulin-like growth factor 1 (IGF1), in a process that was dependent on activation of the NLRC4 inflammasome. The high levels of IGF1 then stimulated the IGF1-phosphatidylinositol 3-kinase (PI3K)-AKT pathway in skeletal muscle, preventing muscle loss.

ORIGINAL RESEARCH PAPER Palaferri Schieber, A. M. *et al.* Disease tolerance mediated by microbiome *E. coli* involves inflammasome and IGF-1 signaling. *Science* **350**, 558–563 (2015)