IN BRIEF

TECHNIQUES & APPLICATIONS

Novel strategy to prevent otitis media caused by colonizing *Streptococcus pneumoniae*

McCullers, J. A. *et al. PloS Pathog.* **3**, e28 (2007)

The middle-ear infection otitis media (OM) is one of the most commonly diagnosed diseases of early childhood, with *Streptococcus pneumoniae* being one of the most common bacterial pathogens associated with this disease. In a recent *Plos Pathogens* paper, Vincent Fischetti and colleagues first describe the creation of a new animal model of OM before going on to show how a phage lysin could be used as an effective therapeutic agent against the disease. The animal model created by McCullers *et al.* is a non-invasive mouse model in which infection was established by intranasal infection with a piliated *S. pneumoniae* strain that had been modified to express luciferase. Mice that had been colonized in this way were then infected with influenza virus, as the disease state in OM is also thought to involve respiratory viruses. Using this new mouse model, the authors demonstrated that the *S. pneumoniae*-specific lysin Cpl-1 could eliminate colonization with *S. pneumoniae* and prevent the development of OM.

BACTERIAL PATHOGENICITY

Mycobacterium tuberculosis produces pili during human infection

Alteri, C. J. *et al. Proc. Natl Acad. Sci USA* **104**, 5145–5150 (2007)

Alteri and colleagues present ultrastructural, biochemical and genetic data indicating that the causative agent of tuberculosis, *Mycobacterium tuberculosis*, produces pili during human infection. Transmission electron microscopy analysis of the *M. tuberculosis* laboratory strains H37Rv and H37Ra and the clinical strain CDC1551 revealed the presence of 2–3-nm-wide coiled-coil aggregated fibres, which the authors named MTP (*M. tuberculosis* pili). The nature of the pilin subunit was investigated by mass spectrometry, and the MTP-associated sequence that was identified was shown to correspond to a predicted protein encoded by the H37Rv Rv3312A open reading frame, which the authors named *mtp*. The ability of purified MTP to bind to host proteins was assessed and the authors found that MTP bind the extracellular matrix component laminin. In the future, MTP might prove to be an attractive vaccine candidate.

VIROLOGY

Structure of a herpesvirus-encoded cysteine protease reveals a unique class of deubiquitinating enzymes

Schlieker, C. *et al. Mol. Cell* **25**, 677–687 (2007)

The host ubiquitination pathway is a key point of regulation for various cellular processes, and so is an obvious target for subversion by both bacterial and viral pathogens. Previous work using a functional proteomics approach had identified a deubiquitinating activity in cells infected with herpes simplex virus 1 (HSV-1), which was mapped to the N-terminal region of the UL36 protein, a constituent of the HSV-1 tegument. This activity was confirmed in the UL36 homologues in many other herpesviruses. The crystal structure of the ubiquitin-specific protease domain of the murine cytomegalovirus US36 homologue ($M48^{USP}$) complexed with a ubiquitin-based suicide inhibitor was reported in a recent issue of *Molecular Cell*. Based on the structural details, the authors conclude that $M48^{USP}$ is the founder member of a new class of deubiquitinating enzymes, which the authors call herpesvirus tegument ubiquitin-specific proteases.