Journal Highlights

New Insight Into Acute Rheumatic Fever Pathogen

Identifying strains of *Streptococcus pyogenes* that cause acute rheumatic fever (ARF) is notoriously difficult, as the symptoms often appear after the infection, when the bacteria are long gone. Now Matthew T. G. Holden of the Wellcome Trust Sanger Institute, Cambridge, United Kingdom, and others show that the Manfredo strain, isolated 50 years ago from a patient with ARF, carries multiple bacteriophage genomes that often differ between strains. One in seven genes is on a prophage, including virulence genes that might therefore be readily transferred between strains. "We now have a clearer view of the genetic makeup of strains that cause this enigmatic disease, and we have gained some insight into the wider pathogenesis of *S. pyogenes*," says Holden. "More important, the research community can use the variation we have detected to search for regions that are important to ARF." That data is available at www.sanger.ac.uk/Projects/S_pyogenes/.

(M. T. G. Holden, A. Scott, I. Cherevach, T. Chillingworth, C. Churcher, A. Cronin, L. Dowd, T. Feltwell, N. Hamlin, S. Holroyd, K. Jagels, S. Moule, K. Mungall, M. A. Quail, C. Price, E. Rabbinowitsch, S. Sharp, J. Skelton, S. Whitehead, B. G. Barrell, M. Kehoe, and J. Parkhill. 2007. Complete genome of acute rheumatic fever-associated serotype M5 *Streptococcus pyogenes* strain Manfredo. J. Bacteriol. 189:1473–1477.)

(See also Guest Commentary, A. Podbielski. 2007. Flexible architecture of the *Streptococcus pyogenes* FCT genome region: finally the clue for understanding purulent skin diseases and long-term persistence? J. Bacteriol. 189:1189–1184.)

How DivIVA Controls Morphology During Cell Division in *S. pneumoniae*

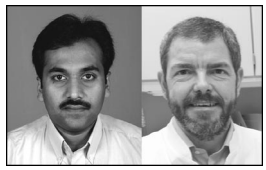
Fadda (l) and Masidda

Many aspects of cell division are still poorly understood, and some actors, including the protein DivIVA, have proven more difficult to study than others. Now Orietta Massidda of the University of Cagliari, Cagliari, Italy, and others show that in *Streptococcus pneumoniae*, DivIVA acts as a cytoskeletal scaffold that ensures a correct division, through positioning the peptidoglycan hydrolytic enzymes, and possibly the late cell division proteins, thereby determining the formation and maturation of the distinctive pointed-shape streptococcal poles. "We think that the results may help in understanding how the cell division machinery works in *S. pneumoniae* and closely related bacteria, including other gram-positive pathogens for which new antimicrobial inhibitors are urgently needed," says Massidda. "The work . . . suggests new ideas on how [DivIVA] may contribute to transformation of the midcell into two pointed poles that result in duplication of the cell volume with no net increase in cell diameter, a mechanism that prevents changes in the surface-to-volume ratio during growth and division," Miguel Vicente and Marta García-Ovalle write in a Guest Commentary.

(D. Fadda, A. Santona, V. D'Ulisse, P. Ghelardini, M. G. Ennas, M. B. Whalen, and O. Massidda. 2007. *Streptococcus pneumoniae* DivIVA: localization and interactions in a MinCD-free context. J. Bacteriol. 189: 1288–1298.)

(See also Guest Commentary, M. Vicente and M. García-Ovalle. 2007. Making a point: the role of DivIVA in streptococcal polar anatomy. J. Bacteriol. 189:1185–1188.)

Newly Discovered Gene Inhibits Virulence in *M. tuberculosis*

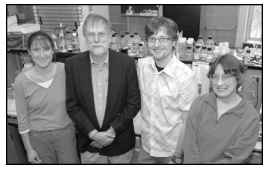


Robinson (l) and Plum

Inhibition of phagosome maturation is an important mechanism for virulence in *Mycobacterium tuberculosis*. Although it was discovered in 1971, the molecules that orchestrate it still have not been identified, despite the fact that the components of the rather peculiar cell wall have been well studied. Now, using a genetic screen, Georg Plum, Nirmal Robinson, and colleagues of the University of Cologne, Germany, have identified a novel gene, *pmiA*, which is involved in production of a specific cell wall glycolipid, which, in turn, plays a role in preventing phagosome maturation. "We believe that this glycolipid is of general importance for mycobacterial virulence as *pmiA* is only one of a number of genes identified by our screen involved in the synthesis of this particular lipid," says Plum. "Elucidation of the structure and the pathways to its synthesis are under way and may yield novel, urgently needed chemotherapeutic targets for mycobacterial infections."

(N. Robinson, M. Wolke, K. Ernestus, and G. Plum. 2007. A mycobacterial gene involved in synthesis of an outer cell envelope lipid is a key factor in prevention of phagosome maturation. Infect. Immun. 75:581–591.)

Ciliates Mop Up Viruses in Water



(l-r) Power, Bols, Pinheiro, and Butler

The impact of viruses on water quality appears more complex than previously thought. Viruses are the most abundant biological entities in water. Niels C. Bols and Mary E. Power of the University of Waterloo, Ontario, Canada, et al. show that as ciliates continuously vacuum water, they inadvertently inactivate viruses. This inactivation "appears nonsaturable, in that the rate of virus removal continued to increase as we increased the phage:ciliate [T4 bacteriophage: *Tetrahymena*] ratio," says Power. The results raise questions the researchers intend to pursue: how general is this type of inactivation? Are there mechanisms of inactivation besides macropinocytosis (in which phage are enclosed in vesicles in the buccal cavity and inactivated when vesicles fuse, presumably with lysosomes)? How significant is this inactivation to bacterial populations? "From a biotechnological perspective, ciliates might be exploited in wastewater treatment to improve the removal of viruses that are pathogenic to humans, if ciliates inactivate these viruses in such a nonspecific and nonsaturable manner," says Power.

(M. D. O. Pinheiro, M. E. Power, B. J. Butler, V. R. Dayeh, R. Slawson, L. E. J. Lee, D. H. Lynn, and N. C. Bols. 2007. Use of *Tetrahymena thermophila* to study the role of protozoa in inactivation of viruses in water. Appl. Environ. Microbiol. 73:643–649.)

Phage Therapy Effective Against *P. aeruginosa* in Murine Gut-Derived Sepsis

Matsumoto

Clinical use of phage therapy dates back to the discovery of bacteriophages by Felix d'Herelle in 1915, but it was forgotten by western medicine after the advent of antibiotics. It has been making a comeback due to the emerging threat of antibiotic-resistant bacteria. Now, phage therapy demonstrates efficacy in mice against *Pseudomonas aeruginosa*, in a study by Tetsuya Matsumoto of Tokyo Medical University and others. "We used an animal model of sepsis that closely resembles the clinical pathophysiology of diseases in humans, and we showed that oral administration of phage may be protective against gut-derived sepsis," says Matsumoto. "Growing levels of antibiotic resistance and the exit of major pharmaceutical companies from antibiotic development will increase in demand for alternatives to antibiotics. So, we are now planning further studies for the widespread use of phage treatment as a clinical therapy for humans."

(R. Watanabe, T. Matsumoto, G. Sano, Y. Ishii, K. Tateda, Y. Sumiyama, J. Uchiyama, S. Sakurai, S. Matsuzaki, S. Imai, and K. Yamaguchi. 2007. Efficacy of bacteriophage therapy against gut-derived sepsis caused by *Pseudomonas aeruginosa* in mice. Antimicrob. Agents Chemother. 51:446–452.)