RESEARCH HIGHLIGHTS

IN BRIEF

BACTERIAL PATHOGENESIS

An interspecies role for SpA

Pathogens often colonize the host as polymicrobial communities; however, much remains to be learnt about how microbial interspecies interactions alter bacterial behaviour. Co-infection with Staphylococcus aureus and Pseudomonas aeruginosa is common in patients with cystic fibrosis and has been associated with increased virulence and pulmonary decline. In this study, Armbruster et al. report that the S. aureus adhesin, staphylococcal protein A (SpA; an extracellular virulence factor that impedes host immune responses) inhibits the formation of biofilms by specific clinical isolates of P. aeruginosa and IgG-mediated phagocytosis by host neutrophils. The authors went on to show that SpA exerts these effects by binding to Psl polysaccharide and the PilA protein component of type IV pili, two surface molecules of P. aeruginosa that have been implicated in adhesion and cell-cell interactions. Thus, the results of this study suggest that secreted SpA alters persistence and host interaction of P. aeruginosa during co-infection.

ORIGINAL ARTICLE Armbruster, C. A. *et al.* Staphylococcus aureus protein A mediates interspecies interactions at the cell surface of *Pseudomonas aeruginosa. mBio* **7**, e00538-16 (2016)

VIRAL INFECTION

Moving and splicing M1 mRNA

Influenza virus M1 mRNA is translated into the matrix protein M1, whereas the ion channel protein M2 is produced after the splicing of M1 mRNA into M2 mRNA. Mor et al. now show that M1 mRNA and M2 mRNA accumulate at nuclear speckles, which are enriched for splicing factors, following transcription. On the basis of their data, they propose a model whereby M1 mRNA is trafficked to nuclear speckles by the viral protein NS1 bound to cellular NS1-BP for hnRNP K-dependent splicing into M2 mRNA and nuclear export. The interaction of SON (a cellular factor that is involved in the assembly of nuclear speckles and alternative splicing) with NS1, NS1-BP, hnRNP K and M1 mRNA further supports the notion that influenza virus subverts nuclear speckles to promote efficient splicing. Finally, nuclear export was shown to be coupled to splicing and to be mediated by cellular export factors. In sum, this study reveals a previously unknown role for NS1 in mRNA targeting to nuclear speckles and splicing. ORIGINAL ARTICLE Mor, A. et al. Influenza virus mRNA trafficking through host nuclear speckles. Nat. Microbiol. http://dx.doi.org/10.1038/nmicrobiol.2016.69 (2016)

BACTERIAL GENOMICS

Finding the connection

In this study, Peters et al. used CRISPR interference to produce a knockdown library of essential genes in Bacillus subtilis. The functional analysis of the essential gene network revealed numerous connections between genes that are involved in related processes and connections that were not previously identified, which highlights the extent of the functional circuits between core processes. Next, the authors determined growth characteristics and found that a slight decrease in essential gene products significantly reduced stationary-phase survival without affecting maximal growth rate. Finally, for most essential genes, complete depletion, in contrast to knockdown to basal levels, altered morphological phenotypes. This work provides a framework for the high-throughput analysis of essential gene functions that can be applied to various bacteria. ORIGINAL ARTICLE Peters, J. M. et al. A comprehensive, CRISPR-based functional analysis of essential genes in bacteria. Cell http://dx.doi.org/10.1016/j.cell.2016.05.003 (2016)