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IN BRIEF

ANTIMICROBIALS

ABC-F proteins protect bacterial ribosomes

Members of the ABC-F subfamily of ATP-binding cassette proteins mediate resistance to a wide range of clinically important classes of antibiotic that target protein translation in Gram-positive pathogens; however, their mechanism of action has long been debated. Previously, antibiotic efflux and ribosomal protection were proposed as two competing hypotheses, and a new study by Sharkey *et al.* provides evidence for the latter. The authors reported that purified ABC-F proteins, VgaA and LsaA, rescued translation from antibiotic-mediated inhibition *in vitro* in a dose-dependent manner, which suggests that the ABC-F protein family protects the bacterial ribosome. They went on to show that LasA prevents the binding of the antibiotic to staphylococcal ribosomes and, furthermore, that it displaces the antibiotic that is bound to the ribosome. In sum, this study provides insights into a possible mechanism of resistance that involves ribosomal protection by ABC-F proteins.

ORIGINAL ARTICLE Sharkey, L. K. R, Edwards, T. A. & O'Neill, A. J. ABC-F proteins mediate antibiotic resistance through ribosomal protection. *mBio* **7**, e01975-15 (2016)

VIRAL INFECTION

Zika virus structure, epidemiology and evolution

The current Zika virus (ZIKV) epidemic in the Americas and the potential link to an increase in the number of cases of birth defects in regions where the virus is circulating has caused worldwide concern. ZIKV belongs to the *Flaviviridae* family of positive-strand RNA viruses; however, its structure, tropism and pathogenesis were largely unknown. Now, Sirohi *et al.* have solved the cryo-electron microscopy structure of mature ZIKV isolated from a patient that was infected during the French Polynesia epidemic in 2013–2014 at 3.8 Å resolution. They found that the structure was similar to those of the flaviviruses dengue virus (DENV) and West Nile virus (WNV); however, the authors noted structural differences in the region surrounding the Asn154 glycosylation site in the viral envelope glycoproteins, a region that might be important for attachment to host receptors and may govern cellular tropism and disease outcome.

In another study, Faria *et al.* used phylogenetic, epidemiological and travel data to investigate the evolution of ZIKV and its introduction to the Americas. Using next-generation sequencing they generated seven complete ZIKV coding sequences from samples that were collected during the outbreak in Brazil, including four self-limited cases, one blood donor, one fatal adult case, and one newborn with microcephaly and congenital malformations. A comparison of these genomes with other available Brazilian strains showed that the isolates differ at several nucleotide sites in the coding region. Furthermore, the authors found that all of the viruses that were sampled in the Americas share a common ancestor with the ZIKV strain that circulated in French Polynesia in 2013 and, using molecular clock analysis, they estimated that a single introduction of ZIKV into the Americas had occurred between May 2013 and December 2013, a time period that coincided with an increase in air travel from ZIKV endemic regions and with reported outbreaks in the Pacific Islands. Finally, they found that viral genomes from Brazil are phylogenetically interspersed with those from other countries in South America and the Caribbean.

ORIGINAL ARTICLES Sirohi, D. *et al.* The 3.8 Å resolution cryo-EM structure of Zika virus. *Science* http://dx.doi.org/10.1126/science.aaf5316 (2016) | Faria, N. R. *et al.* Zika virus in the Americas: Early epidemiological and genetic findings. *Science* http://dx.doi.org/ 10.1126/science.aaf5036 (2016)