Staphylococcus aureus gets a helping *van*(d) from *Enterococcus faecalis*

One of the last lines of treatment against *Staphylococcus aureus*, including the methicillin-resistant strains (MRSA), has been vancomycin. Strains with decreased susceptibility to vancomycin (VISA) have been isolated previously, but recently a vancomycin-resistant strain (VRSA) was isolated from a dialysis patient in Michigan. Vancomycin-resistant *Enterococcus faecalis* and *E. faecium* (VRE) has been a major problem for the last decade. The resistance genes in VRE are carried on the mobile genetic element, transposon Tn*1546*, with the potential for interspecies transfer to, for instance *S. aureus*.

Weigel *et al.* [7] isolated plasmids from the Michigan VRSA strain and two co-isolates from the same patient, a VRE and a vancomycin-susceptible MRSA. Both VRSA and VRE plasmids contained Tn*1546*, while the MRSA did not, suggesting that the MRSA acquired the transposon from the VRE, thus generating a VRSA. The VRSA and VRE plasmids were shown to be conjugative plasmids that can be transferred *in vitro* to *S. aureus* and *E. faecalis*, respectively.

When the complete sequence of the VRSA plasmid was determined, it revealed a composite structure with homologies to several multidrug resistance plasmids and conjugative plasmids. The integrated transposon encoding the VR gene cluster was identical to the prototype Tn*1546*.

In addition to the Tn*1546*, genes encoding putative resistances against several other antibiotics and disinfectants were identified.

This study convincingly shows that VRSA can arise from inter-species conjugation and/or transduction events of mobile genetic elements, most likely originating from co-infecting vancomycin-resistant enterococci, but also raises serious concerns about continuous intra-species dissemination among *S. aureus.*

7 Weigel, L.M. (2003) Genetic analysis of a high-level vancomycin-resistant isolate of *Staphylococcus aureus*. *Science* 302, 1569–1571

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Business

Announcements

UniProt is launched

The EMBL-European Bioinformatics Institute (EBI), the Swiss Institute of Bioinformatics (SIB) and Georgetown University Medical Center's Protein Information Resource (PIR), have announced the launch of UniProt, a new universal protein resource that will be the most comprehensive catalogue of information on proteins.

This venture was made possible by funding from the US National Institutes of Health, totalling US$15 million over three years, with the National Human Genome Research Institute (NHGRI) as the primary funding body.

Peter Good, the NHGRI programme director in charge of the UniProt project, said: 'The UniProt databases will be a critical resource for investigators trying to unlock the secrets in genome sequences, both to understand biology and to translate basic research into improvements in healthcare.'

Rolf Apweiler, UniProt's Principal Investigator, explained, 'UniProt's structure resembles that of a wedding cake. Each tier of the cake represents a different database, optimized for different uses.'

The next layer of the 'wedding cake', and the centrepiece of activities for the three institutes – collectively known as the UniProt Consortium – is the UniProt Knowledgebase, which is unified from Swiss-Prot, TrEMBL and PIR-PSD. 'This is the place to go if you want to know everything there is to know about a specific protein,' explains Maria-Jesus Martin, Sequence Coordinator for EBI.

UniProt can be accessed at http://www.uniprot.org.

Collaborations

Entelos expands research with Johnson & Johnson

Entelos (http://www.entelos.com) has announced its expansion of its research collaboration with Johnson & Johnson Pharmaceutical Research and Development (J&JPRD; http://www.jnj.com), to include target validation, lead optimization and clinical development in obesity.

In addition, J&JPRD sister company – McNeil Nutritionals – will join the collaboration. This announcement coincides with the first annual meeting of the Diabetes Research Forum, which is a research effort between Entelos, the American Diabetes Association and the pharma industry, to advance research in the treatment of type 2 diabetes.

James Karis, President and CEO of Entelos, said that he was pleased that J&JPRD had expanded their collaboration to include obesity and that McNeil Nutritionals has joined the collaboration.

Entelos employs disease level system biology technologies to identify and validate targets, biomarkers and compounds for human efficacy.

Cellzome in collaboration with Bayer Healthcare

Cellzome (http://www.cellzome.com) have announced a collaboration with Bayer Healthcare (http://www.bayer.com), where Cellzome's drug proteomics platform will be leveraged to profile Bayer's lead compounds.

Cellzome's chemical proteomics approach will be used to identify the protein interaction profiles of several lead compounds from a variety of therapeutic areas, facilitating drug development at Bayer.

David Brown, Chief Executive at Cellzome, commented: '… [we] believe this is the first step towards a long-term strategic relationship between the companies.'

Cellzome is a drug discovery company building an R&D pipeline in chronic diseases, with a primary focus on Alzheimer's disease, whose combination of chemical proteomics and pathway expansion focuses on the interface between validated disease pathways, tractable medicinal chemistry and druggable targets.

Business was written by *Joanne Clough*

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