E052

2-hour Educational Workshop

Whole genome sequencing - what the heck?

Whole genome sequencing for microepidemiological investigations: can person-to-person transmission be identified?

M. Holden[1]

[1]*University of St Andrews, St Andrews, United Kingdom*

The application of whole genome sequence (WGS) as a high-resolution typing tool has provided clinical microbiologists with the ability to distinguish bacterial isolates that differ by as little as a single nucleotide in their genetic makeup. Consequently, WGS has become a very powerful epidemiological tool for investigating outbreaks of infectious diseases. The ability of WGS to define the genetic relatedness of isolates can be used to distinguish distantly related isolates from those that shared a common ancestor more recently, and thereby potential identify isolates that have a common origin. In the context an outbreak investigation, this can help investigators rule-in and rule-out isolates from the outbreak, and also infer routes of transmission from person-to-person. However, the use of WGS in epidemiological investigations is still in its infancy. There is currently a dearth of knowledge surrounding pathogen diversity with the host, and pathogen evolution during disease and asymptomatic carriage, which redistricts the interpretation of WGS data from micro-epidemiological investigations. In this talk I will focus on the healthcare-associated pathogen *Staphylococcus aureus*, and discuss how deep sequencing has been used to investigate the population structure and transmission dynamics of *S. aureus* in hospitals, and also considerations for using WGS to identify person-to-person transmissions.