Key Session 1

[O2] PROSPECTS FOR WHOLE GENOME SEQUENCING FOR DIAGNOSTICS

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Bacterial whole genome sequencing has the potential to replace much of routine laboratory microbiology, including in the investigation of potential bone and joint infection.
Approaches using whole genome sequencing to reliably identify bacteria and determine antimicrobial susceptibilities will be discussed. Most proof of principal studies to date have relied on prior culture of bacteria before sequencing, however methods in development to allow the presence of bacteria, species and susceptibilities to be determined directly from clinical samples will also be presented. Specific challenges include selective identification of limited amounts of bacterial DNA in the presence of large amounts of human DNA, and determining diagnostic thresholds for the amount of bacterial DNA associated with clinically significant infection.

Novel sequencing technology, such as Oxford Nanopore sequencing, is likely to significantly enhance diagnostics with clinical samples sequenced directly within hours using a device the size of a USB-drive connected to a laptop. Emerging 'read-until' technology offers the prospect of selectively sequencing pathogen DNA, while rejecting human DNA from the sequencing pore. In contrast to the short reads generated by current technology, the longer reads produced potentially enable improved matching of species identification and resistance prediction in polymicrobial infections.

Whole genome sequencing offers the potential for rapid culture-free diagnostics in bone and joint infection. Where distinguishing contamination from true infection is important, sequences from multiple samples can be compared directly rather than having to rely on proxies such antimicrobial susceptibilities. Additionally, whole genome sequencing has the potential to enhance our understanding of the aetiology of bone and joint infection; data collected for routine diagnostic purposes may concurrently yield insights into pathogenicity and virulence determinants. Comparison of patient and environmental flora with sequences from infections may also reveal sources of infection and allow their better control.