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P2511 Investigating the utility of MicroDTTect® and rapid metagenomic sequencing for the detection of prosthetic joint infection

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Background:

Prosthetic Joint Infections (PJI) occur when bacteria colonize a prosthesis, forming a biofilm. The incidence of PJI is between 1% and 2% and requires prosthetic joint revision surgery, costing an estimated £200 million annually in the UK. Routine culture of tissue biopsy is the current gold-standard for the diagnosis of PJI. However, culture is slow and low in sensitivity, with fastidious organisms and commensal contamination making diagnosis difficult. Rapid metagenomics combined with whole prosthesis sampling could potentially provide better results in a shorter timeframe.

Materials/methods:

We tested the MicroDTTect® system, which removes biofilm from whole prostheses, followed by metagenomic sequencing and BacT/Alert® culture on 19 patients with suspected PJI or Aseptic Loosening and controls. The metagenomics pipeline utilises differential lysis for human DNA depletion and MinION® nanopore sequencing. We compared the performance of MicroDTTect® fluid metagenomics and BacT/Alert® culture for the detection of PJI with routine microbiology (4-9 peri-prosthetic tissue samples - ≥2 containing the same bacterium classified as positive).

Results:

The metagenomics pipeline and MicroDTTect® BacT/Alert® culture had sensitivities of 60% and specificities of 86% compared to routine culture. In one sample *Streptococcus pneumoniae* was found only by metagenomics, backed up by a probe-based *S. pneumoniae* qPCR and a Gram stain of Gram-positive cocci in synovial fluid taken during surgery. In another sample, *Staphylococcus warnerii* was found by both metagenomics and MicroDTTect® culture, but not by routine culture, demonstrating how whole prosthesis sampling may improve diagnostic sensitivity. There were two cases where metagenomics failed to detect organisms found by routine culture: one containing *Pseudomonas aeruginosa,* found in 2/7 tissue samples (and MicroDTTect® culture) and the other containing *Propionibacterium acnes*, a common skin contaminant (not detected by MicroDTTect® culture). In two samples, *Staphylococcus epidermidis* was cultured from MicroDTTect® fluid but not reported by either sequencing or routine culture, suggesting MicroDTTect® may be susceptible to some contamination.

Conclusions:

MicroDTTect® combined with metagenomics shows potential for a rapid and efficient diagnosis of PJI. Direct MinION® sequencing can provide results in hours rather than days, providing guidance for appropriate antibiotic treatment, improving patient outcomes and improving antimicrobial stewardship.