

## TITLE

Evaluating Contamination Risk when Aspirating a Prosthetic Joint using Microbial Next Generation DNA Sequencing: An In-Vitro study

## ABSTRACT

**Background:** A challenge in periprosthetic joint infection is the detection of microbiota. Next-generation sequencing (NGS) of microbial ribosomal DNA is one detection method, but false-positive results are of concern. We conducted a simulated joint aspiration study to assess false-positive rates with NGS testing.

**Methods:** The simulated joint was a 50-mL bottle of sterile saline. Four techniques (n = 20 per technique) were tested. Fluid aspirates were inserted into sterile vacutainers with different needle exchanges analyzed for potential contamination points. The negative control group (n = 20 per technique) consisted of 80 sterile saline bottles tested directly at the NGS laboratory.

**Results:** Eighty simulated aspirations were performed, two NGS tests per “joint.” In three simulated techniques, the positive detection rate was 0.8%. In the fourth technique, where 10 mL of ambient air was aspirated into the syringe, the rate was 10%. The positive detection rate among the negative control bottles was 1.2%.

**Conclusion:** NGS detected DNA signals from sterile saline aspirations using a sterile technique. However, the false-positive rate was low (0.8%). We theorize that positive DNA signals originated from errant microbe contamination from ambient air drawn into the testing needle bore. We advocate needle exchange at every fluid transfer point.