Section 1: Abstract Title

Clinical Uses of Nanopore Sequencing in Recurrent Acute and Chronic Otitis Media

Section 2: Author Names

Ben Holtzlander[1], Sarah Burgin[2], Grace Perkins[3], Guang-Sheng Lei[3], Thomas Davis[3]

Section 3: Author Department and School Affiliation

[1]Indiana University School of Medicine; [2]Indiana University School of Medicine, Department of Otolaryngology; [3]Indiana University School of Medicine, Department of Pathology

Background. Otitis Media (OM) is a widespread problem that has an incidence of 10.85% worldwide, 51% occurring under the age of 5. Emergence of drug resistant bacteria contribute to high incidence of recurrent acute otitis media (AOM) and chronic otitis media with effusion (COME). Despite this, the standard of care for treatment is empiric antibiotics. Molecular microbiology diagnostics may enable clinicians to provided pathogen directed antibiosis. Nanopore sequencing is a highly accurate method of identifying a broad range of pathogens when compared with multiplex PCR. We hypothesize that nanopore sequencing is an effective method for detection of pathogens in the middle ear and nasopharynx of patients with recurrent or chronic OM.

Methods. Bacterial Culture, multiplex PCR (BioFire PNA panel), and nanopore sequencing (MinIon, Oxford Nanopore Technologies) were tested on 60 middle ear and nasopharynx samples. Chi-Square test was used to examined differences in bacterial identification among the methods.

Results. Bacterial identification using nanopore proves to be more sensitive in identification of 16 of the 18 unique pathogens when compared with multiplex testing. Of the 5 most common OM bacterial pathogens (*S. pneumoniae, M. catarrhalis, H. influenza, S. aureus, P. aeruginosa*), nanopore identified 3 pathogens (*S. pneumoniae, M. catarrhalis, P. aeruginosa)* at higher levels, 1 at the same rate (*H. influenza*), and 1 did not receive any readings (*S. aureus*).

Conclusion. This is the first study to utilize nanopore sequencing to assess pathogens in the middle ear fluid of children with OM. While nanopore genomic sequencing is still in the early stages of use, it has potential to comprehensively identify bacteria with more sensitivity when compared to the current clinical standards. The next step of data analyzation will include bacterial identification in nanopore that multiplex PCR and traditional bacterial cultures cannot test for.