

# Real-Time Bacterial Identification for Acute Otitis Media

## Summary

Vanderbilt researchers have developed an optical-based method for real-time characterization of middle ear fluid in order to diagnose acute otitis media, also known as a middle ear infection. The present technique allows for quick detection and identification of bacteria and can also be applied to other biological fluids *in vivo*.

## Addressed Need

Otitis media is the leading cause of physician visits and medication prescription for children, with over 350 million cases per year. The diagnosis of otitis media is currently subjective and symptom-dependent. Furthermore, since current diagnoses do not identify specific bacteria, the treatment often involves the use of broad spectrum antibiotics thereby increasing the chances of developing multi-drug resistant organisms (MDROs) in patients.

## Technology Description

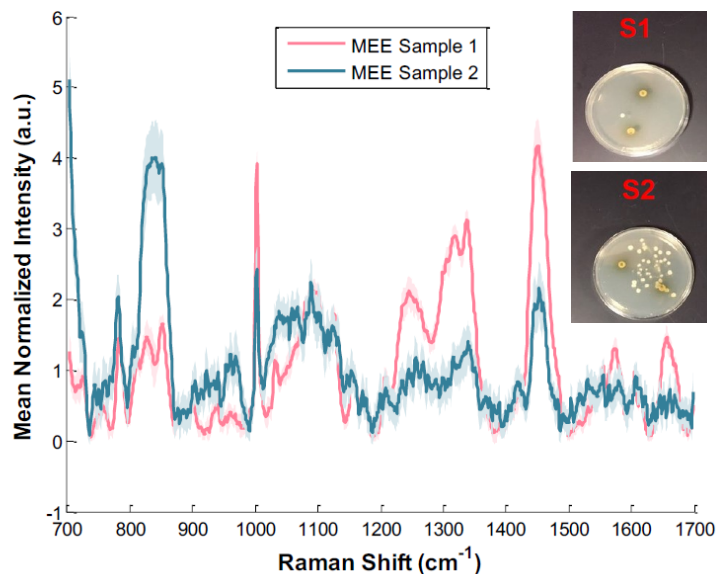
The present technology uses Raman spectroscopy to generate a spectral signal from the fluid sample, which is then compared against a database of known biomarkers. At this point, the presence or absence of known bacteria that cause middle ear infections can be determined using statistical analysis. The treatment regime can then be tailored for the specific bacteria, thereby improving the patient's response to the treatment and reducing the prevalence of MDROs.

## Technology Features

- ◇ Uses a non-invasive, light-based approach to identify bacteria
- ◇ Is able to distinguish in real-time between bacterial and non-bacterial causes of acute otitis media, enabling more targeted antibiotic prescription
- ◇ Able to be made hand-held for physician usage in the clinic

## Intellectual Property and Technology Development Status

- ◇ Patent application has been filed
- ◇ Raman spectroscopy has been used to characterize and distinguish the three main bacteria that cause acute otitis media
- ◇ Continued development is ongoing, including a prototype handheld device



The Raman spectra of two middle ear effusion samples is shown. The microbial colonies present in the samples were successfully classified for each sample.

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