Comparison of Sinus Flora Using Various Next-Generation Sequencing Techniques Versus Standard Culturing

Benjamin Kistler[1], Manav Patel[1], Thomas Davis[2], Guang-Sheng Lei[2], Danielle Schreiber[2], Vijay Ramakrishnan[3]

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

Background:

Next generation sequencing methods are being developed to help diagnose infectious diseases at the point of care and to help resolve discrepant results. These new methods hope to replace longer, more tedious sequencing methods such as Sanger/shotgun sequencing and less sensitive culture results to provide a clinical diagnosis and start appropriate treatment sooner. In lieu of dated techniques, with next generation sequencing the physician could analyze samples in their clinic with relative ease and receive a sensitive diagnosis in a fraction of the time.

Objective:

To compare percent agreement between standard culturing results of swabbed sinus samples on blood and chocolate agar to BIOFIRE® FILMARRAY® results, and use Oxford Nanopore and 16s illumina sequencing results to resolve discrepancies.

Study design:

Swabs were taken of the nasal sinuses of 21 patients and flash frozen. Some of these swabs (15/21) were sequenced with 16s illumina sequencing. All these swabs were put into a saline solution and plated on blood and chocolate agar plates as a 1:100 loop dipped into the solution and as the original swab. These solutions were sequenced through the BIOFIRE® FILMARRAY® Torch System on a pneumonia and blood culture (BCID2) panel and through the Oxford Nanopore® MinION Mk1C® system.

Results:

The pneumonia panel had 36% agreement with blood agar and 52% agreement with chocolate agar plates. Using the top 3 genus results, either Nanopore or 16s illumina sequencing resolved

92% of discrepancies between the pneumonia panel and blood agar and 90% of discrepancies between the pneumonia panel and chocolate agar plates.

The blood culture panel had 43% agreement with blood agar and 57% agreement with chocolate agar plates. Nanopore or 16s illumina sequencing resolved 92% of discrepancies between the blood panel and blood agar and 89% of discrepancies between the blood panel and chocolate agar.