ORAL ABSTRACTS

119. Identification of Infectious Agents in Pediatric Bronchoalveolar Lavage Specimens Using Standard versus Molecular Diagnostic Methods

Sruti Nadimpalli, MD MPH[1]; Paul Planet, MD, PhD[2]; Smith Hannah, BS[3]; Coscia Gina, MD[4]; Tobin Hammer,[5]; Henley Jessica,[5]; Andrei Constantinescu, MD PhD[4]; Prakash Satwani, MD[6]; Fierer Noah, PhD[5]; Lisa Saiman, MD MPH[1]; Marc Foca, MD[6]; [1]Department of Pediatrics, Columbia University Medical Center, New York, NY; [2]Pediatrics, Columbia University, New York, NY; [3]Columbia University Medical Center, New York, NY; [4]Columbia University Medical Center, Department of Pediatric Pulmonology, New York, NY; [5]University of Colorado, Department of Ecology, Boulder, CO; [6]Columbia University College of Physicians & Surgeons, New York, NY

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Background. New molecular diagnostic strategies are being developed to improve detection of infectious pathogens. We examined the use of these strategies for bronchoalveolar lavage (BAL) specimens.

Methods. We performed a pilot study to evaluate different diagnostic strategies for BAL specimens. We compared standard culture-based methods, commercially available molecular methods for respiratory viruses (FilmArray, Biofire, Inc.) and herpes viruses, and the investigational methods 16S ribosomal Sanger and Illumina sequencing which amplify DNA to identify bacteria from variable regions of the 16S ribosomal subunit gene. Eligible subjects were ≤18 years of age and underwent BAL from May 2013 to February 2014 for potential infection or structural anomalies. Mixed commensal flora (MCF) was not considered pathogenic.

Results. Thirty-three subjects underwent BAL; 9 had cystic fibrosis (CF); 4 had oncologic disease; 4 had laryngotracheomalacia; 2 had heart transplants; 2 had asthma; 8 had other conditions, e.g., foreign body, plastic bronchitis and interstitial lung disease; and 4 had chronic respiratory symptoms, but no identified diagnosis. Overall, 30/33 (91%) subjects had positive BALs for 51 potential pathogens (30 bacteria, 14 viruses, 7 fungi). Concordant results were noted for 4/4 subjects with nasopharyngeal swab sent for RT-PCR within 3 days of BAL. 16S Sanger sequencing was 75% (6/8) concordant with bacterial cultures, and deeper Illumina sequencing was 67% (16/24) concordant. Both methods detected potential pathogens in 2 other BAL. The yield of standard versus molecular methods is shown (table).

Positive BAL Specimens: Standard versus Molecular Methods

Pathogen[1]	Culture-based	Molecular-Viruses	16S	Illumina
Bacteria	23	NA	8	18
MCF	6	NA	NA	NA
Virus	NA	13	NA	NA
Fungal	7	NA	NA	NA
Overall	27/33 (82%)	13/25 (52%)	8/25 (32%)	18/24 (75%)

[1]11 subjects had co-infections.

Conclusion. Most subjects had a pathogen detected by available techniques. However, 16S sequencing identified potential pathogens not identified by standard methods. Future studies should assess the utility of the relative organism burden derived from 16S sequencing as well as amplified DNA for fungal and mycobacterial pathogens.

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