Pulmonary Metagenomic Sequencing Suggests Missed Infections in Immunocompromised Children

Matt S. Zinter,1,2 Christopher C. Dvorak,2 Madeline Y. Mayday,1 Kensho Iwanaga,3 Ngoc P. Ly,3 Meghan E. McGarry,2 Gwynne D. Church,3 Lauren E. Faricy,4 Courtney M. Rowan,1 Janet R. Hume,6 Marie E. Steiner,6,7 Emily D. Crawford,8,9 Charles Langelier,10 Katrina Kalantar,9 Eric D. Chow,9 Steve Miller,11 Kristen Shimano,3 Alexis Melton,3 Gregory A. Yanik,12 Anil Sapru,13 and Joseph L. DeRisi8,9

Hospital for Children, Indiana University School of Medicine, Indianapolis; Divisions of 6Critical Care and 7Hematology/Oncology, Department of Pediatrics, Masonic Children’s Hospital, University of Minnesota School of Medicine, Minneapolis; 8Chan Zuckerberg Biohub, and 9Department of Biochemistry & Biophysics, 10Division of Infectious Diseases, Department of Internal Medicine, and 11Department of Laboratory Medicine, University of California–San Francisco School of Medicine; 12Division of Oncology, Department of Pediatrics, Motts Children’s Hospital, University of Minnesota School of Medicine, Minneapolis; 13Division of Critical Care, Department of Pediatrics, Benioff Children’s Hospital, University of California, San Francisco School of Medicine; 14Division of Pulmonology, Department of Pediatrics, University of Vermont School of Medicine, Burlington; 15Division of Critical Care, Department of Pediatrics, Riley Hospital for Children, Indiana University School of Medicine, Indianapolis; Divisions of 1Critical Care and 2Allergy, Immunology, and Blood & Marrow Transplantation, and 3Pulmonology, Department of Pediatrics, Benioff Children’s Hospital, University of California, San Francisco, 550 16th St, San Francisco, CA 94143 (matt.zinter@ucsf.edu).

Background. Despite improved diagnostics, pulmonary pathogens in immunocompromised children frequently evade detection, leading to significant mortality. Therefore, we aimed to develop a highly sensitive metagenomic next-generation sequencing (mNGS) assay capable of evaluating the pulmonary microbiome and identifying diverse pathogens in the lungs of immunocompromised children.

Methods. We collected 41 lower respiratory specimens from 34 immunocompromised children undergoing evaluation for pulmonary disease at 3 children’s hospitals from 2014–2016. Samples underwent mechanical homogenization, parallel RNA/DNA extraction, and metagenomic sequencing. Sequencing reads were aligned to the National Center for Biotechnology Information nucleotide reference database to determine taxonomic identities. Statistical outliers were determined based on abundance within each sample and relative to other samples in the cohort.

Results. We identified a rich cross-domain pulmonary microbiome that contained bacteria, fungi, RNA viruses, and DNA viruses in each patient. Potentially pathogenic bacteria were ubiquitous among samples but could be distinguished as possible causes of disease by parsing for outlier organisms. Samples with bacterial outliers had significantly depressed alpha-diversity (median, 0.61; interquartile range [IQR], 0.33–0.72 vs median, 0.96; IQR, 0.94–0.96; P < .001). Potential pathogens were detected in half of samples previously negative by clinical diagnostics, demonstrating increased sensitivity for missed pulmonary pathogens (P < .001).

Conclusions. An optimized mNGS assay for pulmonary microbes demonstrates significant inoculation of the lower airways of immunocompromised children with diverse bacteria, fungi, and viruses. Potential pathogens can be identified based on absolute and relative abundance. Ongoing investigation is needed to determine the pathogenic significance of outlier microbes in the lungs of immunocompromised children with pulmonary disease.

Keywords. intensive care units, pediatric; immunocompromised host; metagenomics; respiratory tract infections; microbiota.

Last year in the United States, approximately 15,000 children were diagnosed with cancer, 2000 underwent solid organ transplantation, and 2500 underwent hematopoietic cell transplantation (HCT) for an increasingly broad set of life-threatening diseases [1–3]. Despite improved safety of antineoplastic and transplantation-based therapies, the risk of infectious complications such as pneumonia remains high [4, 5]. Due to the inhibitory effect of antimicrobial pretreatment on culture growth, impaired serologic immunity, and the limited preselected targets of multiplex assays, current microbiologic diagnostics frequently fail to identify pathogenic organisms [6]. The significant mortality associated with undiagnosed pulmonary infections is evident in postmortem case series of pediatric HCT patients, in whom previously undetected pulmonary pathogens have been identified in 30%–50% [7].

Unlike assays that target the 16S and/or 28S/ITS ribosomal RNA amplicons, unbiased metagenomic next-generation sequencing (mNGS) can detect bacteria, viruses, and fungi and has shown promising results for diagnosing neurologic and ocular infections [8–10]. However, the identification of filamentous molds such as Aspergillus spp. remains difficult due to thick extracellular matrices and the relatively small inoculum required to induce disease [11–14]. Unfortunately, off-the-shelf assays for respiratory biospecimens have proven inadequate to survey the variety of organisms present in thick and mucoid respiratory secretions. As such, unlike the better-characterized...
microbiomes of the human gastrointestinal tract and nasopharynx, data describing the composition of the pulmonary microbiome are sparse and insufficient to reliably discriminate between health and disease [15].

Therefore, we conducted a pilot study aimed to develop a highly sensitive mNGS assay capable of detecting myriad pulmonary bacterial, fungal, and viral pathogens and to test that assay on a retrospective cohort of immunocompromised children who underwent lower respiratory tract sampling as evaluation for suspected pulmonary infection. We hypothesized that an optimized mNGS assay could improve characterization of the pulmonary microbiome and identify potential pulmonary pathogens in this high-risk population.

METHODS

Development of Optimized mNGS Assay

We created mock-positive bronchoalveolar lavages (BALs) by spiking Aspergillus niger broth into aliquots of BAL containing known Haemophilus influenzae/Human Adenovirus B coinfection (Supplementary Material 1). An Aspergillus species was chosen as an optimization benchmark given its thick polysaccharide cell wall and extreme clinical importance of invasive mold in this patient population [16].

Sample Preparation

We tested nucleic acid extraction conditions by combining 200 μL of mock-positive BAL with either 600 μL DirectZol, 600 μL lysis buffer, or 200 μL DNA/RNA Shield (Zymo), followed by mechanical homogenization with either 0.1 mm or 0.5 mm glass bashing beads (Omnip) for 2, 5, or 8 cycles of 25 seconds, bashing at 30 Hz with 60 seconds rest on ice between each cycle (TissueLyser II, Qiagen). Samples homogenized in DNA/RNA shield also underwent enzymatic mycolysis with either 0.15 mg or 0.38 mg proteinase K at 23°C for 30 or 60 minutes (Zymo) or with 0.4 mg, 1.2 mg, 4 mg, or 8 mg Yatalase (Takara Bio Inc.) at 23°C or 37°C for 60 or 90 minutes. Subsequently, all samples underwent 10 minutes of centrifugation at 4°C, and the supernatant was used for parallel DNA/RNA extraction (Zymo ZR-Duet DNA/RNA MiniPrep Kit). Aspergillus niger nucleic acid yield was measured using an orthogonal digital droplet polymerase chain reaction (PCR) assay with pan-Aspergillus primers (Supplementary Material 2) [17]. RNA and DNA sequencing libraries were prepared in parallel (New England Biolabs NEBNext Ultra-II Library Prep) and underwent 125 nucleotide paired-end sequencing on an Illumina HiSeq 4000 instrument (Supplementary Material 3).

Bioinformatics Pipeline

Resultant.fastq files were processed using a previously described pipeline that consisted of several open-source components [8, 9]. Briefly, reads underwent iterative removal of host (Hg38/PanTro), low-quality, low-complexity (Lempel–Ziv–Welch [LZW] compression ratio >0.45), and redundant sequences using STAR, Bowtie2, PriceSeqFilter, and CD-HIT-DUP [18–21]. The remaining sequences were aligned to the National Center for Biotechnology Information (NCBI) nonredundant nucleotide database using GSNAPL for assignment of taxonomic IDs [22]. Microbes were described as potentially pathogenic or typically nonpathogenic based on a priori literature review (Supplementary Material 4).

Controls

To assess microbial contaminants in our reagents and laboratory environment, we sequenced 8 control samples containing spiked-in HeLa RNA (Supplementary Material 5).

Analysis

The prevalence of each microbe in each respiratory sample was described using 2 criteria: abundance relative to other microbes in the same sample, wherein we normalized sequencing reads per million total sequencing reads (rpm), and (2) abundance relative to the same microbe in other samples in the cohort, wherein we normalized sequencing reads as the number of standard deviations above or below the mean log_{10}-transformed rpm for the total cohort (Z-score).

Given the anticipated wide array of respiratory bacteria and the paucity of knowledge regarding the significance of low-level viruses and fungi, we aimed to maximize specificity for bacterial pathogens and to maximize sensitivity for viral and fungal pathogens [15, 23, 24]. Therefore, we defined microbial outliers as those with Z-score ≥2 and ≥10 rpm (bacteria) or ≥1 rpm (viruses/fungi). The Simpson diversity index was used to associate the loss of bacterial diversity with the presence of outlier microbes (Supplementary Material 6) [25].

Validation

Respiratory samples with outlier pathogens that were not identified on clinical testing were sent to reference laboratories for orthogonal confirmatory testing (Supplementary Material 7).

Patients

To test the optimized mNGS assay, we prospectively screened and approached immunocompromised patients age ≤25 years undergoing clinically indicated lower respiratory sampling between September 2014 and April 2016 at the University of California San Francisco Benioff Children’s Hospital, Indiana University Riley Hospital for Children, and the University of Minnesota Masonic Children’s Hospital. Patients were enrolled with consent. After respiratory samples were collected for clinical purposes, excess volume was separated, placed on dry ice within 10 minutes of the original procedure, and banked at −70°C until processing (Supplementary Material 8). This study was approved by each site’s institutional review board.

RESULTS

Development of Optimized mNGS Assay

Iterative optimizations demonstrated that mechanical homogenization of BAL using 0.5-mm glass bashing beads for 5 cycles...
in DNA/RNA shield without mycolytic enzymes yielded the highest quantity of *A. niger* nucleic acid (Supplementary Material 9, Supplementary Figure 1a–1d). This extraction protocol performed similarly when applied to clinical isolates of *A. fumigatus* (Supplementary Figure 1e). When sequencing RNA to a depth of 25 million reads per 200 µL BAL, this protocol improved the lower limit of detection (LLOD) of *A. niger* by approximately 100-fold (59.60 colony-forming units [CFU] preoptimization; 95% confidence interval [CI], 37.70–95.36 vs 0.42 CFU postoptimization; 95% CI, 0.12–1.40; paired T test \( P < .001 \); Supplementary Figure 2). However, sequencing simultaneously extracted DNA to the same depth yielded a 10-fold inferior *A. niger* LLOD (6.13 CFU; 95% CI, 4.16–9.04; paired T test \( P < .001 \); Figure 1). The optimization did not change the detection of *H. influenzae* or *Human Adenovirus B* (\( T \) test \( P = .343 \) and \( P = .420 \), respectively).

**Application of mNGS Assay**

Using the optimized protocol described above, we conducted mNGS on 41 clinical samples obtained from 34 patients (Table 1). Sequencing results are summarized below, with sequencing quality reported in Supplementary Tables 1 and 2, raw sequencing files available in NCBI dbGaP (https://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs001684.v1.p1), and detailed patient results in Appendix 1. Negative controls demonstrated minimal environmental contamination (<1 rpm of pathogenic bacteria and no pathogenic fungi or viruses Supplementary Table 3).

**Bacteria**

The vast majority of taxa derived from bacterial alignments were present at low abundance and in quantities similar across all samples in the cohort. Specifically, 81.7% of bacterial genera were identified at approximately 100-fold (59.60 colony-forming units [CFU] preoptimization; 95% confidence interval [CI], 37.70–95.36 vs 0.42 CFU postoptimization; 95% CI, 0.12–1.40; paired T test \( P < .001 \); Supplementary Figure 2). However, sequencing simultaneously extracted DNA to the same depth yielded a 10-fold inferior *A. niger* LLOD (6.13 CFU; 95% CI, 4.16–9.04; paired T test \( P < .001 \); Figure 1). The optimization did not change the detection of *H. influenzae* or *Human Adenovirus B* (\( T \) test \( P = .343 \) and \( P = .420 \), respectively).

**Fungi**

Relative to bacterial alignments, fungal alignments were significantly less prevalent in the cohort. Further, 92.1% of fungal genera were quantified below 1 rpm (Figure 2B). Evidence supporting these alignments is limited by the rarity of the reads themselves. Only 3.4% of fungal genera met outlier criteria; these included potentially pathogenic fungi identified in 7/41 patient samples (*Alternaria, Aspergillus, Candida*,...
**Table 1. Characteristics of Enrolled Patients**

| Demographics (n = 34 patients) | Descriptor |
|------------------------------|-----------|
| Age (median years, IQR)" | 11.2 (IQR, 4.3–16.2) |
| Sex                          |           |
| Female                       | 16 (47%)  |
| Male                         | 18 (53%)  |
| Race                         |           |
| White                        | 26 (76%)  |
| Black                        | 1 (3%)    |
| Asian                        | 1 (3%)    |
| Hawaiian/Pacific Islander    | 1 (3%)    |
| Other                        | 1 (3%)    |
| Unknown                      | 4 (12%)   |
| Ethnicity                    |           |
| Hispanic/Latino              | 9 (26%)   |
| Not Hispanic/Latino          | 24 (74%)  |
| Primary medical condition    |           |
| Allogeneic HCT"              | 20 (59%)  |
| Autologous HCT               | 3 (9%)    |
| Acute leukemia (without HCT) | 2 (6%)    |
| Primary immunodeficiency (without HCT) | 4 (12%) |
| Severe aplastic anemia (without HCT) | 2 (6%) |
| Solid tumor (without HCT)    | 1 (3%)    |
| Solid organ transplantation   | 2 (6%)    |
| Clinical course (n = 41 episodes) |    |
| Lower respiratory sample type|           |
| BAL                          | 33 (80%)  |
| Mini-BAL                     | 4 (10%)   |
| ETT aspirate                 | 4 (10%)   |
| Therapies (median number of therapies, IQR) | |
| Antibacterials               | 4 (1–5)   |
| Antivirals                   | 1 (0–2)   |
| Antifungals                  | 1 (0–2)   |
| Immunomodulation             | 2 (0–2)   |
| Patients with identified pathogen |        |
| Any pathogen                 | 13 (32%)  |
| Bacteria only                | 5 (12%)   |
| Fungi only                   | 1 (2%)    |
| Viruses only                 | 4 (10%)   |
| Multiple pathogens           | 3 (7%)    |
| Outcomes                     |           |
| Required pediatric intensive care unit admission | 21 (51%) |
| Required >24 hours mechanical ventilation | 17 (41%) |
| Hospital death"             | 10 (29%)  |

Abbreviations: BAL, bronchoalveolar lavage; ETT, endotracheal tube; HCT, hematopoietic cell transplantation; IQR, interquartile range.

"Age at first specimen collection.

"Indications for allogeneic HCT were acute leukemia (12/20), primary immunodeficiency (3/17), severe aplastic anemia (2/17), myeloproliferative/myelodysplastic disorder (2/17), and osteopetrosis (1/17).

"Hospital death n = 10/34 (29%).

Cladosporium, Cryptococcus, Fusarium, and Pneumocystis). While Aspergillus RNA levels were detectable in 14/41 patient samples, only 1 was positive for invasive pulmonary aspergillosis (IPA) by both culture and galactomannan assay (Figure 2B, labeled). Although the remaining 13 were all culture negative, 12/13 had received fungicidal or fungistatic anti-Aspergillus pharmacotherapy within 48 hours of sample collection, suggesting that empiric antifungal pharmacotherapy significantly confounds the association between Aspergillus RNA and growth in culture. Aspergillus RNA levels did not correlate with growth in culture (T test P = .148) but demonstrated weak association with BAL galactomannan (P < .001; Supplementary Figure 3).

**Virtuses**

In contrast with bacteria and fungi, a significantly larger portion of RNA alignments to viral genera were present at high abundance, and 30.5% met outlier criteria (Figure 2C and 2D). Communicable respiratory viruses with abundant alignments were identified in approximately one third of all patient samples (13/41) and included Adenoviruses A and C, Bocavirus, Coronavirus 229E and OC43, Influenzaviruses A and C, Parainfluenzavirus 3, and Rhinoviruses A and C. Although 4 Rhinoviruses met outlier criteria, an additional 3 Rhinoviruses were abundant but had Z-scores between +0.92 and +1.78. Additionally, 2 patients had viral coinfections (Parainfluenza-3 and Influenza-C; Adenovirus-C and Rhinovirus-A). Although there were no cases of clinically suspected herpesvirus pneumonitis, Epstein-Barr virus, Cytomegalovirus, HHV-6, and HHV-7 were identified in low abundance in 9/41 samples. Viral genera of uncertain or unlikely pathogenicity were also identified in 21/41 samples and included Papillomaviruses, WU and KI Polyomaviruses, and Torquetenuviruses (2, 5, and 18 samples, respectively).

**Comparison to Clinical Testing**

Clinical testing identified causative pathogens in 41.4% of samples (n = 17; Figure 4). Of these, 11 were concordantly identified as outliers by mNGS, and 3 of these 11 contained outlier quantities of RNA aligning to a second previously undetected potential copathogen (Bocavirus, Corynebacterium, and Influenza-C). An additional 3 were identified by mNGS but were not classified as outliers (2 cases of Aspergillus diagnosed by galactomannan and 1 case of Rhinovirus-A), and another 3 had a different outlier pathogen identified by mNGS (Coronavirus 229E twice and Coronavirus OC43 once). Clinical testing did not identify any pathogens in 58.5% of samples (n = 24). Here, mNGS was able to identify statistically outlying potential pathogens in 11/24 cases, including a variety of bacteria (ie, P. aeruginosa, E. cloacae, M. pneumoniae), fungi (ie, C. glabrata), and viruses (ie, Rhinovirus-A).

**Orthogonal Validation**

Statistical approaches to separate commensals from pathogens are inherently imperfect; therefore, we undertook orthogonal validation as an independent means to verify these results. Organisms detected by mNGS but not clinical testing were validated with commercially available Clinical Laboratory Improvement Amendments (CLIA)-approved assays performed...
on aliquots of the original unprocessed sample (Supplementary Material 7). All validation tests were concordant with mNGS with 1 exception: 28S/ITS amplicon DNA sequencing failed to identify *C. glabrata* in sample 37. For this sample, we confirmed the presence of this organism with 3 separate species-specific reverse-transcription primer sets followed by Sanger sequencing. These data demonstrate that mNGS has significantly greater sensitivity for detecting potential pulmonary pathogens than current clinical diagnostics (McNemar’s *P* < .001).

**DISCUSSION**

In this study, we developed and optimized an mNGS assay with adequate sensitivity to identify bacteria, fungi, and both RNA and DNA viruses within the lower respiratory tract of immunocompromised children. In doing so, we identified a rich molecular portrait of the pulmonary microbiome in this vulnerable population. Further, by comparing the quantity of microbial nucleic acid to that of other microbes within a sample and to other samples within the cohort, we were able to identify outlying potential pathogens in approximately half of clinically negative samples.

Due to inherent challenges in sampling the lower respiratory tract, the pulmonary microbiome was not one of the original sites studied in the 2008 Human Microbiome Project, and its exploration has lagged decades behind similar analyses of human intestinal, cutaneous, and nasopharyngeal microbiomes [26]. In addition, studies of the pulmonary microbiome in children necessarily lack healthy matched controls due to the inherent risks of anesthesia and bronchoscopy [27]. In this study, we found that many potentially pathogenic bacteria such as *Pseudomonas* and *Streptococcus* are ubiquitous, and hence their abundance needs to be contextualized by cohort-specific norms. For example, 100% of samples had detectable *Pseudomonas* RNA, but only sample 29 had *Pseudomonas* RNA detected more than 2 standard deviations above the cohort mean. Normalizing...
population-dependent measurements is common in pediatrics and appears well suited to describe aspects of the pulmonary microbiome [28–30].

To date, the majority of metagenomic sequencing assays have targeted amplicons within the 16S or 28S rRNA subunits, allowing detection of pulmonary bacteria or fungi, but not both, and not viruses [31]. Recently, unbiased mNGS assays have allowed detection of both bacterial and viral nucleic acid but have lacked ideal sensitivity for detecting filamentous mold [11, 12]. Although the European Aspergillus PCR Initiative has described ideal methodology for extracting fungal nucleic acid from blood, the optimal extraction conditions for respiratory specimens remain less well defined [32, 33]. This study confirms the need for aggressive mechanical homogenization in stabilizing media in order to detect molds such as Aspergillus while simultaneously preserving the detection of bacteria and viruses [34–36]. As the majority of commercial sequencing assays measure DNA, this study adds to the literature by demonstrating that RNA sequencing is >10 times more sensitive for the detection of such fastidious organisms, which we speculate may be due to high copy numbers of particular RNA templates present in active organisms [37].

Using optimized mechanical homogenization, Aspergillus RNA was detected in 34.1% of samples and no negative controls, suggesting that the lungs of immunocompromised children are frequently exposed to low levels of potentially viable Aspergillus organisms. These data are novel in the pediatric population and are congruous with surveillance data from neutropenic and nonneutropenic adults [38, 39]. However, as only 10% of samples originated from patients with suspected IPA, patient-specific factors such as antifungal pre-treatment, immune reconstitution, alloreactive inflammation, and impaired mucociliary clearance remain crucial in determining which child might develop IPA [16]. While this study was not powered to assess performance characteristics of this assay for IPA, pan-fungal and Aspergillus-specific PCR have demonstrated 76%–79% sensitivity and 93%–95% specificity for probable/proven IPA [14, 40–47]. Combining nucleic acid tests with galactomannan can hasten diagnosis and improve detection of both bacterial and viral nucleic acid but have lacked ideal sensitivity for detecting filamentous mold [11, 12]. Although the European Aspergillus PCR Initiative has described ideal methodology for extracting fungal nucleic acid from blood, the optimal extraction conditions for respiratory specimens remain less well defined [32, 33]. This study confirms the need for aggressive mechanical homogenization in stabilizing media in order to detect molds such as Aspergillus while simultaneously preserving the detection of bacteria and viruses [34–36]. As the majority of commercial sequencing assays measure DNA, this study adds to the literature by demonstrating that RNA sequencing is >10 times more sensitive for the detection of such fastidious organisms, which we speculate may be due to high copy numbers of particular RNA templates present in active organisms [37].

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Figure 3. Respiratory samples with outlier pathogens have depressed bacterial alpha-diversity. Diversity of the bacterial microbiome was significantly decreased in samples with potentially pathogenic bacteria present at ≥10 rpm of the pulmonary bacterial microbiome and Z-score ≥2 (median, 0.61; interquartile range [IQR], 0.33–0.72; n = 13 vs median, 0.96; IQR, 0.94–0.96; n = 28; P < .001). Simpson diversity index cutoffs of ≥0.8 or ≥0.9 showed 90.3% (95% confidence interval, 77.6–96.2) and 100% negative predictive value for the presence of an outlier bacterial pathogen, suggesting that the identification of bacterial dysbiosis may be a useful screen for recognizing possible bacterial infections.

Figure 4. Comparison of clinical laboratory results vs metagenomic next-generation sequencing (mNGS) results. Clinical laboratory results were determined by review of medical charts. n = 17 patients had samples with a pathogen detected clinically, as determined by interpretation of clinical microbiologic testing by the treating physician. Of these, n = 11 had concordant pathogens of outlier quantities on mNGS (Adenovirus/Rhinovirus, Aspergillus fumigatus, Enterobacter cloacae, Escherichia coli, Haemophilus influenzae, Haemophilus influenzae/Parainfluenza virus, Mycoplasma pneumoniae [n = 2], Pneumocystis jiroveci/Rhinovirus-A, Rhinovirus-C, and Staphylococcus aureus); n = 3 had concordant pathogens identified on mNGS but not in outlier quantities (Aspergillus [n = 2] and Rhinovirus-A); and n = 3 had an alternative pathogen identified on mNGS (Human coronavirus 229E [n = 2] and Human coronavirus OC43), n = 24 patients had samples without a pathogen detected clinically. Of these, n = 11 had a potential pathogen present in outlier quantities on mNGS (Candida glabrata, Cytomegalovirus, Cryptococcus [n = 2], Enterobacter cloaceae, Human herpesvirus-6, Mycoplasma pneumoniae, Rhinovirus-A, Pseudomonas aeruginosa/Influenza-A, Staphylococcus epidermidis, and Streptococcus pneumoniae) and n = 13 did not. Abbreviation: mNGS, metagenomic next-generation sequencing.
Our study has several strengths. First, we optimized the extraction of *Aspergillus* spp. RNA while preserving detection of bacterial and viral nucleic acid. Second, we proposed a logical analytical framework that ranks organism abundance both within a sample and relative to other samples. Third, outlier pathogens identified by mNGS that were not detected clinically were subsequently validated by orthogonal assays. Fourth, we provided, to our knowledge, the first evaluation of the pulmonary microbiome in immunocompromised children.

Our study has several limitations. First, while the Z-score was useful in deemphasizing commonly abundant organisms (ie, *S. pneumoniae*), it may have overvalued uncommon organisms with less abundant transcripts (ie, CMV); additional larger studies will naturally strengthen the utility of Z-score analyses. Second, because the relationship between microbe quantity and sequencing reads varies across organisms based on nucleic acid accessibility and the availability of annotated reference genomes, future clinical application of an mNGS assay will require validation on numerous clinically relevant species. Third, samples with abundant nucleic acid from human epithelial cells, leukocytes, viruses, and other sources may have reduced detection of sparse or fastidious microbes. Finally, as with all mNGS assays, the identification of microbial nucleic acid does not directly confirm the presence of viable, live organisms; does not directly implicate that microbe as a contributor to pulmonary disease; and does not exclude less abundant organisms as potential contributors to pulmonary disease. Future studies are needed to determine whether prospective use of mNGS in a clinically relevant time frame might affect patient management and improve outcomes. In order to optimize patient outcomes, we advocate for ongoing multidisciplinary collaboration among clinicians, laboratory scientists, and bioinformaticians.

**CONCLUSIONS**

In summary, we present an optimized mNGS assay that revealed a rich bacterial, fungal, and viral pulmonary microbiome in immunocompromised children and identified potential pathogens in half of clinically negative samples. As such, advanced organism detection offers the potential for early implementation of targeted therapy and the possibility for improved clinical outcomes in immunocompromised children. We invite the scientific and clinical community to participate in an ongoing multicenter collaborative clinical trial aimed at further refining this emerging technology [65].

**Supplementary Data**

Supplementary materials are available at *Clinical Infectious Diseases* online. Consisting of data provided by the authors to benefit the reader, the posted materials are not copyedited and are the sole responsibility of the authors, so questions or comments should be addressed to the corresponding author.

**Notes**

**Author contributions.** Study concept and design: M. S. Z., C. C. D., A. S., J. L. D. Acquisition of data: M. S. Z., C. C. D., M. Y. M., K. I., N. P. L., M. E. M., G. D. C., L. E. F., C. M. W., J. R. H., M. E. S., S. M., K. S., A. M., G. A. Y., A. S., J. L. D. Analysis and interpretation of data: M. S. Z., C. C. D., M. Y. M., E. D. C., C. L., K. K., E. D. C., S. M., K. S., A. M., G. A. Y., A. S., J. L. D. Drafting of the manuscript: M. S. Z., C. C. D., M. Y. M., J. L. D. Critical revision of the manuscript for important intellectual content: M. S. Z., C. C. D., M. Y. M., K. I., N. P. L., M. E. M., G. D. C., L. E. F., C. M. W., J. R. H., M. E. S., E. D. C., C. L., K. K., E. D. C., S. M., K. S., A. M., G. A. Y., A. S., J. L. D. Statistical analysis: M. S. Z., M. Y. M., K. K., J. L. D. Administrative, technical, or material support: M. S. Z., C. C. D., M. Y. M., K. I., N. P. L., M. E. M., G. D. C., L. E. F., C. M. W., J. R. H., M. E. S., E. D. C., C. L., K. K., E. D. C., S. M., K. S., A. M., G. A. Y., A. S., J. L. D.

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