Results. The LOD was determined to be 99 IU/mL. Precision was demonstrated with multiple sample replicates over three days of testing, with 100% amino acid concordance within the region of interest (ROI). The assay also accurately identified 100% of amino acids within the ROI of 30 unique CMV-positive de-identified clinical samples. While some polymorphisms were detected, no mutations conferring resistance were identified in the clinical samples tested, which is in agreement with the literature indicating that naturally occurring polymorphisms in the UL56 gene have not been shown to confer resistance to letermovir.

Conclusion. The CMV UL56 antiviral resistance assay was shown to be a rapid and sensitive means of detecting mutations conferring letermovir resistance. This expands current CMV antiviral resistance testing, which includes UL54 and UL97 sequencing, and provides physicians with the ability to monitor for the emergence of antiviral resistance mutations to all current FDA-approved anti-CMV drugs.

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2297. The Diagnostic Yield of 16/18S rRNA PCR of Sterile Site Samples in Pediatric Patients

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Background. 16S ribosomal RNA (rRNA) and 18S rRNA gene polymerase chain reaction (16/18S PCR) with sequencing can provide expeditious bacterial or fungal pathogen identification from sterile site samples (cost $474/PCR). Our objective was to assess the utilization and diagnostic yield of 16/18S PCR of sterile site samples in pediatric patients.

Methods. Patients' sterile site fluid or direct tissue specimens were collected and cultured at Lurie Children's Hospital of Chicago and sent to Northwestern Memorial Hospital for 16/18S PCR as clinically indicated. Clinical data were reviewed including PCRs, cultures, and medical conditions.

Results. 16/18S PCR testing increased over the study period. In total, 177 samples were sent for 16S and/or 18S PCR from 146 patients (January 2016–April 2018). Osteoarticular, CSF, pleural fluid and organ tissue (n = 28; lung=19, chest mass=2, liver=2, spleen=2, etc.) sites were most frequent. The yield of 16/18S PCR by source is listed in Table 1. Twenty-eight of 156 samples for 16S PCR were positive (17.9%); 21 with a single organism ID, one with two organisms, and 6 indeterminate. (Table 2). Of negative 16S PCR samples, one grew *Mycobacterium avium complex* in culture. 18S PCR was performed on 108 unique samples; 7 were positive (6.5%, Table 3). For 4 positive 18S PCRs, a fungus also grew in culture with 3 concordant results and one discordant. Two negative 18S PCR samples grew molds (*Phellinus spp.; Blastomyces dermatitidis*). All patients (100%) with positive 18S PCR were immunocompromised compared with 21% (6/28) with positive 16S PCR. Both 16S and 18S PCRs were sent on 87 samples of which 16S PCR was positive in 5, 18S PCR was positive in 3, and none had both 16/18S PCRs positive.

Conclusion. 16/18S PCR can provide important infectious pathogen diagnostics. 16S PCR should be sent only if bacterial culture is negative with higher yield sites being brain, abscess, pleural effusion, bone/joint and CSF. 16S PCR appears useful if an anaerobic pathogen is likely but conditions are not optimal for recovery. 18S PCR is highest yield in patients at risk of fungal disease. 16 and 18S PCRs were often sent together, likely reflexively. Selective or sequential testing may be advisable for most cases, guided by the clinical index of suspicion. Best practices to optimize resource utilization and clinical impact are evolving.

Table 1

Sample source	Total (n)	16S PCR sent (n)	16S PCR + (n)	18S PCR sent (n)	18S PCR + (n)
Osteoarticular	45	41	6 (15%)	21	1 (0.5%)
Cerebrospinal fluid	34	32	5 (16%)	17	1 (0.6%)
Pleural fluid	28	27	9 (33%)	14	1 (0.7%)
Organ/tissue	28	26	2 (8%)	24	1 (0.4%)
Abscess NOS	7	5	2 (40%)	2	1 (50%)
Lymph node	6	4	0	6	0
Bone marrow	6	6	0	6	0
Peritoneal/biliary	6	5	0	4	0
Brain	5	5	3 (60%)	2	0
Skin	4	0	n/a	4	2 (50%)
Respiratory/bronchial	3	2	1 (50%)	3	0
Sinus	3	1	0	3	0
Pericardial fluid	2	2	0	2	0

Table 2

Sample source	+ 16S PCR organism	Gram stain/culture
Brain abscess	*S intermedius*	-
Brain abscess	*S intermedius*	-
Brain abscess	*S pneumoniae*	-
CSF	*S pneumoniae*	-
CSF	*U parvum*	-
Pleural fluid	*F nucleatum*	-
Pleural fluid	*F nucleatum; S intermedius*	-
Pleural fluid	*Porphyromonas spp.*	-
Pleural fluid	*S pneumoniae*	-
Pleural fluid	*S aureus*	-
Pleural fluid	*S pyogenes*	GPC/-
Bronchial wash	*Granulicatella spp.*	-
Renal mass	*Prevotella spp.*	-
Spleen	*S anginosis*	GPC/-
Ischium bone	*Acinetobacter spp.*	GNR/-
Sternoclavicular bone	*S pneumoniae*	-
Femur bone	*K kingae*	-
Lumbar bone abscess	*B henselae*	-
Left leg abscess	*S mitis*	-
Wrist abscess	*S agalactiae*	-
Vertebral abscess	*S aureus*	*S aureus*
Right leg abscess	*E coli*	*E coli*
Pleural fluid	+ indeterminate*	*E coli + S anginosis*
Pleural fluid	+ indeterminate	-
Pleural fluid	+ indeterminate	-
CSF	+ indeterminate	-
CSF	+ indeterminate	-
CSF	+ indeterminate	-

*positive PCR without bacterial identification; multiple amplicons present

Table 3

Sample source	+ 18S PCR organism	Fungal culture
Leg	*Candida lusitaniae*	*Candida lucitaniae*
Lung	*Cunninghamella spp.*	*Aspergillus fumigatus*
Scalp abscess	*Lichtheimia ramosa*	-
Pleural fluid	*Rhizomucor spp.*	*Rhizomucor spp.*
Skin	*Rhizopus oryzae*	*Rhizopus oryzae*
Skin	*Rhizopus spp.*	-
CSF	*Rhodotorula spp.*	-

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2298. Identifying and Addressing Implementation Barriers to Whole-Genome Sequencing (WGS) in State Public Health Laboratories

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Background. The past decade has witnessed revolutionary advances in DNA sequencing, bioinformatics, and related technologies. The Advanced Molecular Detection (AMD) program at the Centers for Disease Control and Prevention (CDC) is a catalyst for bringing advanced DNA sequencing and related technologies to the forefront for combatting a wide range of infectious disease threats by the US public health system, resulting in quicker detection of outbreaks and more effective public health responses. Bacterial whole-genome sequencing (WGS) has many applications in public health and is now being implemented in several areas both at the CDC and in state public health laboratories (SPHLs). While SPHLs have overcome a variety barriers to the implementation of WGS technology, only a small percentage of SPHLs using bacterial WGS (3 out have 51) have validated workflows that comply with regulations set forth by the Clinical Laboratory Improvement Amendments of 1988 (CLIA). If a piece of data has the potential to make it back to a patient's record, then the laboratory