Conclusion. Our study showed that restricting the ordering of GIP to the first 72 hours of hospitalization and directing providers to standalone C. difficile NAAT testing resulted in a reduction of GIPs performed. There were marginal changes in the test positivity rate of GIP. A limitation of our study is that the timing of post-intervention coincided with the COVID-19 pandemic, which had unpredictable effects on hospital practice and patient admissions. Ideally, future quality improvement projects should increase the test positivity of pathogens other than C. difficile while lowering the GIP use in diagnosing C. difficile colitis.

Disclosures. John C. O’Horo, Sr., MD, MPH, Bates College and Elsevier Inc (Consultant)

Abundance of bacteria and fungi detected on plasma mcf-DNA-seq test. Data classified by organism and level of immunosuppression. Abundance is expressed in microbial cell free DNA per microliter. Warmer colors towards red represent higher abundance.

Figure 1. Bacteria abundance from date of symptom onset.

There was no clear trend in bacterial abundance over time from symptom onset. Most bacteria detected were not considered clinically pathogenic.

Figure 2. Fungi abundance from date of symptom onset

There was an increasing trend in the abundance of fungi detected from time of symptom onset. Seven of the 8 fungi detected were considered clinically pathogenic.

Conclusion. Plasma-mcf-DNA assisted in making critical management changes including initiation of treatment for identified organisms and de-escalation of antimicrobials. Plasma-mcf-DNA is a promising approach for a non-invasive rapid diagnosis.

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670. Precision Metagenomic (PM) Sequencing Outperforms Conventional Urine Culture in Detecting Clinically Relevant Microorganisms

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Session: P-30. Diagnostics: Typing/sequencing

Background. Morbidity from urinary tract infection (UTI) is high. Urine culture is the reference method for UTI diagnosis. Its diagnostic yield is limited as prior antibiotic use prevents growth of established uropathogens, many emerging uropathogens do not grow under routine culture conditions, and results interpretation can be subjective. Faster, more comprehensive diagnostics could help manage recurrent and/or drug-resistant infections. We evaluated the diagnostic yield of a precision metagenomic (PM) workflow for pathogen detection & antimicrobial resistance (AMR) characterization directly from urine.

Methods. Residual urine samples from symptomatic adults evaluated by culture & susceptibility were identified by a combination of consecutive & stratified random sampling (n=480; 79% culture positive). DNA was extracted with modifications to the Quick-DNA Urine Kit (Zymo). Libraries were generated with Illumina DNA Prep kits using a library prep kit designed for Illumina technology. Libraries were sequenced on the Illumina MiSeq platform. A bioinformatics pipeline was used to process the sequencing reads. Bioinformatics was performed using custom scripting (Bash and Python) and open source software (FastQC, Trimmomatic, STAR, HISAT2, BWA, Bowtie2, STAMP, QIIME, R). Pathogen detection was performed using the PathGroup Lab System, a PM sequencing and bioinformatics platform designed for clinical use. AMR was predicted using the Antibiogram module (QIIME2).

Results. Thirty-six adult patients included: 92% immunosuppressed (11 with T cell deficits; 8 with B-cell deficits; 14 with both (hematologic stem cell transplant, aplastic anemia)). Most tests evaluated fever & susceptibility were identified by a combination of consecutive & stratified random sampling (n=480; 79% culture positive). DNA was extracted with modifications to the Quick-DNA Urine Kit (Zymo). Libraries were generated with Illumina DNA Prep kits using a library prep kit designed for Illumina technology. Libraries were sequenced on the Illumina MiSeq platform. A bioinformatics pipeline was used to process the sequencing reads. Bioinformatics was performed using custom scripting (Bash and Python) and open source software (FastQC, Trimmomatic, STAR, HISAT2, BWA, Bowtie2, STAMP, QIIME, R). Pathogen detection was performed using the PathGroup Lab System, a PM sequencing and bioinformatics platform designed for clinical use. AMR was predicted using the Antibiogram module (QIIME2).