Table 1. Pre- and Post-Intervention Test Positivity Rate of Specific Pathogens in GIP

Pathogen	Pre-intervention n (%)	Post-intervention n (%)	% Change	*p*-value
Bacteria				
Campylobacter (jejuni, coli, and upsaliensis)	13 (0.83)	13 (1.21)	0.38	0.32
Clostridioides difficile (toxin A/B)	238 (15.18)	164 (15.28)	0.11	0.94
Enteroaggregative *Escherichia coli*	16 (1.02)	5 (0.47)	-0.55	0.12
Enteropathogenic *E. coli*	59 (3.76)	32 (2.98)	-0.78	0.28
Enterotoxigenic *E. coli*	8 (0.51)	3 (0.28)	-0.23	0.37
Shiga-like toxin-producing *E. coli*	10 (0.64)	6 (0.56)	-0.08	0.8
Shigella/Enteroinvasive *E. coli*	6 (0.38)	-	-0.38	-
Plesiomonas shigelloides	-	2 (0.19)	0.12	-
Salmonella	10 (0.64)	5 (0.47)	-0.17	0.56
Yersinia enterocolitica	4 (0.26)	5 (0.47)	0.21	0.36
Vibrio species	1 (0.06)	-	-0.06	-
Viruses				
Adenovirus F40/41	2 (0.13)	1 (0.09)	-0.03	0.8
Astrovirus	4 (0.26)	3 (0.28)	0.02	0.9
Norovirus GI/GII	74 (4.72)	70 (6.52)	1.8	**0.04**
Rotavirus A	21 (1.34)	-	-1.34	-
Sapovirus (I, II, IV, and V)	10 (0.64)	9 (0.84)	0.2	0.55
Parasites				
Cryptosporidium	6 (0.38)	7 (0.65)	0.27	0.33
Cyclospora cayetanensis	4 (0.26)	2 (0.19)	-0.07	0.72
Entamoeba histolytica	-	-		
Giardia lamblia	4 (0.26)	3 (0.28)	0.02	0.9

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)

669. Metagenomic Plasma Microbial Cell Free DNA-Sequencing Assists in Diagnosis of Infections and Critical Antimicrobial Changes in Immunocompromised Hosts

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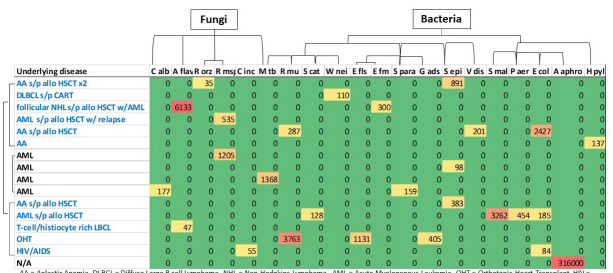
Session: P-30. Diagnostics: Typing/sequencing

Background. Metagenomic next-generation sequencing of plasma cell-free DNA (Karius®) (plasma mcf-DNA-seq) is a noninvasive approach that may have a unique role for the diagnosis of infectious complications in immunocompromised patients. The rapid turnaround time and noninvasive nature makes this a promising supplement to standard of care.

Methods. The aim of this study is to investigate the utility of plasma-mcf-DNA-seq in clinical practice; how it changes management, correlations between organism abundance over time from symptom onset and the value of negative tests. Retrospective review of plasma-mcf-DNA-seq performed, January 2020 -March 2021. Organism abundance was displayed as a heat map and graphed over time from initiation of antimicrobials. Management changes and concordance with standard of care results were compared for positive and negative tests. This study was approved by the Virginia Commonwealth University Institutional Review Board.

Results. Thirty-six adult patients included: 92% immunosuppressed (11 with T cell deficits (solid organ transplant, malignancy, human immunodeficiency virus), 8 with B-cell deficits (hematologic malignancy, diabetes mellitus), and 14 with both (hematopoietic stem cell transplant, aplastic anemia)). Most tests evaluated fever (67%) and/or pneumonia (72%). Patients received a median 7 days of antimicrobials prior to testing. Twenty-one (58%) tests detected 1-5 organisms (14/21 bacteria, 8/21 fungi, and 6/21 viruses). A positive test prompted therapy changes in 14/21 patients. Of the bacterial species identified, 8/20 were considered clinically pathogenic, 3 prompted targeted treatment; 7/8 fungi identified were clinically pathogenic and resulted in antifungal therapy changes to target the species identified. Antimicrobials were de-escalated in 3 patients with negative tests. There was an exponential relationship between the abundance of pathogenic fungi over time from symptom onset, but no such relationship was seen with bacteria.

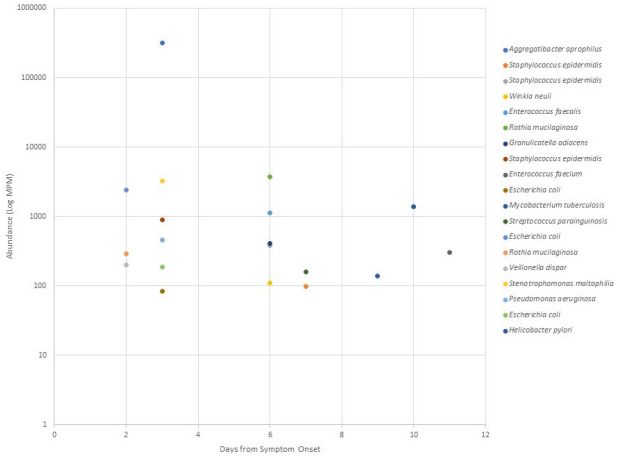
Abundance of fungi and bacteria detected on plasma mcf-DNA-seq test



AA = Aplastic Anemia, DLBCL = Diffuse Large B cell lymphoma, NHL = Non-Hodgkins Lymphoma, AML = Acute Myelogenous Leukemia, OHT = Orthotopic Heart Transplant, HIV = Human Immunodeficiency Virus, AIDS = Acquired Immunodeficiency Syndrome, LBCL = Large B Cell Lymphoma, C alb = *Candida albicans*, A flav = *Aspergillus flavus*, R orz = *Rhizopus oryzae*, R msp = *Rhizopus microspores*, C inc = *Candidabolus incongruous*, M tb = *Mycobacterium tuberculosis*, R mu = *Rothia mucilaginosa*, S cat = *Streptomyces cattleya*, W nei = *Winkia neuii*, E fs= *Enterococcus faecalis*, E fm = *Enterococcus faecium*, S par = *Streptococcus parasanguinosis*, G ads = *Granulicatella adiacens*, S epi = *Staphylococcus epidermidis*, V dis = *Veillonella dispar*, S mal = *Stenotrophomonas maltophilia*, P aer = *Pseudomonas aeruginosa*, E col = *Escherichia coli*, A aphro = *Aggregatibacter aprophilus*, H pyl = *Helicobacter pylori*

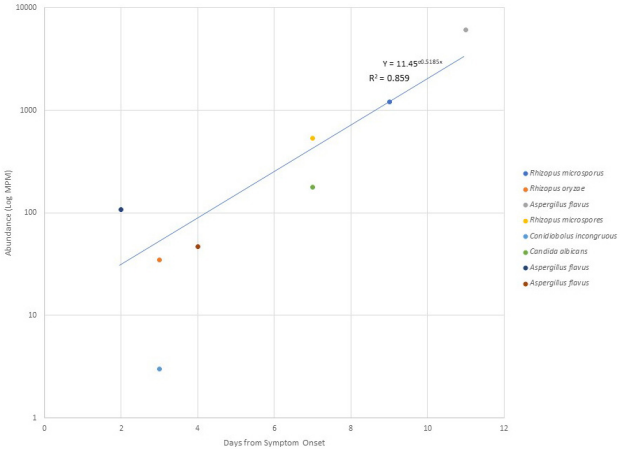
Abundance of bacteria and fungi detected on plasma mcf-DNA-seq test. Data classified by organism and level of immunosuppression. Abundance is expressed in microbial cell free DNA per microliter. Warmer colors towards red represent higher abundance.

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.

Disclosures. **All Authors**: No reported disclosures

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