Conclusion. Our efforts to perform 'Reference-assisted assembly' followed by K-mer based taxonomic annotation of cfDNA data, led to development of a novel and accurate pathogen detection protocol.

Disclosures. Rohita Sinha, PhD, Viracor-Eurofins (Employee) Steve Kleiboeker, DVM, PhD, Viracor-Eurofins (Employee) Michelle Altrich, PhD, Viracor-Eurofins (Employee) Ellis Bixler, MS, Viracor-Eurofins (Employee)

1211. Response to Fecal Microbiota Transplant (FMT) in Refractory Clostridioides difficile Infection (CDI) is Modest Compared to Recurrent CDI in Hospitalized Patients

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Session: P-54. Microbiome in Health and Disease

Background. There are limited options for *Clostridioides difficile* infection (CDI) refractory to conventional antibiotic therapy (metronidazole, vancomycin, or fidaxomicin). Fecal microbiota transplant (FMT) is considered a safe and effective treatment for recurrent CDI but has not been widely utilized for refractory CDI due to concerns about safety. Even when included in studies, refractory CDI has not been analyzed separately from recurrent CDI. We reviewed cases of FMT performed in the inpatient setting for CDI to evaluate its safety and efficacy for refractory CDI.

Methods. Patients who received FMT inpatient at University of Virginia Health System for recurrent or refractory CDI after Infectious Diseases and Gastroenterology consultation signed informed consent acknowledging that FMT was considered investigational use in CDI not responding to standard of care as per 2014 FDA guidance. Charts were reviewed as part of quality improvement efforts to evaluate safety and efficacy of FMT in inpatient setting.

Results. Starting in July 2014, 13 patients received FMT for CDI as inpatients. Six received FMT for recurrent CDI, with four having complete resolution, one had recurrent CDI, and one had persistent *C. difficile*-negative diarrhea, for cure rate of 83%, comparable to published studies. Seven patients received FMT for refractory CDI, with three resulting in complete resolution. One responded to FMT but refused further care, one died from multiorgan failure after initial response to FMT that was possibly related to CDI, strongyloides, and/or CMV. Two patients had ongoing diarrhea suggestive of post-infectious irritable bowel syndrome, one was *C. difficile*-negative and one was not tested. The cure rate was 57%, lower than that of the recurrent CDI, but without any clear evidence of microbiologic failure.

Outcome of patients undergoing FMT for CDI in the inpatient setting at University of Virginia Health System

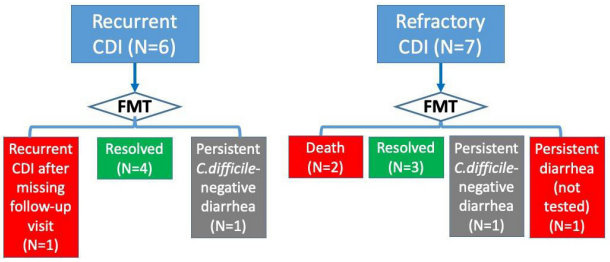

Figure 1. Outcome of patients undergoing FMT for CDI in the inpatient setting at University of Virginia Health System

Conclusion. Cure rate for FMT for refractory CDI was lower than recurrent CDI, but review of the cases of treatment failures did not reveal any microbiologic evidence of failure. FMT should be considered an alternative option when treating refractory CDI.

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

1212. Temporal Dynamics of the Plasma Microbiome in Recipients at Early Post-liver Transplantation

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Session: P-54. Microbiome in Health and Disease

Background. Immunosuppression during liver transplantation (LT) enables the prevention and treatment of organ rejection, but poses a risk for severe infectious diseases. Antimicrobials are often required for patients after LT. Recently, the genomes of multiple microorganisms have been detected in blood, which is essentially sterile. Immune modulation and antimicrobials affect the blood microbiome. Thus, determining the impact of immunosuppression and antimicrobials on the microbiome may be important to understand immunocompetence, predict clinical adverse events after LT such as acute cellular rejection (ACR), and treat infectious diseases.

Methods. Fifty-one patients who received LT at Nagoya University Hospital from 2016 to 2018 were enrolled. Plasma samples were retrospectively collected within a week after LT, 4±1 weeks after LT, 8±1 weeks after LT, and within 2 days after a positive blood culture. A total of 111 plasma samples were analyzed using shotgun next-generation sequencing (NGS). Sequence data were imported into the custom-made analysis pipeline PATHDET.

Results. The relative abundance of *Anelloviridae*, *Nocardiaceae*, *Microbacteriaceae*, and *Enterobacteriaceae* significantly changed during the postoperative period (figure 1). Microbiome diversity was higher within a week after LT than at 8 weeks after LT. Antimicrobials were significantly associated with the microbiome of LT recipients. In addition, the proportion of *Enterobacteriaceae* was significantly decreased (figure 2) and the plasma microbiome diversity was significantly higher in patients with ACR than in non-ACR patients. Finally, sequencing reads of bacteria isolated from blood cultures were predominantly identified by NGS in 8 of 16 samples (figure 3), and human herpesvirus 6 was detected as a causative pathogen in one recipient with severe infectious diseases.

Change in the relative abundance of each microorganism at the family level of taxonomic hierarchy in plasma samples after liver transplantation

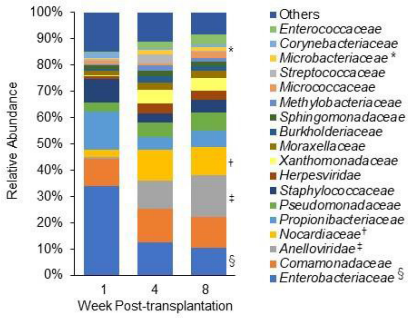

Figure 1. Change in the relative abundance of each microorganism at the family level of taxonomic hierarchy in plasma samples after liver transplantation
Microbacteriaceae (*), *Nocardiaceae* (†), and *Anelloviridae* (‡) abundance increased in samples collected at week 4 or 8 post-transplantation in comparison with samples collected at week 1 post-transplantation (*Anelloviridae*: week 4 vs. week 1, $p = 0.62$, week 8 vs. week 1, $p < 0.001$; *Nocardiaceae*: week 4 vs. week 1, $p = 0.003$, week 8 vs. week 1, $p = 0.36$; *Microbacteriaceae*: week 4 vs. week 1, $p < 0.001$, week 8 vs. week 1, $p = 0.002$). *Enterobacteriaceae* (§) abundance decreased in samples collected at week 4 or 8 post-transplantation in comparison with samples collected at week 1 post-transplantation (week 4 vs. week 1, $p < 0.001$, week 8 vs. week 1, $p < 0.001$).

Comparison of the plasma microbiome at the family level in patients with and without acute cellular rejection

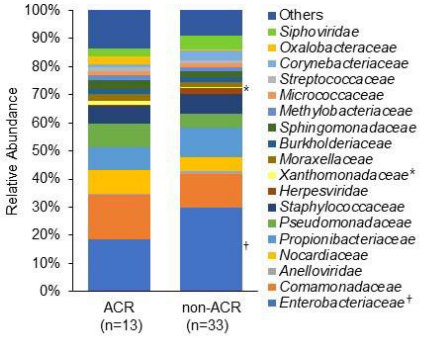

Figure 2. Comparison of the plasma microbiome at the family level in patients with and without acute cellular rejection (ACR)
Xanthomonadaceae (*) abundance was significantly increased in the ACR group in comparison with the non-ACR group ($p = 0.047$). In contrast, *Enterobacteriaceae* (†) abundance was significantly decreased in the ACR group in comparison with the non-ACR group ($p = 0.045$).

Relative abundance of microorganisms at the species level in plasma from patients with positive blood cultures

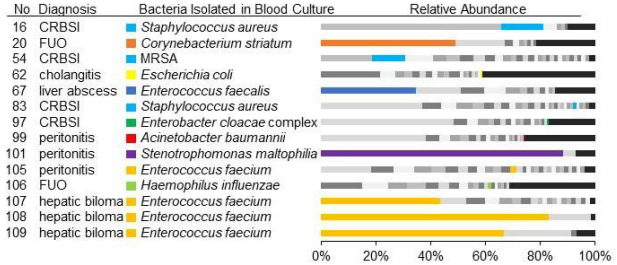

Figure 3. Relative abundance of microorganisms at the species level in plasma from patients with positive blood cultures
Representative results of 14 patients are shown. Colored bars indicate that the same bacteria were isolated from next-generation sequencing and blood culture samples. Black bars indicate microorganisms with < 1% relative abundance. CRBSI, catheter-related bloodstream infection; FUO, fever of undetermined origin; MRSA, methicillin-resistant *Staphylococcus aureus*.

Conclusion. The metagenomic NGS technique has great potential in revealing the plasma microbiome and is useful as a comprehensive diagnostic procedure in clinical settings. Temporal dynamics of specific microorganisms may be used as indirect markers for the determination of immunocompetence and ACR in LT recipients.

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

1213. A TRAIL/IP-10/CRP Signature Distinguishes between Viral and Bacterial Infection in Chronic Obstructive Pulmonary Disease Patients

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Session: P-55. New Approaches to Diagnostics

Background. Challenges in determining the etiology of acute exacerbations of chronic obstructive pulmonary disease (COPD) lead to significant overuse of antibiotics. A new host-response assay that integrates the levels of three proteins (TRAIL, IP-10, and CRP) was shown to exhibit high performance in distinguishing between bacterial and viral disease in two double-blind pediatric validation studies. Here we sought to evaluate its ability to differentiate bacterial from viral infection in adult COPD patients with suspicion of lower respiratory tract infection (LRTI).

Methods. The study population included 492 febrile adult patients prospectively recruited in "Observer", an EU Horizon 2020 funded study (grant #684589). Patient etiology was determined by majority expert panel based on clinical, laboratory, multiplex PCR, radiological and follow-up data. We compared the expert panel diagnosis with the assay that gives three possible outcomes: viral, bacterial (including viral with bacterial coinfection) or equivocal.

Results. 45 out 492 adult patients prospectively recruited with suspicion of LRTI had a medical history of COPD. Of these, 20 cases were assigned as suspected viral infections and 19 as suspected bacterial infections (Figure 1). Antibiotics were prescribed to 19/19 bacterial infections and 16/20 viral infections. The assay correctly classified 19/19 bacterial infections and 12/20 viral infections, with 2 viral cases classified by the assay as bacterial and 6 receiving an equivocal outcome. These data support the assay's potential to reduce antibiotic overuse from 16/20=80% to 8/20=40% (P=0.01).

FIgure 1: Flow through of COPD patients in prospective performance validation study "Observer"

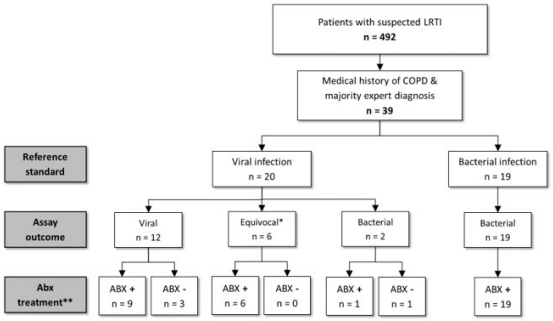

Figure 1: Flow through of COPD patients in prospective diagnostic performance validation study "Observer"
*Equivocal= an equivocal outcome dose not provide diagnostic information. **Abx treatment as reported on medical record.

Conclusion. A new TRAIL/IP-10/CRP signature has potential to significantly reduce antibiotic overuse for patients with suspected LRTI and a history of COPD without missing bacterial infection.

Disclosures. Meital Paz, MD, MeMed Ltd. (Employee) Noa Avni, PhD, MeMed (Employee) Michal Stein, MeMed Ltd. (Employee) Liran Shani, MD, MeMed Ltd. (Employee) Tanya Gottlieb, PhD, MeMed (Employee) Kfir Oved, MD, PhD, MeMed (Employee) Eran Eden, PhD, MeMed (Employee)

1214. Clinical characteristics of patients with adrenal insufficiency presenting fever

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Session: P-55. New Approaches to Diagnostics

Background. The aim of the present study is to analyze the clinical characteristics of adrenal insufficiency patients presenting fever.

Methods. A single-center retrospective study was conducted in an 846-bed tertiary hospital in South Korea. All hospitalized adult patients (age ≥19 years) who diagnosed with adrenal insufficiency between March 1, 2018 and June 30, 2019 were recruited. Only the first event per patient was included and patients were excluded if they: (1) had proven structural problems with adrenal or pituitary gland, (2) had a history of chemotherapy within 6 months prior to the diagnosis of adrenal insufficiency, and (3) had other medical conditions which may cause fever.

Results. A total of 150 cases were included: 45 (30.0%) had fever and 105 (70.0%) did not have fever at the time of diagnosis of adrenal insufficiency. The proportion of female patients was lower in patients with fever compared to those without fever (44.4% vs. 67.6%, P =0.008). In addition, patients with fever were diagnosed at 13.98 ± 14.51 days, which was later than 6.47 ± 6.91 of patients without fever (P < 0.001). Higher proportion of patients with fever had history of surgical procedure within 6 months (33.3% vs. 11.4%, P =0.001) and antibiotic usage at the time of diagnosis (80.0% vs. 17.1%, P < 0.001) compared to those without fever. Among clinical manifestations, general weakness (91.1% vs. 66.7%, P =0.002), headache (15.6% vs. 4.8%, P =0.044), and cough (17.8% vs. 4.8%, P = 0.022) were more frequently observed in patients with fever. There were no significant differences in clinical outcomes between two groups. According to the multivariate analysis, female sex (OR =0.32, 95% CI: 0.12–0.86, P = 0.024) lowered the risk for adrenal insufficiency with fever. In comparison, history of surgical procedure within 6 months (OR = 4.35, 95% CI: 1.23–15.39, P =0.023), general weakness (OR = 7.21, 95% CI: 1.71–30.37, P =0.007), and