with positive ESIs identified by BioFire FilmArray Blood Culture Identification (BCID) Panel® or Accelerate PhenoTest Blood Culture kit® 2 between January 2018 – July 2019 were evaluated and pertinent data was collected.

Results. Rapid diagnostic technologies identified 108 bloodstream infections due to gram positive, 36 due to gram negative, and 6 due to Candida organisms. Mean time to optimal antimicrobial therapy was significantly lower when pharmacist recommendations was accepted versus when primary care team consulted ID for recommendation or did not accept pharmacist recommendation. Mean time to optimal therapy was 14.7, 34.3, and 271.3 hours (p < 0.0001) respectively. Median total cost of visit per patient, calculated using the average wholesale price of antibiotics multiplied by the number of doses received, was significantly lower when pharmacist recommendations were accepted ($864.40, $147.95, and $239.41, respectively).

Baseline characteristics

| Baseline patient characteristics (%) | All (N=9) | ID consulted (N=6) | ID not consulted (N=3) |
|-------------------------------------|----------|------------------|----------------------|
| Gender (female)                     | 62%      | 62%              | 67%                  |
| Age (years)                         | 56 (48, 63) | 54 (44, 65)      | 67 (53, 72)          |
| Chronic kidney disease              | 67%      | 67%              | 100%                 |
| Organ-specific infection            | 67%      | 67%              | 100%                 |
| Indole negative                     | 67%      | 67%              | 100%                 |
| Urea negative                       | 67%      | 67%              | 100%                 |
| Arginine positive                   | 67%      | 67%              | 100%                 |
| Esculin positive                    | 67%      | 67%              | 100%                 |

Microbiological isolates

| Primary isolates (%)                  | All (N=9) | ID consulted (N=6) | ID not consulted (N=3) |
|---------------------------------------|----------|------------------|----------------------|
| Time to optimal antimicrobial therapy (hr) | 20.7 (4.2, 41.4) | 20.7 (4.2, 41.4) | 20.7 (4.2, 41.4) |

Primary outcomes: Time to Optimal Therapy

Conclusion. The establishment of a pharmacist run antimicrobial stewardship program in conjunction with rapid diagnostic tools for identifying bacteria led to a decrease in time to optimal antimicrobial therapy and cost savings. Introduction of similar services at community hospitals with limited ASP staffing is justified. Larger studies to further investigate whether ASP partnered with rapid diagnostics have an impact on patient-related outcomes such as mortality and length of stay is warranted.

Secondary outcomes

Missed cost savings

| Variable                           | Median | Mean | IQR | Cost savings |
|------------------------------------|--------|------|-----|--------------|
| Actual cost of visit (USD)         | 427.28 |
| Hypothetical cost of visit saved   | 268.34 |
| Potential cost savings (USD)       | 213.32 |

Disclosures. All Authors: No reported disclosures

644. Phenotypic and Genomic Analysis of Novel, Fastidious, Gram-negative Bacilli Isolated from Clinical Wound Specimens

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Session: P-29. Diagnostics: Bacteriology/mycobacteriology

Background. Animal bites are considered the thirteenth leading cause of nonfatal ED visits. Epidemiology studies have shown a rise in dog bites during the COVID-19 pandemic in the US. In Oct. 2020, we received a facultatively anaerobic, non-hemolytic Esp-like (OL1) isolate from a dog bite wound for identification. 165 rRNA gene sequencing showed OL1 was 95.9% identical to Ottowia pentelensis in the family Comamonadaceae. Our historical sequence database revealed 8 additional isolates (OL2-OL9) from hand wounds/abscesses (including 3 dog bites) since 2012 that had ≥ 99.8% identity with OL1. Most other Ottowia sp. have been isolated from industrial and food sources, with no reports from patient samples. As these clinical isolates likely represent a novel Ottowia species, we aimed to characterize them using both phenotypic and genomic approaches.

Methods. The OL isolates were tested in API 20 NE panels (8 conventional and 12 assimilation tests) for 4 d. Paired-end genomic DNA libraries (Nextera DNA Flex Library Prep, Illumina) were sequenced as 150 nt reads by Illumina NovaSeq. De novo assembly, annotation, funGial prediction, and phylogenetic analyses were performed with Geneious, PATRIC, and web-prediction databases. Strain comparison was done with StrainTypeMer.

Results. All 9 OL isolates were negative for indole, urea, arginine, esculin, PNPG, glucose fermentation and carbohydrate assimilation tests. Potassium glutonate assimilation and gelatin hydrolysis were positive for 5 and 4 isolates, respectively. StrainTypeMer showed the isolates from different patients were not closely related, but 2 from the same patient were indistinguishable. The estimated genome size of scale was ~3.1 Mbp, with 66.1% G/C, and ~3523 coding genes. Potential virulence factors (BrkB and MviM), multidrug efflux systems (MdtABC-TolC and Bcr/Cila), and 1-2 intact prophages were identified. Genomic phylogenetic analysis with RAxML showed the OL isolates clustered separately from all known Ottowia spp.

Conclusion. These OL isolates are fastidious, Gram-negative bacilli from clinical wound specimens, and are associated with dog bites. Genomic and 16S rRNA gene sequence analysis suggests these isolates constitute a novel species within the family Comamonadaceae.

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645. Rapid Diagnosis of Disseminated Mycobacterium kansasii infection in Renal Transplant Recipients Using Plasma Microbial Cell Free DNA Next Generation Sequencing

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Session: P-29. Diagnostics: Bacteriology/mycobacteriology

Background. Disseminated Mycobacterium kansasii infection is rare in kidney transplant recipients. The diagnosis may not be suspected readily due to non-specific clinical presentation. The diagnosis and treatment can be further delayed due to poor sensitivity of culture (especially of extra-pulmonary sites) and slow growth in culture media. Accurate and rapid diagnosis of disseminated M. kansasii infections in transplant recipients is important for antimicrobial management.

Methods. Two cases of disseminated M. kansasii infections with unusual presentation in which rapid diagnosis was made using the Karius test (KT) are presented. The KT is a CLIA certified/CAP-accredited next-generation sequencing (NGS) plasma test that detects microbial cell-free DNA (mcfDNA). After mcDNA is extracted and NGS performed, human reads are removed, and remaining sequences are aligned to a curated database of >1400 organisms. Organisms present above a statistical threshold are reported.

Results. Case 1: A 31-year female kidney transplant recipient presented with a thyregoidal duct cyst, as well as swelling of her right metacarpophalangeal joint and left 3rd finger. AFB culture of the resected graft was confirmed as M. kansasii. The KT is a CLIA certified/CAP-accredited next-generation sequencing (NGS) plasma test that detects microbial cell-free DNA (mcfDNA). After mcDNA is extracted and NGS performed, human reads are removed, and remaining sequences are aligned to a curated database of >1400 organisms. Organisms present above a statistical threshold are reported.

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Rapid diagnosis of disseminated M. kansasii infection

**Conclusion.** Open-ended NGS plasma testing for mcDNA identified disseminated M. kansasii infection much earlier than standard microbiology and thus helped in initiation and modification of pathogen directed treatment.

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646. Increasing Use of Interferon-Gamma Release Assay to Test for Pediatric Tuberculosis in a Low-Burden Setting
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**Background.** The American Academy of Pediatrics recommends tuberculin skin tests (TSTs) or interferon gamma release assays (IGRAs) to test for tuberculosis (TB) infection in children ≥2 years old, and prioritizes IGRA testing in Bacille Calmette-Guérin vaccine recipients due to cross-reactivity. TSTs require a return visit, which frequently results in loss to follow up. Growing evidence supports accuracy of IGRA testing in pediatric patients, including young children, leading to calls for preferential use of IGRA over TST. We sought to evaluate trends in IGRA use in children over time.

**Methods.** We identified all TB infection tests conducted in children 5-17 years old at 2 academic medical systems in Boston from October 2015–January 2021. TSTs were identified using medication administration records, and IGRAs were identified using laboratory records. We computed the proportion of tests per month that were IGRA and TST. We used Pearson correlation to determine the association between month of testing and proportion of tests that were IGRA.

**Results.** 21,471 TB infection tests were obtained from 16,778 patients during our study period. Median age of testing was 13.4 years (IQR 9.2 – 16.2 years). During the study period, there was a significant increase in the monthly proportion of TB infection tests that were IGRA (Pearson correlation coefficient 0.92, P < 0.001). The total number of tests performed per month also increased, with seasonal increases in testing in late summer and early fall and a substantial decline in testing early in the COVID-19 pandemic.

**Conclusion.** Use of IGRAs among patients age 5-17 years of age increased significantly overall and compared to TST in two large Boston healthcare systems over a 5-year period. These results suggest a shift towards blood-based TB infection testing in a low-burden setting, which may improve completion of the pediatric TB infection care cascade. Future research is needed to determine reasons for changing testing modalities, and similar patterns in other settings.

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