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, 56 due to gram negative, and 6 due to Candida organisms. Mean time to optimal antimicrobial therapy was significantly lower when pharmacist recommendations were accepted ($86.40, $147.95, and $239.41, respectively).

### Baseline characteristics

| Variable | ASP pharmacist recommendation accepted | ID team recommended (h) | ASP pharmacist recommendation accepted | p-value |
|----------|---------------------------------------|-------------------------|---------------------------------------|---------|
| Gender: Female | 63 (87.6%) | 12.0 (4.6) | 31.9 (3.4) | 0.0090 |
| Age | 65 (95.5%) | 20.9 (6.1) | 21.3 (3.0) | 0.7307 |
| Race | 85 (99.1%) | 19.9 (3.9) | 21.5 (4.9) | 0.0068 |
| Organism Identified: Gram Negative | 69 (89.6%) | 22.3 (5.1) | 27.0 (3.7) | 0.0470 |
| | Gram Positive | 10 (12.8%) | 16.2 (3.4) | 16.6 (3.6) | 0.0173 |
| | Candida | 2 (2.5%) | 27.0 (6.3) | 27.0 (6.3) | 0.1713 |

**Primary outcomes: Time to Optimal Therapy**

**Conclusion.** The establishment of a pharmacist run antimicrobial stewardship program in conjunction with rapid diagnostic tools for identifying bacteremia led to significant savings in cost and length of stay. Further studies are needed to fully understand the impact of ASP recommendations on outcomes.

### Microbiological isolates

| Primary isolates (%) | ASP pharmacist recommendation accepted | ID team recommended (h) | ASP pharmacist recommendation accepted | p-value |
|----------------------|---------------------------------------|-------------------------|---------------------------------------|---------|
| Time to optimal antimicrobial therapy (h) | R: 11 (92.3%) | 25.7 (17.2, 46.4) | 261.2 (97.3, 850.0) | < 0.0001 |

**Primary isolates (%)**

| Variable | ASP pharmacist recommendation accepted | ID team recommended (h) | ASP pharmacist recommendation accepted | p-value |
|----------|---------------------------------------|-------------------------|---------------------------------------|---------|
| Total cost of visit | $86.40, $147.95, $239.41 | $93.00, $157.95, $250.41 | $86.40, $147.95, $239.41 | 0.0068 |
| 30 day mortality | 3/38 (7.9%) | 6/40 (15.0%) | 7/39 (17.9%) | 0.0850 |
| 90 day mortality | 7/38 (18.4%) | 13/40 (32.5%) | 12/39 (30.8%) | 0.1660 |
| 30 day readmission | 11 (28.9%) | 15 (37.5%) | 10 (25.6%) | 0.4111 |
| 90 day readmission | 12 (31.5%) | 21 (52.5%) | 14 (35.9%) | 0.2415 |
| Length of stay | 10.4 (8.1, 15.0) | 15.0 (9.6, 18.0) | 11.8 (8.1, 12.0) | 0.0003 |
| Length of stay from diagnosis | 5.0 (2.6, 9.9) | 10.3 (7.0, 16.0) | 8.0 (4.9, 14.0) | 0.0134 |

**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/mycobiology

**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 U.S. In Oct. 2020, we received a facultatively anaerobic, non-hemolytic organism (OL1) from a dog bite wound for identification. 16S 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 spp. 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 genomics 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, functional 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, PNP, glucose fermentation and carbohydrate assimilation tests. Potassium gluconate 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 sizes were ~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/CIA), 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.

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

### 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/mycobiology

**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 mcfDNA 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 thyroglossal duct cyst, as well as swelling of her right metacarpophalangeal joint and left 3rd finger. AFB culture of the thyroglossal cyst aspiration done on post admission day (PAD) 2 took 27 days to be identified as M. kansasii (on PAD 29) whereas plasma sent for KT on PAD 5 reported a positive test for M. kansasii at 284 molecules/micro-liter (MPM) in 4 days (on PAD 9). Case 2: A 29-year male kidney transplant recipient presented with generalized weakness, arthralgia, pericardial effusion, cytopenia, weight loss and intermittent fevers. Plasma sent for KT on PAD 12 was reported positive for M. kansasii at 1314 MPM in 3 days (on PAD 15). PET CT done simultaneously was consistent with an infection of an old AV graft in the left upper extremity. The AFB culture of the resected graft was confirmed as M. kansasii in 22 days on PAD 36. After the KT was available (before confirmation of M. kansasii on culture), the first patient underwent modification of empiric treatment and the second patient was started on specific treatment for M. kansasii.