with positive BSI 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 recommendation 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 ($86.40, $147.95, and $239.41, respectively).

Baseline characteristics

Baseline patient characteristics (N= 170)				
Variable	ASP Pharmacist recommendation accepted (n=90)	ID team consulted (n=38)	ASP Pharmacist recommendation NOT accepted (n=42)	p-value
Gender: Female Male	 45 (50%) 45 (50%)	 13 (34.2%) 25 (65.8%)	 21 (50%) 21 (50%)	0.2280
Age	73 ± 16.1 (median = 75.5)	69.6 ± 15.1 (median = 71)	74.1 ± 15.1 (median = 78)	0.3267
Organism identified Gram Negative Gram Positive Yeast	 29 (32.2%) 56 (62.2%) 5 (5.6%)	 12 (31.6%) 25 (65.8%) 1 (2.6%)	 15 (35.7%) 27 (64.3%) 0 (0%)	0.7105

Microbiological isolates

Microbiological isolates (N= 170)	
Gram Positive Organisms (n=108)	
Methicillin susceptible *Staphylococcus aureus*	48
Methicillin susceptible *Staphylococcus aureus*	**8**
Streptococcus spp.	33
***Enterococcus* spp.**	**15**
Other	4
Gram Negative Organisms (n=56)	
Escherichia coli	37
Klebsiella pneumoniae	**7**
Other	12
Yeast (n=6)	
Candida spp.	6

Primary outcome (N= 170)				
Variable	ASP Pharmacist recommendation accepted (n=90)	ID team consulted (n=38)	ASP Pharmacist recommendation NOT accepted (n=42)	p-value
Time to optimal antimicrobial therapy (hr)	8.1 (3.9, 24.1)	25.7 (17.2, 44.5)	241.2 (118.0, 352.5)	<0.0001

Primary Outcome: 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 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 warrented.

Secondary outcomes

Secondary outcomes (N= 170)				
Variable	ASP Pharmacist recommendation accepted (n=90)	ID team consulted (n=38)	ASP Pharmacist recommendation NOT accepted (n=42)	p-value
Total cost of visit (USD)	86.4 (51.02, 295.03)	147.95 (87.84, 342.11)	239.41 (158.61, 512.18)	0.0002
Mortality during admission	8 (8.9 %)	3 (7.9%)	5 (11.9 %)	0.8317
30-Day mortality	2 (2.2 %)	0 (0.0%)	3 (7.14 %)	0.1696
30-day unscheduled readmission	15 (16.7 %)	4 (10.5%)	7 (16.7 %)	0.6111
Microbiological clearance at 48 hours: No No follow-up cultures Yes	 12 (13.3 %) 11 (12.2 %) 64 (71.1 %)	 9 (23.7%) 1 (2.6%) 28 (73.7%)	 8 (19.0 %) 6 (14.3 %) 27 (64.3 %)	0.2415
Length of stay	10.0 (6.0, 16.0)	13.5 (7.0, 28.0)	11.0 (6.0, 17.0)	0.0933
Length of stay from time of PharmD notification	8.0 (5.0, 14.0)	10.0 (6.0, 20.0)	9.0 (4.5, 15.0)	0.0753

Missed cost savings

Variable	N	Mean	Median (IQR)	25th Pctl	75th Pctl
Actual cost of visit (USD)	42	892.49	239.41	158.61	512.18
Hypothetical cost of visit had ASP pharmacist recommendation been accepted (USD)	42	648.73	111.80	62.88	235.34
Potential cost savings (USD)	42	263.62	112.32	15.80	323.72

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

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

Benjamin Liu, MD, PhD[1]; Keith Simmon, MS[2]; Mark Fisher, PhD, D(ABMM)[3]; [1]University of Utah School of Medicine/ARUP, Salt Lake City, Utah; [2]ARUP, Salt Lake City, Utah; [3]ARUP Infectious Diseases Laboratory, Salt Lake City, UT

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 U.S. In Oct. 2020, we received a facultatively anaerobic, non-hemolytic Gram-negative rod (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* 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, 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, PNPG, 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 size 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/CflA), 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

Tosin Ogunsiakan, MD[1]; Kristen D. Fajgenbaum, MD[2]; Gautam Phadke, MD[3]; Thomas Montgomery, M.D.[4]; Kiran Gajurel, MD[5]; [1]Carolinas Medical Center, Atrium Health, Charlotte, NC; [2]Atrium Health - Carolinas Medical Center, Charlotte, NC; [3]Metrolina Nephrology, Charlotte, NC; [4]Atrium Health, Charlotte, NC; [5]Carolinas Medical Center, Charlotte, NC

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 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/microliter (MPM) in 4 days (on PAD 9). Case 2: A 59-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*.