

864 (12%) urine cultures were repeats. Of the 864 index cultures, 75% were negative. The median time to repeat urine culture was 4 days. When negative index cultures were repeated at 0-3 days, the diagnostic yield for detecting a new bacteriuria was only 9%. Diagnostic yield at 3-6 days was 10%, not significantly higher compared to 0-3 days ($p=0.620$). Diagnostic yield at 6-9 days was 19%; this increase was significant compared to the 0-3 days group ($p=0.014$). When positive index cultures were repeated at 0-3 days, the diagnostic yield for detecting a new bacteriuria was only 8%. Diagnostic yield at 3-6 days was also 8%. Yield increased significantly to 15% at 6-9 days from index culture ($p=0.013$). When the threshold for significant bacteriuria was adjusted to 10,000 CFU/mL, more bacteriuria was detected overall, but primarily of gram-positive organisms. Whether the threshold for significant bacteriuria was 100,000 CFU/mL or 10,000 CFU/mL, the rate of detection of new gram-negative bacteriuria was similar, and remained less than 10% until 6-9 days from index culture (Figure 1). **Conclusions:** Among inpatients, most urine cultures repeated at less than 6 days provide redundant information. This unnecessary retesting offers an opportunity for diagnostic stewardship.

Antimicrobial Stewardship & Healthcare Epidemiology 2025;5(Suppl. S2):s87-s88

doi:10.1017/ash.2025.311

Presentation Type:

Poster Presentation

Subject Category: Diagnostic Stewardship

Blood Culture Utilization: How Many Follow-Up Cultures Are Needed?

George Jones¹ and Jennifer Hanrahan²

¹Eastern Virginia Medical School at Old Dominion University and ²Eastern Virginia Medical School

Background: Follow-up blood cultures (BCx) are ordered after an initial positive culture in many instances. The number of follow-up cultures needed is not clear. Obtaining unnecessary BCx may cause unintended consequences. The optimal balance between stewardship and patient safety warrants investigation. We sought to assess the frequency with which a third set is positive after a negative second BCx. **Methods:** We conducted a retrospective study of BCx submitted to the microbiology laboratory from 1/1/18-11/1/23. We included all patients ≥ 18 years who had at least two follow-up BCx drawn 24-72 hours after an initial positive culture. Data were collected from electronic medical records. Cultures obtained within two hours of each other were counted as one set. Different strains of an organism were considered to be different organisms. Patients were divided into four groups based on BCx positivity, with a focus on the cohort with a positive culture after a negative follow-up set. **Results:** 28,875 patients had an initial positive BCx, of which 2,636 had at least two follow-up cultures drawn in the selected timeframe. Within this group, 585 (22.2%) had two positive follow-up sets, 1500 (56.9%) had two negative, 431 (16.4%) had a positive followed by a negative, and 120 (4.6%) had a negative followed by a positive. Of this cohort, 71 (2.7%) grew the same organism in the initial and second follow-up cultures, while 49 (1.9%) did not. In the same-organism subset, the most commonly identified bacteria were coagulase-negative staphylococci ($n=21$; 0.8%), gram-negative bacteria ($n=17$; 0.6%), methicillin-sensitive *Staphylococcus aureus* ($n=13$; 0.5%), and methicillin-resistant *S. aureus* ($n=7$; 0.3%). The most frequently isolated organisms in this subset were *S. aureus* ($n=20$; 0.8%), *Staphylococcus epidermidis* ($n=16$; 0.6%), and *Escherichia coli* ($n=11$; 0.4%). In the different-organism subgroup, 35 (1.3%) of the second follow-up sets had suspected contamination, though true bacteremia from skin/soft tissue ($n=4$; 0.2%), central line ($n=4$; 0.2%), unknown ($n=3$; 0.1%), and other sources was observed, often due to *S. aureus* ($n=4$; 0.2%), *E. coli* ($n=2$; 0.1%), and *Candida* ($n=2$; 0.1%). **Conclusion:** The number of patients with ongoing bacteremia that would have been missed with one follow-up BCx was small. The skip phenomenon has been described with *S. aureus* but was seen with gram-negatives as well. The second follow-up cultures were sometimes positive for contaminants. Further data are needed to determine when two follow-up sets should be obtained rather than one.

Antimicrobial Stewardship & Healthcare Epidemiology 2025;5(Suppl. S2):s88

doi:10.1017/ash.2025.312

Presentation Type:

Poster Presentation

Subject Category: Diagnostic Stewardship

Evaluating appropriateness and clinical impact of a GI PCR panel: A Retrospective Study

Pranav Ramamurthy¹, Jennifer Schimmel², Sherin Samuel³, Elisha Shah⁴, Kevin Groudan⁵, Lydia D'Agostino⁵ and Yesenia Greeff⁵

¹UMass Chan - Baystate Medical Center; ²Baystate Health; ³University of Massachusetts Chan Medical School - Baystate; ⁴UMass Chan -Baystate and

⁵University of Massachusetts Chan-Baystate

Background: Acute gastroenteritis and diarrheal illnesses have a significant burden on the United States healthcare system, with over 500,000 estimated hospitalizations annually. Testing for these conditions is often ordered inappropriately at significant cost to the healthcare system. This study aimed to determine the appropriateness of ordering of gastrointestinal PCR panel (GIP) testing in our hospital system to guide improvements in ordering practices. It also aimed to evaluate the impact of a GIP in our system. **Method:** This was a retrospective chart review with the objective of quality improvement. The appropriate measures for ordering a GIP test included documentation of diarrhea in addition to fever, blood in stool, signs of sepsis or immunocompromise and without history of laxative use in preceding 48 hours. The result of a positive versus negative GIP test was measured in terms of its effect on isolation time and appropriate de-escalation of antibiotics. **Result:** Of the 402 records which were reviewed, 204 (50.7%) were deemed to have had an appropriately ordered test per our criteria. However, of these patients, 21 were noted to have either been on tube feeds or had received bowel regimen medications within the past 48 hours. When these patients were excluded, this left 183 (45.5%) patients with an appropriately ordered GIP test. Of note, 16 of these patients had a positive concomitant *C. difficile* test. Of the 93 (23.1%) positive tests, only 36 positive results were from appropriately ordered tests of which 9 tests impacted clinical management. Of the 57 remaining tests, 11 impacted clinical management. A negative test led to discontinuation of isolation precautions in 159 (76.1%) patients who had isolation placed for diarrheal illness prior to testing. Negative tests also led to discontinuation of antibiotics in 51 (39.5%) patients. There was no difference between these groups regardless of whether the test was ordered appropriately or not. **Conclusion:** The GIP test to detect a variety of gastrointestinal pathogens is not being ordered appropriately in our health system over half the time. It bears further investigation as to whether the monetary cost to patients and the health system of this test is offset by the apparent antibiotic stewardship and cost benefits in discontinuing isolation precautions and antibiotics. Interestingly, testing appeared to have utility regardless of appropriateness. Based on this finding, an updated set of guidelines to educate physicians in the appropriate ordering and interpretation of this test is required.

Antimicrobial Stewardship & Healthcare Epidemiology 2025;5(Suppl. S2):s88

doi:10.1017/ash.2025.313

Presentation Type:

Poster Presentation

Subject Category: Diagnostic Stewardship

Community-acquired pneumonia work-up in areas where coccidioidomycosis is endemic: Undertested, underdiagnosed, and untreated

Kent Carpenter¹, Pooja Rangan², Sumit Agarwal², Justin Hayes², Neil Ampel³ and Jonas Marschall⁴

¹University of Arizona College of Medicine Phoenix; ²University of Arizona College of Medicine; ³University of Arizona and ⁴University of Arizona College of Medicine - Phoenix

Background: The dimorphic fungus *Coccidioides* is endemic in the Southwestern USA and most commonly causes respiratory infection ("Valley Fever"). While the true community prevalence of this respiratory