cultures met inclusion criteria. Baseline illness severity and identified pathogens were similar between cohorts. Clinical outcomes and antimicrobial DOT are reported in Tables 1 and 2.

Conclusion. Following our implementation of AXDX, clinical outcomes including LOS, TTO, total DOT, BGN DOT, and frequency of achieving optimal therapy were significantly improved compared with a historical cohort. Addition of RTN for AXDX results in the setting of an already active ASP did not further improve these metrics. However, compared with historical arm, AXDX with RTN did significantly impact specific subsets of antibiotic use while AXDX alone did not. This may be due to the different patient selection criteria. These results support the benefit of integration of AXDX into healthcare systems with an active ASP even without the resources to include real-time notification.

Table 1: Clinical Outcomes comparing historical, intervention-1, and intervention-2 arms

| Clinical Outcomes       | Historical | Intervention 1 | Intervention 2 | P value |
|-------------------------|-----------|----------------|----------------|---------|
| LOS, days (mean ± SD)   | 11.89 (10.9) | 6.54 (9.0) | 10.00 (14.4) | ≥0.05*  |
| ICU LOS, days (mean ± SD)| 5.17 (4.1)  | 6.20 (8.9) | 5.55 (8.0)  | 0.76    |
| TTOF, days (mean ± SD)  | 2.49 (1.8)  | 1.58 (1.5) | 1.48 (1.1)  | ≥0.05*  |
| Antibiotic Per Patient  | 204.6 (41.6) | 145.0 (45.1) | 156.0 (45.1) | 0.01*   |

*Statistical significance (p value ≤0.05)

Disclosures. All authors: No reported disclosures.

2138. Follow-up Investigation of Antibody Titters and Diagnostic Antibody Cut-Off Values in Scrub Typhus Patients in Korea

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Background. Scrub typhus is a mite-borne infectious disease caused by Orientia tsutsugamushi. There have been few follow-up studies assessing antibody titers using serologic tests from various commercial labs.

Methods. A prospective investigation to assess antibody titers of scrub typhus patients and seroreversion for health checkup individuals were evaluated. The antibody titers of former patients diagnosed with scrub typhus at least 1 year and a maximum of 13 years were also investigated. The following tests were performed simultaneously: (i) immunofluorescence antibody assays (IFAs) that detect immunoglobulin (Ig) M and IgG, (ii) IFA that detects total Ig by a commercial lab, (iii) antibody tests using two commercially available kits.

Results. In prospective analyses with cutoff values set to ≥1:16 for IgM, ≥1:256 for IgG, the positive antibody rates of 162 confirmed scrub typhus patients were 44%, 35.3%, and 57.6%, respectively, in the first week after symptom onset. Among 91 former patients recovered, the follow-up IgM, IgG, and total Ig positivity rates were 38.5% (35/91), 22.0% (20/91), and 76.9% (70/91), respectively. In overall cohort of 216 health checkup subjects, 4.2% (9/216) IgM and 0% (0/216) IgG seroprevalence was observed.

Conclusion. The IFA from KCDC and commercial lab, and rapid commercial kits cannot differentiate between former patients recovered from scrub typhus and current scrub typhus. In Korea and other countries where low antibody cut-off titer values have been used as criteria for diagnosing and reporting scrub typhus, upward adjustments of cut-off values may be necessary.
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2139. *Rickettsia typhi* Detection in Clinical Infections by the Karius Test, a Plasma Microbial Cell-free DNA Next-Generation Sequencing Test

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**Background.** *Rickettsia typhi* typically causes a nonspecific syndrome characterized by fever, rash, and headache but can rarely progress to severe disease. *R. typhi* is transmitted by the rat flea and there has been an increased incidence in Houston, TX. Establishing the diagnosis can be challenging and is often made by serological studies. Prompt therapy with doxycycline is important especially in severe disease.

**Methods.** Karius Test results from the prior 2 years (Redwood City, CA) were reviewed for detections of *R. typhi*. The Karius Test 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 sequences are removed and remaining sequences are aligned to a curated pathogen database of >1,000 organisms. Organisms present above a statistical threshold are reported. Chart review was conducted on the cases of *R. typhi* identified by the Karius Test.

**Results.** The Karius Test detected *R. typhi* in 6 adult patients, 4 women and 2 men, from a medical center in Houston, TX. In 2 patients, *R. typhi* mcfDNA was present in the raw sequencing data but at an abundance below validated statistical thresholds. *R. typhi* mcfDNA was not found in negative controls run simultaneously with the samples. All patients presented with fever, 4 presented with headache, 3 presented with gastrointestinal symptoms, 3 developed rash, one presented with hypotension. Laboratory data were available for 5 patients. Four patients developed thrombocytopenia, 5 had anemia, 4 had WBC < 5, 4 had transaminase elevation and 3 developed hyponatremia. 3 out of 5 had *R. typhi* serologies sent; all 3 were positive (including two of the patients with *R. typhi* mcfDNA levels below threshold). In the two other patients the Karius test was the means of establishing the diagnosis. 3 out of 5 patients where data were available were treated with doxycycline.

**Conclusion.** The Karius test was able to detect *R. typhi* in a cluster of 6 patients in one medical center in Houston, TX. NGS for mcfDNA offers a rapid means of detecting *R. typhi* infection. Accurate, rapid diagnosis of *R. typhi* has important public health implications given its vector-borne mechanism of transmission.

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2140. Utility of Respiratory Specimen Gram Stain for Predicting Final Culture Result in Patients with Clinically Diagnosed Pneumonia

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**Background.** Obtaining a high-quality respiratory tract specimen for Gram stain and culture in patients with suspected lower respiratory tract infections is recommended by the IDSA guidelines. However, conflicting results correlating Gram stain with final culture growth has led to questions about the utility of a respiratory specimen Gram stain. The purpose of this study was to assess the correlation of Gram stain with final culture in patients with pneumonia.

**Methods.** A retrospective chart review was conducted to evaluate adult inpatients with a diagnosis of pneumonia (based on the CDC surveillance definition) who had a respiratory specimen submitted for Gram stain and culture. A specimen was considered acceptable if less than ten epithelial cells were visualized under low power field. Each Gram stain was compared with the corresponding final culture. The primary outcome was to evaluate the correlation of Gram stain with final culture using positive predictive value (PPV), negative predictive value (NPV), sensitivity, and specificity. A culture was considered negative if no bacteria were isolated or if only normal flora grew. Secondary outcomes were PPV and NPV based on antibiotic exposure prior to specimen collection, semi-quantitative number of bacteria on Gram stain, and collection method. Additionally, discordance between Gram stain and final culture morphology was evaluated.

**Results.** A total of 269 acceptable specimens were assessed. Of the 72 specimens with a positive Gram stain, 41 yielded bacteria in final culture (PPV: 56.9%). In contrast, 154 of the 197 specimens with a negative Gram stain were associated with negative final culture (NPV: 76.7%). The NPV of Gram stain was decreased when antibiotics were given for > 24 hours pre-specimen. The PPV of Gram stain improved as an increasing amount of bacteria were reported. Less invasive collection methods had a lower PPV but a higher NPV in comparison to invasive collection methods. Finally, the discordance rate between Gram stain and final culture morphology was low.

**Conclusion.** This study shows inconsistent results regarding the ability of Gram stain to predict final culture. Pneumonia should continue to be managed clinically and cultures submitted prior to adjusting empiric antimicrobial regimens based solely on the Gram stain.

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