narrowing or discontinuation of 1 or more antimicrobial therapies <3 days after sepsis onset. **Results:** Overall, 277 patients were included (DEG, 90 patients, 32%; NDG, 187 patients, 68%). The groups were similar in terms of sex, comorbidities, length of stay, and severity of illness: septic shock (47% DEG vs 49% NDG; $P = .693$) and ICU stay (27% DEG vs 32% NDG; $P = .406$). DEG patients were slightly older than NDG patients: (DEG age, 63+16 years vs NDE age, 58+16 years; $P = .028$). There was no difference in hospital mortality (8% DEG vs 12% NDE; $P = .257$). Nearly half of the patients in both groups (46% DEG and 47% NDG) had no causative microorganisms identified using conventional microbiology culture. The common sources of primary infection were respiratory, urinary tract, and gastrointestinal infections, and these were not different between groups. Also, 69% of DEG patients and 79% of NDG patients received antibiotics for >7 days ($P = .002$). Empiric intravenous vancomycin was initiated in 83% in DEG patients and 74% in NDG patients at sepsis diagnosis. Although organisms covered by intravenous vancomycin were isolated from only 17% of patients in DEG and 23% in NDG, vancomycin was continued for >5 days in 34% of DEG patients and 50.3% of NDG patients ($P < .001$). 60% of patients in DEG and 61% in NDG were seen by infectious diseases specialists (ID). Patients with infectious diseases consultations had significantly more comorbidities, were more frequently in the ICU, had higher MDRO isolation and longer hospital stays, but they were still de-escalated without a difference in mortality. **Conclusions:** Microbiology data did not contribute to early de-escalation of antibiotics in this study. This finding may be related to the high percentage of negative culture and unavailability of rapid molecular diagnostic tests. Shorter duration of antibiotics (including vancomycin) was not associated with worse outcome in these severely ill patients.

Presentation Type:
Poster Presentation
Decision Support Tool for Screening of Tuberculosis Exposed Individuals Seeking Care at a Public Academic Health System
Stephanie Cobb, UT Southwestern; Stephanie Nguyen, UT Southwestern; Deepa Raj, UT Southwestern Medical Center; Dena Taherzadeh, Parkland Health and Hospital System; Pranavi Sreeramoju, University of Texas Southwestern Medical Center

Table 1.

Location	Mean Exposure			F Statistic	P
	Borderline (n = 57)	Negative (n = 747)	Positive (n = 313)		
Person-nights exposure to smear-positive TB					
Shelter 1	25.14	22.95	33.57	2.835	.059
Shelter 2	0.00	0.00	0.00	0	
Shelter 3	23.21	11.51	29.89	13.279	.000
Shelter 4	0.00	0.01	0.00	0.446	.641
Person-nights exposure to smear-negative TB					
Shelter 1	11.70	11.52	13.99	0.675	.510
Shelter 2	0.00	0.02	0.05	2.595	.075
Shelter 3	6.21	4.89	9.66	4.609	.010
Shelter 4	0.00	0.04	0.00	0.778	.460

Background: *Mycobacterium tuberculosis* (TB) is one of the leading causes of morbidity and mortality worldwide. At our health system, 50–100 patients are diagnosed with tuberculosis every year. One risk factor for TB is residence within a homeless shelter. In response to an increased number of cases in local homeless shelters, the health department sought assistance with contact tracing of individuals potentially exposed to tuberculosis. We report the results of contact tracing performed at our health system. **Methods:** The setting is a 770-bed, safety-net, academic hospital with community clinics and a correctional health center. Name, date of birth, and social security number of contacts potentially exposed during February 2009 to July 2013 were programmed into the electronic medical records to create a decision support tool upon entering the health system. The best practice alert (BPA) informed physicians of the exposure and offered a link to a screening test, T-spot.TB, and a link to an information sheet. This intervention was implemented from July 2013 to July 2015. After excluding patients with active TB, data on the magnitude of exposure in each homeless shelter and screening test results were analyzed with ANOVA using SPSS v 26 software. **Results:** Of the 8,649 identified exposed contacts, 2,118 entered our health system. Of those for whom the BPA was triggered, 1,117 had a T-spot.TB done, with 313 positive results and 57 borderline results. Table 1 shows that shelter 3 was correlated with a positive T-spot.TB. **Conclusions:** The BPA, which prompted physicians to evaluate an individual for TB, was effective at capturing high-risk, exposed individuals. Clinical decision support tools enabled our safety-net health system to respond effectively to a local public health need.

Presentation Type:
Poster Presentation
Effect of delays in concordant antibiotic treatment on mortality in patients with hospital-acquired Acinetobacter spp. bacteremia in Thailand: a 13-year retrospective cohort
Cherry Lim, Mahidol Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Thailand/ Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, United Kingdom; Mo Yin, Mahidol Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Thailand/ Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, United Kingdom/ Division of infectious disease, University Medicine Cluster, National University Hospital, Singapore, Singapore; Prapit Teparrukkul, Department of Internal Medicine, Sunpasitthiprasong Hospital, Ubon Ratchathani, Thailand; Maliwan Hongsuwan, Mahidol Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Thailand; Nicholas P.J. Day, Mahidol Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Thailand/ Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, United Kingdom; Direk Limmathurotsakul, Mahidol Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Thailand/ Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, United Kingdom; Ben S. Cooper, Mahidol Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol