

codes, and treatment regimens, we developed a novel algorithm to classify patient records into LTBI categories: definite, probable or possible. We used multivariable logistic regression, with a referent group of all cohort patients not classified as having LTBI or TB, to identify associations between TB risk factors and LTBI.

**Results.** Among 2,190,686 patients, 6.9% (n=151,195) had a TB screening test; among those, 8% tested positive. Non-U.S.-born or non-English-speaking persons comprised 24% of our cohort; 11% were tested for TB infection, and 14% had a positive test. Risk factors in the multivariable model significantly associated with being classified as having LTBI included preferring non-English language (adjusted odds ratio [aOR] 4.20, 95% confidence interval [CI] 4.09–4.32); non-Hispanic Asian (aOR 5.17, 95% CI 4.94–5.40), non-Hispanic black (aOR 3.02, 95% CI 2.91–3.13), or Native Hawaiian/other Pacific Islander (aOR 3.35, 95% CI 2.92–3.84) race; and HIV infection (aOR 3.09, 95% CI 2.84–3.35).

**Conclusion.** This study demonstrates the utility of EHR data for understanding TB screening practices and as an important data source that can be used to enhance public health surveillance of LTBI prevalence. Increasing screening among high-risk populations remains an important step toward eliminating TB in the United States. These results underscore the importance of offering TB screening in non-U.S.-born populations.

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### 1666. Yield of Tuberculosis Contact Tracing among Veterans after Outpatient Exposure

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**Session:** P-72. Tuberculosis and other Mycobacterial Infections

**Background.** Tuberculosis contact tracing (TBCT) is essential to detecting transmission. High priority contacts for TBCT include children less than 5 and those with prolonged, close contact with a tuberculosis (TB) case. Other populations considered high priority include those with certain comorbidities. While data are limited, there is evidence for transmission in outpatient settings with short duration/casual contact. We describe the yield of TBCT among a high priority cohort after exposure in to active TB in VA clinics.

**Methods.** Between 2016-2019, VA Northern California performed 4 episodes of TBCT in the outpatient setting. In TBCT 1, the index case was an AFB smear positive healthcare worker (HCW) with 30-minute patient appointments. In TBCT 2-4, the index cases were patients, 2 of whom were AFB smear positive. TBCT included patients seen by the HCW (TBCT 1) and those with appointments one hour before or after the index patient in the same clinic (TBCT 2-4). Contacts were offered interferon-gamma release-assay (IGRA). Staff contacts were tested by purified protein derivative (PPD). Comorbidities, prevalent and new cases with positive TB testing were calculated and compared between different groups.

**Results.** Fifty-one percent of veteran contacts had comorbidities placing them in a high priority group for TBCT. Among the 593 patients who had an IGRA during TBCT, 40 (6.7%) tested positive. Twenty-six (4.4%) had no known history of prior positive TB test of whom 6 reported a previous TB exposure history. Veterans exposed to the HCW did not have a higher prevalence of IGRA positivity or a new positive IGRA compared to TBCT 2-4 (5.5% vs 8.0%, p-value 0.22 and 3.4% vs. 5.3%, p-value 0.26). Among the 130 staff tested in TBCT 1-4, one (0.7%) converted during TBCT 1.

**Conclusion.** After extensive TBCT, the prevalence of latent TB among short duration/casual contacts of TB was 6.7%, similar to the baseline prevalence of latent TB of 6% in California. In this high priority population for TBCT, no difference was seen when there was face-to-face contact versus a shared waiting room with the index case. Staff conversion rate was extremely low. While decisions to perform TBCT in outpatient settings need to be individualized, the yield of TBCT in this population of veterans was low.

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### 1667. Change in characteristics of community-onset ciprofloxacin-resistant E. coli isolates causing community-acquired acute pyelonephritis in South Korea

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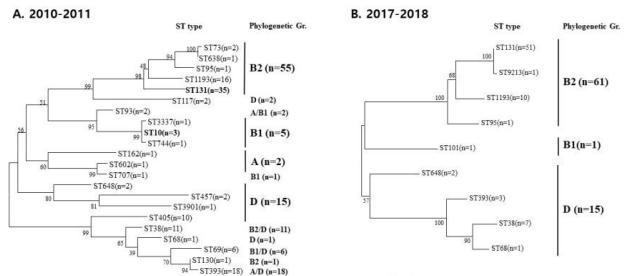
**Session:** P-73. UTIs

**Background.** The aim of this study was to examine the change in characteristics of community-onset ciprofloxacin-resistant (CIP-R) *E. coli* isolates causing community-acquired acute pyelonephritis (CA-APN) in South Korea between 2010-2011 and 2017-2018.

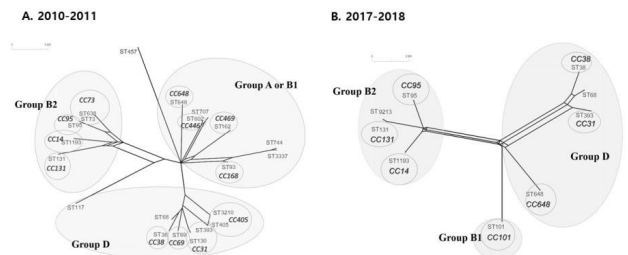
**Methods.** *E. coli* samples isolated from the blood or urine were collected from patients with CA-APN aged 19 years and more who were admitted to 8 Korean hospitals from September 2017 to August 2018, respectively. One isolate was collected from each patient. Phylogenetic typing, multilocus sequence typing (MLST), and molecular characterization of  $\beta$ -lactamase resistance and plasmid-mediated quinolone resistance (PMQR) determinants were performed. The data were compared with those from the previous study with same design in 2010-2011.

**Results.** A total of 346 and 300 isolates were collected during 2017-2018 and 2010-2011, respectively. Among them, 76 (22.0%) and 77 (25.7%) were CIP-R isolates. Significantly higher antimicrobial resistance against ampicillin (75.7% vs. 100%,  $P < 0.001$ ) and cefotaxime (23.9% vs. 77.9%,  $P < 0.001$ ) were observed for isolates in 2017-2018 compared to those in 2010-2011. The proportion of phylogenetic group B2 had increased significantly (44.7% vs. 79.2%,  $P < 0.001$ ). As for MLST, the proportion of ST131 (27.6% vs. 66.2%,  $P < 0.001$ ) had increased while that of ST393 (18.4% vs. 3.9%,  $P = 0.004$ ) had decreased significantly. Higher proportion of CIP-R *E. coli* isolates in 2017-2018 had extended-spectrum  $\beta$ -lactamase (ESBL)/plasmid-mediated AmpC  $\beta$ -lactamase (PABL) (23.7% vs. 79.2%,  $P < 0.001$ ) and PMQR determinant (11.8% vs. 40.8%,  $P < 0.001$ ) compared to those in 2010-2011.

Phylogenetic tree



Analyzed by SplitsTree



**Conclusion:** Among uropathogenic CIP-R *E. coli* isolates in South Korea, ST131 predominance had become more prominent and the proportion of containing ESBL/PABL and/or PMQR determinants had increased.

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### 1668. Clinical Risk Score Model for Predicting Extended Spectrum Beta Lactamase (ESBL)-Positive Urinary Tract Infection among Hospitalized Filipino Patients: a Retrospective Single-Center Study

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**Session:** P-73. UTIs

**Background.** Infections caused by Extended-Spectrum B-lactamases (ESBL) organisms are an emerging health concern worldwide. In the background of progressive rise of antibiotic resistant organisms, efforts should be started to minimize