were 70.97% (95%CI 58.05%-81.80%) and 56.32% (95%CI 45.26%-66.94%) respectively. While for FluoroSpot, the AUROC was 0.906 (95 CI 0.856-0.957), the sensitivity and specificity of differentiating ATB from LTBI were 80.65% (95%CI 68.63% - 89.58%) and 88.51% (95%CI 79.88% - 94.35%) respectively.

Figure 2. Correlation between the frequencies of total IFN-γ-secreting T cells detected by FluoroSpot assay and those of T-SPOT.TB. (A) Stimulated by EAST-6, (B) Stimulated by CFP-10.

Figure 3. ROC curves and the corresponding AUROC for measurement of frequencies of specific T cells in differentiating ATB and LTBI under stimulation of ESAT-6 or CFP-10. The blue line is drawn with the frequency of IFN-γ-secreting T cells detected by T-SPOT.TB, and the AUC is 0.609 (95% CI 0.574-0.765). The red line is drawn with combination of the frequencies and proportion of single IFN-γ-single IL-2-single TNF-α-dual IFN-γ/IL-2-dual IFN-γ/TNF-α-dual IL-2/TNF-α-secreting T cells detected by FluoroSpot, and the AUC is 0.906 (95% CI, 0.856-0.957).

Table 1. Diagnostic value of T-SPOT.TB and FluoroSpot for differentiating ATB from LTBI

## Conclusion

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Table 1. Diagnostic value of T-SPOT.TB and FluoroSpot for differentiating ATB from LTBI

**Conclusion.** Compared with T-SPOT.TB, the IFN-γ/IL-2/TNF-α FluoroSpot assay may be helpful to distinguish ATB from LTBI, and the results need to be verified by large sample prospective cohort study.

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

**404. Hepatitis B and C Prevalence in Patients with Active and Latent Tuberculosis in an Ethnically Diverse Area of London, UK**

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**Session:** P-80. Tuberculosis and other Mycobacterial Infections

**Background.** North West London has one of the highest tuberculosis (TB) rates in the UK, at 24.8 per 10,000. The UK prevalence of hepatitis B virus (HBV) is 0.1-0.5% and for hepatitis C virus (HCV) is 0.5-1%. Chronic infection with HBV or HCV can lead to an increased risk of adverse treatment outcomes, such as drug-induced liver injury (DILI) in patients with active or latent TB. National guidelines recommend routinely screening for HBV/HCV prior to initiating TB treatment. Our objectives were to 1) evaluate the HBV/HCV screening practice in local TB clinics, 2) establish the prevalence of HBV/HCV in patients receiving TB treatment.

**Methods.** Retrospective analysis of laboratory and medical records of patients treated for active or latent TB identified from the London TB register and clinic records from 01/01/2018 to 31/12/2020 from London North West NHS Trust.

**Results.** 1409 patients received treatment for TB during the time period of interest; 574 (40.7%) had active disease and 835 (59.3%) had latent infection. 966/1409 from 01/01/2018 to 31/12/2020 from London North West NHS Trust. Our objectives were to routinely screen for HBV/HCV in patients receiving TB treatment.

**Discussion.** Compared with T-SPOT.TB, the IFN-γ/IL-2/TNF-α FluoroSpot assay may be helpful to distinguish ATB from LTBI, and the results need to be verified by large sample prospective cohort study.

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

## 1407. The Latent Tuberculosis Infection Cascade of Care during the COVID-19 Pandemic Response in a Mid-Sized US City

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**Session:** P-80. Tuberculosis and other Mycobacterial Infections

**Background.** The COVID-19 pandemic response may unintendly disrupt multiple public health services, including tuberculosis control programs. We aimed to assess the cascade of care of latent tuberculosis infection (LTBI) in an urban US city during the COVID-19 pandemic response.

**Methods.** We conducted a retrospective cohort study of adult patients who presented for LTBI evaluation at the Hamilton County Public Health Tuberculosis Clinic in Ohio between 2019 and 2020. We defined 01/2019 to 02/2020 as the pre-COVID-19 response period, and 04/2020 to 12/2020 as the COVID-19 pandemic period. We reviewed electronic medical records and extracted sociodemographic information, medical history, and follow-up and treatment data to define steps in the LTBI cascade of care. Logistic regressions were used to assess factors associated with LTBI treatment acceptance and completion, adjusted by potential confounders and COVID-19 period.

**Results.** Data from 312 patients were included. There was a significant decrease in the number of monthly LTBI referrals (median, 18 vs. 8, p < 0.02) and LTBI evaluations (median, 17.5 vs. 7, p < 0.01) during COVID-19. There was a decrease in the proportion of patients followed up (40% vs. 31%, p < 0.01) and the LTBI treatment acceptance rate (76% vs. 64%, p = 0.02). LTBI treatment completion rates (65% vs. 63%, p = 0.85) in a multivariate analysis, LTBI treatment acceptance was associated with Hispanic ethnicity, younger age, male sex, IGRA use, no comorbidities, and non-healthcare occupation, independent of COVID-19 period. LTBI treatment completion was associated with taking a rifamycin-containing regimen, independent of COVID-19 period.

**Conclusion.** We observed a significant decline in the number of monthly LTBI referrals and evaluations during COVID-19. Our findings indicate an unintended negative impact of the COVID-19 response in LTBI screening efforts in our region. LTBI treatment acceptance and completion rates were not affected during COVID-19.

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

## 1408. Population-based Nontuberculous Mycobacteria Surveillance in Four Emerging Infections Program Sites, October 2019–March 2020

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**Session:** P-80. Tuberculosis and other Mycobacterial Infections

**Background.** Nontuberculous mycobacteria (NTM) cause pulmonary (PNTM) disease and extrapulmonary (ENTM) disease. NTM infections are difficult to diagnose and treat; environmental exposures occur in both healthcare and community settings. Few population-based studies describe NTM disease epidemiology. Current data indicate NTM disease and ENTM skin and soft tissue infections are increasing. We describe findings from a multi-site pilot of population-based NTM surveillance.
Methods. CDC’s Emerging Infections Program conducted active, laboratory- and population-based surveillance for NTM cases occurring in 4 sites (Colorado [5 counties], Minnesota [2 counties], New York [2 counties], and Oregon [3 counties PNTM; statewide ENTM]) during October 1, 2019–March 31, 2020. PNTM cases were defined according to current published microbiologic criteria, based on isolation of NTM in respiratory cultures or tissue. ENTM cases required NTM isolation from a non-pulmonary specimen, excluding stool or rectal swabs. Demographic, clinical, exposure, and laboratory data were collected via medical record review. We calculated overall incidence per 100,000 population using census data and performed descriptive analyses of medical record data.

Results. Overall, 299 NTM cases were reported [231 [77%] PNTM], M. avium was the most commonly isolated species (Table). NTM incidence was 3.8 per 100,000 (PNTM 5.1/100,000; ENTM 0.7/100,000). Most patients with available data had ≥1 sign or symptom in the 14 days before culture (63 [97%] ENTM, 203 [92%] PNTM). During the surveillance period, 187 (63%) had their first infection–defining culture collected in an outpatient setting (33 [49%] ENTM, 154 [67%] PNTM). Of PNTM cases, 145 (64%) were female, and 154 (67%) had underlying pulmonary disease. Among ENTM cases, 29 (43%) were female, 9 (13%) had diabetes, 8 (12%) had HIV and 27 (40%) had infection at the site of a medical device or healthcare procedure. Common ENTM infection types were lymphadenitis (16 [24%]) and skin abscess (6 [9%]).

Conclusion. Characterizing disease burden and affected populations with population-based NTM surveillance will provide data to inform potential interventions and monitor prevention strategy impact.

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N3C Basic Demographic Data

Methods. COVID-19 is defined by positive lab result (PCR, antigen, or antibody) or COVID-19 coding diagnosis, as defined by N3C. PNTMI phenotype was built with N3C Data Enclave concept set tool, and ATLAS (https://atlas.ohdsi.org/). We limited analysis to adults (18 years-old or older). We used de-identified data sets stripped of protected health information (PHI). We used N3C Data Enclave analytical tools for exploratory data analysis, and descriptive statistics.

Results. We identified five hundred and eighty-six individuals from 19 sites fulfilling the PNTMI phenotype (9.46 cases per 100,000 people). After our age limit, 555 individuals were included for analysis (Figure 2). 340 were females (61.3%), 447 of white race (80.5%), and 30 were Hispanic (5.4%). Additional descriptive statistics and statistical significance testing are provided (Table 1). The most common concept were “Non-tuberculous mycobacterial pneumonia”, and “Pulmonary Mycobacterium avium complex infection”. Four sites accounted for more than 50% of identified patients (Figure 2). We identified 24 individuals with COVID-19 (4.32%), and 44 deaths in this cohort (7.9%). Deaths were unrelated to COVID-19 event.