were 70.97% (95%CI 58.05%-81.80%) and 56.32% (95CI 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.

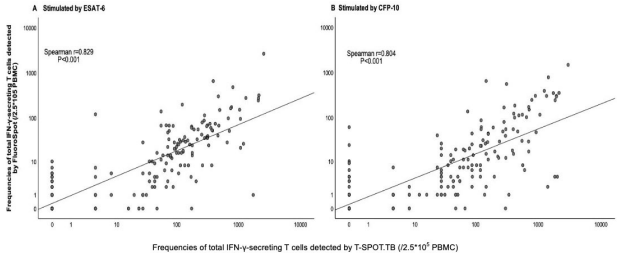

Figure 2. Correlation between the frequencies of total IFN-γ-secreting T cells detected by FluoroSpot assay and those of T-SPOT.TB. (A) Stimulated by EAST-6. (B) Stimulated by CFP-10.

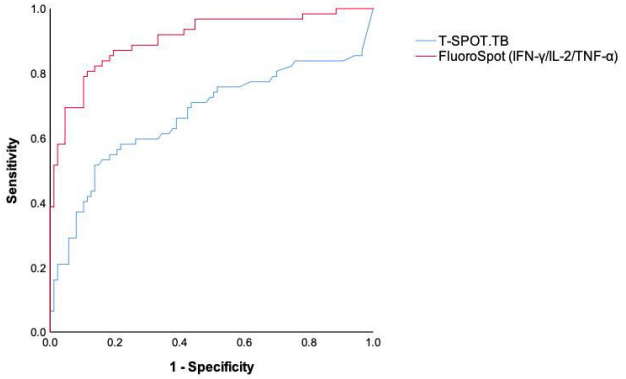

Figure 3. ROC curves and the corresponding AUROC for measurement of frequencies of specific T cells in differentiating ATB and LTBI under stimulation of ESAT-6 or CFP-10. The blue line is drawn with the frequency of IFN-γ-secreting T cells detected by T-SPOT.TB, and the AUC is 0.669 (95%CI, 0.574-0.765). 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

	Sensitivity (%, 95%CI)	Specificity (%, 95%CI)	PLR (%, 95%CI)	NLR (%, 95%CI)	PPV (95%CI)	NPV (95%CI)
T-SPOT.TB	70.97(58.05-81.80)	56.32(45.26-66.94)	1.62 (1.22-2.16)	0.52(0.34-0.79)	53.66(42.30-64.75)	73.13(60.90-83.24
FluoroSpot (IFN-γ/IL-2/TNF-α)	80.65(68.63-89.58)	88.51(79.88-94.35)	7.02(3.87-12.73)	0.22(0.13-0.37)	83.33(71.48-91.71)	86.52(77.63-92.83

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

1406. Hepatitis B and C Prevalence in Patients with Active and Latent Tuberculosis in an Ethnically Diverse Area of London, UK

Amedine Duret, MBBS BA (Hons)[1]; Emma Thorley, MBBS BA (Hons)[1]; Ayolola Eni-Olotu, n/a[2]; Oishi Sikdar, BSc[2]; Padmasayee Papineni, MRCP[1]; [1]London North West University Healthcare NHS Trust, London, England, United Kingdom; [2]Imperial College London, London, England, United Kingdom

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 patients (68.56%) were screened for HBV and HCV. 55.9% of the active TB group and 77.2% of the latent infection group were tested. 66 (6.8%) patients had isolated anti-HBc positivity, 22 (2.3%) were HBV surface antigen positive and 8 (0.8%) were HCV-antibody positive. HBV surface antigens were more prevalent in active TB patients: 9/321 (2.80%) with active TB versus 13/645 (2.02%) with latent TB. 36/321 (11.21%) active TB patients had HBV core antibodies compared to 30/645 (4.65%) latent TB patients ($p < 0.001$). Three patients started antiviral treatment following their viral hepatitis diagnosis (one with HBV, two with HCV).

Conclusion. The prevalence of chronic HBV in the study population was higher than the estimated UK prevalence. Fifteen diagnoses of hepatitis were new, allowing specialist referral for monitoring of fibrosis and development of hepatocellular carcinoma. Three patients required hepatitis treatment. 6.8% of patients were positive for anti-HBc and therefore identified as being at future risk of HBV reactivation if requiring immunosuppressive therapies.TB disproportionately affects marginalised communities; screening for viral hepatitis in TB clinic represents an opportunity to target these hard-to-reach groups to maximise the impact of public health interventions.

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

Trevor M. Stantliff, BS[1]; Lauren Houshel, BS[1]; Rinki Goswami, MD[1]; Serenity Millow, BA[2]; Gabrielle Cook, n/a[1]; Robin Knapmeyer, RN[2]; Christa Easton, RN[2]; Jennifer Mooney, PhD[2]; Moises A. Huaman, MD, MSc[1]; [1]University of Cincinnati, Cincinnati, Ohio; [2]Hamilton County Public Health, Cincinnati, Ohio

Session: P-80. Tuberculosis and other Mycobacterial Infections

Background. The COVID-19 pandemic response may unintendedly 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 response period. We reviewed electronic medical records and extracted sociodemographic information, medical history, and follow-up and treatment data to define steps within 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 immigrants as indication for LTBI testing (30% vs. 9%; $p< 0.01$), and an increase in LTBI diagnoses based on interferon-gamma release assay (IGRA; 30% vs. 49%; $p< 0.01$) during COVID-19. The proportion of people who were recommended LTBI treatment was similar before and during COVID-19 (76% vs. 81%, p=0.41), as well as the LTBI treatment acceptance rates (56% vs. 64%, p=0.28), and LTBI treatment completion rates (65% vs. 63%, p=0.85). In 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

Kelly A. Jackson, MPH[1]; Devra Barter, MS[2]; Christopher A. Czaja, MD, DrPH[2]; Helen Johnston, MPH[2]; Ruth Lynfield, MD[3]; Ruth Lynfield, MD[3]; Paula Snippes Vagnone, MT(ASCP)[4]; Laura Tourdot, MPH[3]; Nancy Spina, MPH[5]; Ghinwa Dumyati, MD[6]; Shantel Peters, MPH[7]; Gabriela Escutia, MPH[8]; Rebecca Pierce, PhD, MS, BSN[8]; Emily Henkle, PhD, MPH[9]; D Rebecca Prevots, PhD, MPH[10]; Max Salfinger, MD[11]; Kevin L. Winthrop, MD, MPH[9]; Kevin L. Winthrop, MD, MPH[9]; Nadege Charles Toney, MS[12]; Shelley Magill, MD, PhD[1]; Cheri Grigg, DVM, MPH[12]; [1]Centers for Disease Control and Prevention, Atlanta, GA; [2]Colorado Department of Public Health and Environment, Denver, Colorado; [3]Minnesota Department of Health, St. Paul, MN; [4]Minnesota Department of Health Laboratory, St. Paul, MN; [5]New York State Department of Health, Albany, NY; [6]New York Rochester Emerging Infections Program at the University of Rochester Medical Center, Rochester, NY; [7]University of Rochester Medical Center, Rochester, New York; [8]Oregon Health Authority, Portland, Oregon; [9]Oregon Health & Science University, Portland, OR; [10]National Institutes of Health, National Institute of Allergy and Infectious Diseases, Bethesda, Maryland; [11]University of South Florida College of Public Health, Tampa, Florida; [12]Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, Atlanta, Georgia

Session: P-80. Tuberculosis and other Mycobacterial Infections

Background. Nontuberculous mycobacteria (NTM) cause pulmonary (PNTM) 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 PNTM 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 3.1/100,000; 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 (12 [18%]).

Table. Characteristics of persons with NTM infection identified in population-based surveillance, October 1, 2019–March 31, 2020.

	Extrapulmonary (n=68)	Pulmonary (n=231)	Total (N=299)
Age: Median (Interquartile range)	41 (22–60.5)	67 (55–76)	64 (43–75)
Ethnicity			
Hispanic	5 (7.3)	7 (3.0)	12 (4.0)
Non-Hispanic	55 (80.9)	205 (88.7)	260 (87.0)
Unknown	8 (11.8)	19 (8.2)	27 (9.0)
Race			
American Indian or Alaska Native	2 (2.9)	1 (0.4)	3 (1.0)
Asian	1 (1.5)	19 (8.2)	20 (6.7)
Black or African American	9 (13.2)	19 (8.2)	28 (9.4)
Native Hawaiian/Other Pacific Islander	0 (0.0)	6 (2.6)	6 (2.0)
White	45 (66.2)	173 (74.9)	218 (72.9)
Unknown	11 (16.2)	13 (5.6)	24 (8.0)
Underlying conditions			
Chronic lung disease[1]	7 (10.3)	154 (66.7)	161 (53.9)
Bronchiectasis	Not collected	89 (38.5)	
Chronic obstructive pulmonary disease	Not collected	49 (21.2)	
Cystic fibrosis	0 (0.0)	21 (9.1)	21 (7.0)
Emphysema	Not collected	9 (3.9)	
Other	Not collected	19 (8.2)	
Diabetes mellitus	9 (13.2)	35 (15.2)	44 (14.7)
HIV infection	8 (11.8)	8 (3.5)	17 (5.7)
NTM species[2,3]			
M. avium complex	28 (41.2)	166 (71.9)	194 (64.9)
M. avium	16 (23.5)	96 (41.6)	112 (37.5)
M. intracellulare subsp. *chimaera*	2 (2.9)	2 (0.9)	4 (1.3)
M. intracellulare subsp. *intracellulare*	5 (7.4)	43 (18.6)	48 (16.1)
Other	0 (0.0)	1 (0.4)	1 (0.3)
Not otherwise specified	5 (7.4)	24 (10.4)	29 (9.7)
Non-*M. avium* complex	39 (57.4)	67 (29.0)	105 (35.1)
M. abscessus complex	9 (13.2)	20 (8.7)	29 (9.7)
M. chelonae complex	13 (19.1)	4 (1.7)	17 (5.7)
M. fortuitum group	8 (11.8)	19 (8.2)	27 (9.0)
M. kansasii	4 (5.9)	6 (2.6)	10 (3.3)
Other	5 (7.4)	17 (7.4)	22 (7.4)
Not otherwise specified	0 (0.0)	1 (0.4)	1 (0.3)
Not TB, not characterized further	1 (1.5)	0 (0.0)	1 (0.3)
Location of culture collection[4]			
Outpatient	33 (48.5)	154 (66.7)	187 (62.5)
Inpatient	35 (51.5)	74 (32.0)	109 (36.5)
Unknown	0 (0.0)	3 (1.3)	3 (1.0)

[1]Defined as one or more of the following: bronchiectasis, chronic pulmonary disease, COPD, cystic fibrosis, and/or emphysema.
[2]Isolated from the first infection-defining culture collected during the surveillance period. The following species were excluded from surveillance: *M. gordonae, M. paragordonae, M. tuberculosis* complex, *M. leprae, M. lepromatosis,* and *M. ulcerans.*
[3]Two PNTM cases had >1 NTM species isolated (1 *M. abscessus* complex and *M. chelonae* complex; 1 *M. abscessus* complex and *M. avium).*
[4]For the first infection-defining culture collected during the surveillance period.

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

Disclosures. **Christopher A. Czaja, MD, DrPH**, **Centers for Disease Control and Prevention** (Grant/Research Support) **Ruth Lynfield, MD**, Nothing to disclose **Ghinwa Dumyati, MD**, **Pfizer** (Grant/Research Support)**Roche Diagnostics** (Advisor or Review Panel member) **Emily Henkle, PhD, MPH**, **AN2** (Consultant, Advisor or Review Panel member)**Zambon** (Advisor or Review Panel member) **Kevin L. Winthrop, MD, MPH**, **Insmed** (Consultant, Grant/Research Support)**Paratek** (Consultant)**RedHill** (Consultant)**Spero** (Consultant) **Kevin L. Winthrop, MD, MPH**, **Insmed** (Consultant, Research Grant or Support)**Paratek** (Consultant)**RedHill Biopharma** (Consultant)**Spero** (Consultant)

1409. Pulmonary Non-tuberculous *Mycobacterium* Infection (PNTMI) and COVID-19: Characterization of the National COVID Collaborative Cohort (N3C)

Carlos E. Figueroa Castro, MD[1]; William Hersh, MD[2]; [1]Medical College of Wisconsin, Milwaukee, Wisconsin; [2]Oregon Health & Science University, Portland, Oregon

N3C RP-1C6E5B

Session: P-80. Tuberculosis and other Mycobacterial Infections

Background. Establishing whether a low-prevalence clinical condition is a risk factor for COVID-19 infection, or serious adverse outcomes, is difficult due to a limited number of patients, and lack of access to patient's data by researchers. The National COVID Collaborative Cohort (N3C), a centralized national data resource to study COVID-19, provides access to structured clinical data derived from electronic health records. As of June 2021, N3C contains data on 6,193,738 patients (2,090,138 with COVID-19, 33.7%) from 55 participating sites (Figure 1). We describe the characteristics of patients with PNTMI based on COVID-19 infection status.

Figure 1

	COVID (N = 2,090,138)	NON-COVID (N = 4,103,600)	OVERALL (N = 6,193,738)
Gender			
Male	951,826	1,826,057	2,777,883
Female	1,133,432	2,274,754	3,408,186
Unknown		2,783	2,783
Age			
0 - 17	195,218	534,149	729,367
18 - 29	400,330	595,930	996,260
30 - 49	629,558	1,124,024	1,753,582
50 - 64	473,244	914,309	1,387,553
65+	361,901	880,655	1,242,556
Unknown	29,887	54,533	84,420
Race			
White	1,126,442	2,703,726	3,830,168
Other	12,744	38,890	51,634
Black or African American	255,942	635,714	891,656
Asian	44,094	125,234	169,328
Pacific Islander	3,796	7,084	10,880
Unknown	587,018	539,355	1,126,373
Ethnicity			
Not Hispanic or Latino	1,348,584	3,162,241	4,510,825
Hispanic or Latino	256,568	448,157	704,725
Unknown	483,065	489,230	972,295

Explore phenotypes for this cohort →

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.

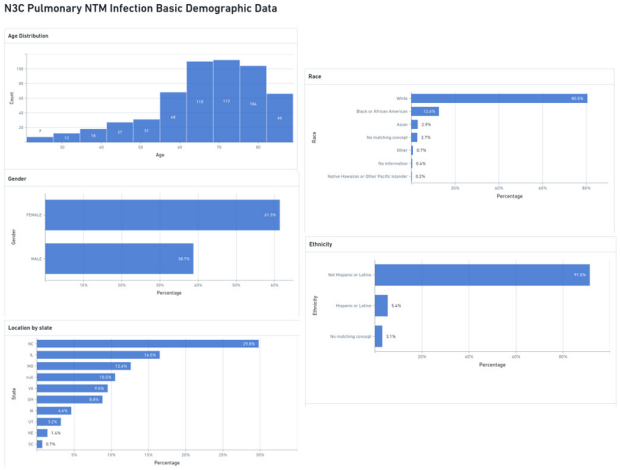

Figure 2. Basic demographic data of pulmonary non-tuberculous Mycobacterium infection phenotype in N3C