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Epidemiology of nontuberculous mycobacteria isolations among central North Carolina residents, 2006–2010[☆]

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Summary *Background:* Nontuberculous mycobacteria (NTM) are environmental mycobacteria associated with a range of infections. Reports of NTM epidemiology have primarily focused on pulmonary infections and isolations, however extrapulmonary infections of the skin, soft tissues and sterile sites are less frequently described.

Methods: We comprehensively reviewed laboratory reports of NTM isolation from North Carolina residents of three counties during 2006–2010. We describe age, gender, and race of patients, and anatomic site of isolation for NTM species.

Results: Among 1033 patients, overall NTM isolation prevalence was 15.9/100,000 persons (13.7/100,000 excluding *Mycobacterium gordonae*). Prevalence was similar between genders and increased significantly with age. Extrapulmonary isolations among middle-aged black males and pulmonary isolations among elderly white females were most frequently detected. Most isolations from pulmonary sites and blood cultures were *Mycobacterium avium* complex;

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rapidly growing NTM (e.g. *Mycobacterium chelonae*, *Mycobacterium fortuitum*) were most often isolated from paranasal sinuses, wounds and skin.

Conclusions: We provide the first characterization of NTM isolation prevalence in the South-eastern United States (U.S.). Variation in isolation prevalence among counties and races likely represent differences in detection, demographics and risk factors. Further characterization of NTM epidemiology is increasingly important as percentages of immunocompromised individuals and the elderly increase in the U.S. population.

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Background

Q2 Nontuberculous mycobacteria (NTM), is a classification group that includes all *Mycobacterium* spp. except *Mycobacterium leprae* and those classified in the *Mycobacterium tuberculosis* complex. These environmental bacteria are isolated from soil, surface waters, water aerosols, and biofilms.^{1–4} Isolation of NTM from the respiratory tract is most often reported among developed countries. Rates of pulmonary NTM isolation vary by subpopulation, geographic area and study, with reports ranging from 1.3 to 22.2/100,000 persons. However, the relationship between isolation in the absence of clinical disease and the progression to disease is poorly characterized.^{5,6} NTM pulmonary infections may be slow to progress to clinical disease and diagnosis, therefore NTM may be isolated from individuals for a relatively long, but variable period of time.⁴ Risk factors for NTM pulmonary disease include: cystic fibrosis, connective tissue disorders, relative immunodeficiency and older age.^{4,7,8} In addition, patients with preexisting lung disease (including but not limited to bronchiectasis, chronic obstructive pulmonary disease, and silicosis) are more susceptible to pulmonary NTM infection.⁹ NTM isolation from extrapulmonary sites are less frequently summarized, and these isolations, particularly those from sterile sites, are likely to represent current disease.²

Reports of NTM isolation and disease are increasing among populations in developed countries.^{4,5,10–14} In the United States (U.S.), NTM diseases are not notifiable with rare exceptions such as extra-pulmonary NTM disease in Oregon.¹⁵ Therefore, population based data are infrequently reported, making it difficult to monitor the epidemiology of NTM over time. We sought to describe the epidemiology of NTM isolation prevalence in three counties within central North Carolina (NC).

Methods

We collected all existing laboratory reports of NTM isolation that occurred during January 1, 2006–December 31, 2010 from all institutions of which we were aware that performed mycobacterial isolations among human biological specimens submitted from Wake, Durham, and Orange counties in NC during the study period. These institutions included hospital-based clinical laboratories, the NC State Laboratory of Public Health, and private clinical laboratories.

However, at one hospital-based clinical laboratory, reports were unavailable for the calendar year 2006 due to a non-searchable laboratory data archive. For this

laboratory, we additionally performed a medical record search using ICD-9-CM codes 031.0–031.9 to identify medical records of patients with NTM diagnoses at the institution during January 1–December 31, 2006. At a second hospital-based clinical laboratory, we were not able to gain access to hospital-based laboratory reports that were generated during 2006–July 2008. However, we collected those few reports that were generated by private clinical laboratories that originated in the institution prior to July 2008, and all reports from that institution that were available from private clinical laboratories during 2006 through the end of the study period. Under the assumption of similar numbers of isolations per institution among study years, we report the average number of reports received during the periods for which data were complete to calculate the estimated number of missing isolation reports.

Laboratory reports included: unique identifiers, date and anatomic site of isolation, species of NTM, age, gender, race and county of residence. For patients with more than one NTM isolation during the study period, only the earliest report that occurred in the study period was included to calculate prevalence rates and descriptive statistics.

Only isolation reports from residents of the three county study area were included. Prevalence rates and 95% confidence intervals (CI) of NTM isolations were calculated as the frequency of individuals with at least one NTM isolation during 2006–2010 divided by the base population of the three counties during this same period and reported per 100,000 persons. Data collected by the U.S. Census Bureau 2010 (www.census.gov) were used to provide a base population for the calculation for each year. Five year period prevalence rates were calculated for the following demographic factors: gender, age groups (i.e., 0–19 years, 20–39 years, 40–59 years, and 60 or more years), race (i.e., White, Black, and all Other races), year of isolation, and county of residence. Categories were compared using the chi-square (χ^2) test, a p-value of 0.05 or less was considered statistically significant. Data analyses were conducted using SAS (version 9.4; SAS Institute, Cary, NC)). **Q3**

NTM were isolated from multiple anatomic locations which were categorized into 1) source categories, and 2) general anatomic sites. Isolate sources were categorized as: 'Pulmonary', 'Sterile site', 'Dermal', 'Catheter', 'Other', and 'Missing/Unknown'. Pulmonary samples originated from the respiratory tract. A Sterile site sample originated from blood, cerebrospinal fluid, pleural fluid, bone marrow, joint fluid, and internal body site specimens obtained from surgery or aspirate from one of the following: lymph node, brain, heart, liver, spleen, vitreous fluid, kidney, pancreas, ovary, and vascular tissue.¹⁶ Dermal isolate sources included

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