

Clinical Chemistry

Trainee Council

PEARLS OF LABORATORY MEDICINE

Non-tuberculous Mycobacteria: Identification and Susceptibility Testing

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Non-tuberculous mycobacteria (NTM)

- **Definition:** all species of mycobacteria other than those in the *M. tuberculosis* complex
- >160 species and subspecies catalogued to date
 - <http://www.bacterio.cict.fr/m/mycobacterium.html>
- Past 15 years: increase in both total number of species and number of species considered to be clinically significant
 - Improved methods for isolation from clinical specimens
 - Increased use of sequencing-based methods
- Opportunistic pathogens in humans (particularly immunocompromised)
- Widely distributed in environment
 - Soil
 - Water (natural and municipal)
- No evidence of human-human or animal-human transmission

NTM clinical disease

- Can cause both asymptomatic infection (colonization) and symptomatic disease in humans
- Various presentations of clinical disease
 - Pulmonary disease (most common)
 - Often associated with structural lung disease (e.g. bronchiectasis, COPD, CF)
 - Can also occur in patients without obvious predisposing factors
 - Lymphadenitis
 - Skin, soft tissue, bone disease
 - Disseminated disease

NTM species most commonly implicated in disease

➤ More common:

- *M. avium* complex (MAC)*
- *M. kansasii*
- *M. abscessus*
- *M. chelonae*
- *M. fortuitum*
- *M. haemophilum*
- *M. marinum*
- *M. scrofulaceum*
- *M. malmoense*
- *M. xenopi*
- *M. celatum*
- *M. ulcerans* (disease-endemic areas)
- *M. leprae* (disease-endemic areas)

➤ Less common:

- *M. genavense*
- *M. smegmatis*
- *M. szulgai*
- *M. simiae*
- *M. mucogenicum*
- *M. immunogenum*
- *M. nonchromogenicum*
- *M. terrae* complex
- *M. asiaticum*

* Most common NTM pathogen in U.S. Includes *M. avium* and *M. intracellulare*.

NTM species: most common associations

➤ Pulmonary Disease

- *M. avium* complex (MAC), *M. abscessus*, *M. kansasii*, *M. malmoense*, *M. xenopi*

➤ Lymphadenitis

- MAC, *M. malmoense*, *M. scrofulaceum*

➤ Disseminated Disease

- MAC, *M. chelonae*, *M. haemophilum*, *M. kansasii*, *M. abscessus*

➤ Skin, Soft Tissue, and Bone Disease

- *M. abscessus*, *M. chelonae*, *M. fortuitum*, *M. marinum*, *M. ulcerans*

➤ Specimen Contaminant

- *M. gordonae* (most common; easily recovered from freshwater, lab faucets, etc.), *M. mucogenicum*, *M. nonchromogenicum*, *M. terrae* complex

Isolating NTM from clinical specimens

- Avoid potential sources of contamination, particularly tap water
- Appropriate clinical specimens:
 - Expecterated or induced sputum (x3), BAL, lung biopsy
 - Body fluid (including stool, urine), abscess fluid, tissue
 - Blood
 - Commercial mycobacterial culture systems
- Specimen processing
 - Manipulations of specimens suspected to contain mycobacteria should be performed either in BSLIII or in BSLII with BSLIII practices
 - Specimens from non-sterile body sites should be digested and decontaminated (NALC-NaOH)
 - 2-5% rate of overgrowth by normal flora is considered optimal

AFB smears

- For primary specimens:
 - Fluorochrome
 - false negatives can occasionally occur with RGM (may be specimen-dependent phenomenon)
 - Kinyoun (carbol fuchsin-based)
 - Ziehl-Neelsen (carbol fuchsin-based)
 - NOT gram stain
- For growth of suspected mycobacteria in culture:
 - Ziehl-Neelsen or Kinyoun
- Semi-quantitative analysis (1+ to 4+)

Culture techniques for NTM recovery

- Cultures should include both liquid and solid media
 - Liquid: higher yield, more rapid results, but more frequently contaminated
 - Media typically contains antibiotics given higher contamination rates
 - Solid: growth rates, colony morphology, separation of mixed species, quantitation
 - LJ (egg-based)
 - Middlebrook 7H10, 7H11 (agar-based)
 - Can add antibiotics (or not) depending on specimen source
- Semiquantitative (0-4+) colony counts recommended
- Some NTMs are fastidious
 - E.g. *M. haemophilum*: media must be supplemented with iron-containing compounds

NTM culture techniques, continued

➤ Temperature

- Most clinically significant NTM grow well at 35-37°C
- *M. chelonae*, *M. haemophilum*, *M. ulcerans*, *M. marinum* grow best at 28-30°C
- All skin, joint fluid, and bone specimens should be cultured at both 28-30°C and 35-37°C
- *M. xenopi* requires higher temperature (40-42°C) for optimal growth

NTM culture techniques, continued

➤ Growth rates in subculture

- “slowly-growing NTM”
 - Most grow in 2-3 weeks on subculture (*MAC*, *M. kansasii*, *M. marinum*)
 - *M. ulcerans* and *M. genovense* can take 8-12 weeks to grow
- “rapidly-growing mycobacteria” (RGM) grow within 7 days on subculture
 - *M. abscessus*, *M. chelonae*, *M. fortuitum*, *M. immunogenum*,
M. smegmatis

➤ Growth rates from primary specimen

- Depend on burden of organism in that specimen
- Liquid media is typically held for 6 weeks and solid media for 8 weeks before being considered culture-negative

Identification of NTM: concepts

- Identify clinical isolates to species level
 - different NTM species have different antimicrobial susceptibility
 - Exception: MAC (differentiation between *M. avium* and *M. intracellulare* is not thought to be clinically significant)
- Context is important. Consider:
 - Clinical setting and host risk factors
 - Pathogenic potential of organism
 - Recovery from multiple specimens or sites
 - Recovery from normally sterile site
 - Quantification of organism
- Communicate with clinician

Identification of NTM: methods

➤ Phenotypic testing

- Growth rate
- Pigmentation
 - Photochromogens, scotochromogens, nonphotochromogens
- Colony morphology

➤ Biochemical testing:

- Time consuming, labor-intensive
- Does not identify many of the newly described NTM species

Identification of NTM: methods

- Molecular probes
 - *MAC, M. kansasii, M. goodii*
- High-Performance Liquid Chromatography (HPLC)
 - Analysis of mycobacterial cell wall fatty acids (mycolic acids)
 - Can be used in combination with or in place of biochemical/molecular methods
 - Can be performed using growth on solid media, AFB-positive broth cultures, or even sediments from smear-positive specimens
 - Not definitive for some species of slowly-growing NTM, and not optimal for distinguishing all species of RGM

Identification of NTM: methods

➤ DNA target sequencing

- PCR-based amplification of genomic DNA target, followed by sequencing of amplicon
- 16S rRNA gene
 - Present in all prokaryotes
 - Contains highly conserved AND variable sequences
- Alternative/additional targets for identification of closely related mycobacterial species: *rpoB*, *hsp65* (also ITS, 23S rRNA gene, *gyrB*, *dnaA*, *recA*, *secA1*)

➤ PCR Restriction Enzyme Analysis (PRA)

- PCR target (e.g. *hsp65* gene), restriction enzyme digest, gel electrophoresis, analysis

➤ MALDI-TOF MS

Antimicrobial Susceptibility Testing (AST) for NTM: concepts

- Role of AST of NTM for guiding patient management remains controversial
- Correlation between in vitro susceptibility and clinical response varies for different NTM species
- AST should be performed on “clinically significant” isolates that exhibit:
 - Variability in susceptibility to clinically useful antimicrobial agents and/or
 - Significant risk of acquired mutational resistance to one or more of these agents
- Optimal susceptibility breakpoints and testing methods remain controversial for many NTM drug-bug combinations
- Clinician needs to be aware of these limitations

Antimicrobial susceptibility testing of NTM: specifics

- Standard is broth microdilution
- MAC
 - Primary drugs: macrolides (test clarithromycin--predicts azithromycin susceptibility).
 - Secondary drugs: moxifloxacin, linezolid (tentative breakpoints)
 - ? EMB, Rifampin, rifabutin, amikacin, streptomycin (breakpoints not established; data emerging for amikacin)
- *M. kansasii*
 - Primary drugs: rifampin, clarithromycin
 - secondary drugs: amikacin, ciprofloxacin, ethambutol, isoniazid, linezolid, moxifloxacin, rifabutin, streptomycin, sulfonamides (only some have breakpoints)
- *M. marinum*
 - Routine susceptibility testing not recommended; treat empirically and test only if patient fails therapy
- RGM
 - Testing panel includes carbapenems, aminoglycosides, quinolones, clarithromycin, ceftazidime, doxycycline, linezolid, TMP-SMX, all with breakpoints
 - Testing should include at least two readings for clarithromycin (day 3 and day 14) to detect inducible macrolide resistance due to presence of *erm* gene

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