



# Laboratory Diagnosis and Susceptibility Testing of Nontuberculous Mycobacteria: The Latest Tips for Clinical Microbiologists

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# LABORATORY DIAGNOSIS OF NTM

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## Numbers of NTM Exploding

**1880–1978 = 46 species (98 years)**

**1979–1995 = 23 species (16 years)**

**1996–2019 = 123 species (~23 years)**

**Total ~ 192 species (September 2019)**

**93 Slow Growers, 99 Rapid Growers**

**More species ID within the past 25 years than  
the >100 years previously!**

Enzeby 2019.

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## Slowly Growing Mycobacteria

**(SGM)**

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## Isolation of the Clinically Significant SGM NTM

- Generally grow at 35° C, >7 days after subculture
- Grows on Middlebrook 7H10/11 but not routine media
- Do not require CO<sub>2</sub>

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## MAC (11 Species Currently)

|                            |                              |
|----------------------------|------------------------------|
| <i>M. arosiense</i>        | <i>M. marseillense</i>       |
| <i>M. avium</i>            | <i>M. timonense</i>          |
| <i>M. bouchedurhonense</i> |                              |
| <i>M. chimaera</i>         | <i>M. vulneris</i>           |
| <i>M. colombiense</i>      | <i>M. yongonense</i>         |
| <i>M. intracellulare</i>   | <i>M. paraintracellulare</i> |

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## ***M. simiae* complex**

***M. europaeum***  
***M. sherrisii***  
***M. simiae***  
***M. stomatepiae* (fish)**  
***M. triplex***

## ***M. kansasii* complex**

***M. kansasii***  
***M. persicum***  
***M. innocens***  
***M. pseudokansasii***  
***M. attenuatum***

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## ***M. terrae* complex**

***M. arupense***                      ***M. minnesotense***  
***M. engbaekii***                      ***M. nonchromogenicum***  
***M. heraklionense***              ***M. senuense***  
***M. hiberniae***                      ***M. terrae***  
***M. kumamotonense***      ***M. virginense***  
***M. longobardum***              ***M. algericum* (goat/fish)**

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## ID of Clinically Significant NTM

- Phenotypic (except pigment, growth)/Bios insufficient
- HPLC – ID not definitive for most species
- MAC ID by probe (except not for “MAC-X”)
- Other slowly growing NTM usually ID by partial 16S sequence
  - DNA Line Probe assays 16S-23S rRNA spacer region and 23S rRNA  
Multiple (approx. 20) species/groups on one strip assay

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## Molecular Methods of ID of NTM

### Nucleic Acid Probes

INNO LiPA (Innogenetics; Ghent, Belgium) reverse hybridization

16S-23S ITS (internal transcribed spacer region)

GenoType (Hain Lifescience GmbH, Nehren, Germany ) – 23S rRNA gene

- Identification of a large number of species by single PCR
- Good specificity and sensitivity but some cross reactions

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## Molecular Methods of ID of NTM (cont'd)

### 16S rRNA Sequence Analysis

#### Background

- Routine sequencing of 1500 NT sequence of the 16S rRNA gene not feasible for most labs.
- 500 bp – Commercially available method
- Many NTM require multi-gene sequencing (e.g., *rpoB*, *erm*)
- Supplementation with in-house database

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## ID of Clinically Significant NTM (cont'd)

Same 16S rRNA gene partial sequence (1<sup>st</sup> 500 bp)

- *M. kansasii* / *M. gastri*
- *M. marinum* / *M. ulcerans*
- Other species generally ID by 16S rRNA gene sequence

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## Matrix-Assisted Laser Desorption Ionization Time of Flight (MALDI-TOF)

- Rapid testing analysis of protein spectra
- Requires inactivation of organisms
- Requires extraction-purification of protein
- Less expensive per test than sequencing
- Identifies large number of NTM species  
~60% ID to highest taxonomic level for both manufacturers.

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## MALDI Can Not Differentiate

- *M. intracellulare* / *chimaera*
- *M. marinum* / *shottsii* / *pseudoshottsii*
- *M. terrae* complex
- *M. goodii* / *paragoodii*

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## MALDI Can Not Differentiate (cont'd)

**MAC (*M. avium*, *M. intracellulare*,  
*M. colombiense* / *chimaera*,  
*M. vulneris*, *M. paraintracellulare*,  
*M. yongonense*, *M. timonense*,  
*M. arosiense*, *M. marseillense*,  
*M. bouchederhonense*)**

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## Rapidly Growing Mycobacteria

### (RGM)

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## Isolation of the Clinically Significant RGM

- Generally 30° C, <7 days after subculture
- Agar-based culture media: Middlebrook 7H10/7H11
- Grow on routine culture media (Blood, Chocolate, TSA)
- Do not require CO<sub>2</sub>
- New media (RGM) not yet commercially available ↑ yield *M. abscessus* ↓ contamination

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## Identification of RGM

- Phenotypic testing/Bios not useful (except growth rate/pigment/colony type)
- HPLC generally only for group ID – not species specific
- AST patterns helpful but not confirmatory

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## Rapidly Growing Mycobacteria

### Group 1

- **Non-pigmented Pathogens**

- M. fortuitum* group

- M. porcinum*

- M. brisbanense*

- M. houstonenense*

- M. neworleansense*

- M. boenickei*

- M. septicum*

- M. fortuitum*

- M. senegalense/*

- M. peregrinum*

- conceptionense*

Schinsky, et al., JSEM 2004

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## Rapidly Growing Mycobacteria

### Group 2

- **Non-pigmented Pathogens**

- M. abscessus* complex

- M. abscessus* subsp. *abscessus*

- M. abscessus* subsp. *massiliense*

- M. abscessus* subsp. *bolletii*

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## Rapidly Growing Mycobacteria

### Group 2 (cont'd)

#### *M. chelonae* complex

*M. chelonae*

*M. immunogenum*

\**M. salmoniphilum*, *M. franklinii*

\*Fish pathogen

Adekambi, et al., J. Clin. Microbiol. 2003  
Brown-Elliott, et al., CMR, 2002  
Adekambi, et al., J. Clin. Microbiol. 2004  
Whipps, et al., IJSEM, 2007  
Adekambi, et al., IJSEM, 2006  
Leao, et al., J. Clin. Microbiol. 2009  
Simmon, Brown-Elliott, EID, 2010

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## Rapidly Growing Mycobacteria

### Group 3

- **Non-pigmented Pathogens**

*M. mucogenicum* group (formerly  
*M. chelonae*-like Organism)

*M. mucogenicum*

*M. aubagnense*

*M. phocaicum*

Adekambi, et al., IJSEM, 2006  
Springer, et al., J. Clin. Microbiol., 1995.

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## Rapidly Growing Mycobacteria

### Group 4

- **Non-pigmented Pathogens**

*M. mageritense/wolinskyi* group

### Group 5

- **Late Pigmenting Pathogens**

*M. smegmatis* group

- *M. smegmatis* (formerly *M. smegmatis* sensu stricto)
- *M. goodii*

Brown BA, et al., IJSB, 1999.

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## Rapidly Growing Mycobacteria

### Group 6

- **Early Pigmenting Species**

|                          |                               |
|--------------------------|-------------------------------|
| <i>M. bacteremicum</i> * | <i>M. monacense</i> *         |
| <i>M. canariasense</i> * | <i>M. neoaurum</i> *          |
| <i>M. cosmeticum</i> *   | <i>M. thermoresistibile</i> * |
| <i>M. elephantis</i> *   | <i>M. flavescens</i>          |
| <i>M. iranicum</i> *     | <i>M. phlei</i>               |
| " <i>M. lacticola</i> "* | <i>M. psychrotolerans</i>     |
|                          | <i>M. vaccae</i>              |

\* **Proven pathogens**

Tortoli, E., FEMS Immunol. Med Microbiol. 2006.  
Shojaei, H., et al. IJSEM. 2012.

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## Molecular Methods of ID of RGM

### 16S rRNA Sequence Analysis (500 bp)

- **Can not discriminate:**
  - *M. chelonae* from *M. abscessus*
  - *M. houstonense* from human isolates of *M. senegalense*
  - *M. peregrinum* from *M. septicum*

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## Molecular Methods of ID of RGM (cont'd)

- *M. chelonae*, *M. abscessus* require sequencing outside first 500 bp as they are same in those regions  
(4 bp difference in complete 16S)
- RGM except for *M. chelonae*, *M. abscessus* contain two copies of 16S rRNA operon
- 1<sup>st</sup> 500 bp 16S sequence not definitive for ID of most *M. fortuitum* group

Tortoli, Clin. Microbiol. Rev. 2003.

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## Molecular Methods of ID of RGM (cont'd)

### Sequencing Secondary Gene Targets

- Heat shock protein (*hsp65*)
- *rpo*  $\beta$  gene
- 16S to 23S rRNA internal transcribed spacer (ITS)
- 32 kDA protein
- Superoxide dismutase gene (*sod*)
- *dnaJ* gene
- *secA* 1 gene
- *recA* gene
- Short sequence analysis of 30 bp in Hypervariable Region

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## MALDI can not differentiate:

- *M. abscessus* subsp. *massiliense*, subsp. *abscessus*, subsp. *bolletii*
- Species within *M. fortuitum* group and *M. mucogenicum* group
- *M. chelonae/salmoniphilum*

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Brown-Elliott, et al., Am. J. Clin. Pathol. 2019

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# ANTIMICROBIAL SUSCEPTIBILITY TESTING

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**CLSI M24, 3<sup>rd</sup> Ed. 2018**  
**CLSI M62, 1<sup>st</sup> ED. 2018**

## Guidelines for AST of NTM

- **Slowly growing NTM**
  - **MAC**
  - ***M. kansasii***
  - ***M. marinum***
- **Rapidly Growing Mycobacteria**

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## Indications for Performing Antimycobacterial Susceptibility Tests (AST)

- Clinically significant isolates
  - Blood, sterile body fluids
  - Tissue
  - Skin/soft tissue lesions
  - Sputum/Respiratory isolates in large numbers, smear (+), or multiple positives
- Failure to eradicate RGM from site after 6 months of appropriate treatment necessitates repeat species confirmation and/or AST

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## Susceptibility Testing: CLSI Guidelines

- Broth microdilution “Gold standard”
- Match 0.5 McFarland turbidity standard
- 2-fold serial dilutions in CAMHB<sub>+</sub> OADC in 96-well microtiter plates
- Organism concentration ~ 10<sup>5</sup> CFU/mL
- Incubation 30° C / 3 days/room air (RGM)  
35° C / 7 days/room air (SGM)

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# Antimicrobial Susceptibility

## Testing (AST) of SGM

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## AST of MAC

- ***In vitro* MIC data for EMB, RMP, RBT show poor correlation with clinical response**
- **Insufficient data using moxifloxacin, linezolid to establish correlation of *in vitro* results to clinical response**
- **Azithromycin is technically difficult to test, so use clarithromycin as “Class drug”**

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CLSI, M24 3<sup>rd</sup> ed., 2018.

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## MAC Amikacin Susceptibility

- New study shows correlation of amikacin MICs with clinical response
- Amikacin MICs >64 µg/mL are associated with mutation in 16S rRNA gene and prior amikacin Rx (position 1408 A→G)
- Amikacin MICs ≤64 µg/mL not associated with mutation in 16S rRNA gene

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## Antimicrobial Susceptibility Breakpoints for *Mycobacterium avium* complex

| Antimicrobial                | MIC (µg/mL) |    |      |
|------------------------------|-------------|----|------|
|                              | S           | I  | R    |
| <b>First Line</b>            |             |    |      |
| Clarithromycin               | ≤8          | 16 | ≥32  |
| Amikacin (IV)                | ≤16         | 32 | ≥64  |
| Amikacin (liposomal inhaled) | ≤64         |    | ≥128 |
| <b>Second Line</b>           |             |    |      |
| Moxifloxacin                 | ≤1          | 2  | ≥4   |
| Linezolid                    | ≤8          | 16 | ≥32  |

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## AST of *M. kansasii*

- Routine testing of Rifampin (RMP) and clarithromycin (CLARI) only
- RMP susceptibility  $\leq 1 \mu\text{g/mL}$
- If RMP susceptible, will be rifabutin susceptible (HIV patients on protease inhibitors)
- Test 2° agents only if RMP resistant (treatment failure generally seen only with RMP resistance; testing other TB drugs can be problematic)
- Repeat MICs at 3 months if still culture (+)

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## Antimicrobial Agents and Breakpoints for Testing Slowly Growing NTM other than MAC

| Antimicrobial   | MIC ( $\mu\text{g/mL}$ ) |    |           |
|---|--------------------------|----|-----------|
|   | S                        | I  | R         |
| Clarithromycin*   | $\leq 8$                 | 16 | $\geq 32$ |
| Rifampin*   | $\leq 1$                 | –  | $\geq 2$  |
| Amikacin  | $\leq 16$                | 32 | $\geq 64$ |
| Ciprofloxacin   | $\leq 1$                 | 2  | $\geq 4$  |
| *First Line for <i>M. kansasii</i> (RMP <sup>s</sup> )<br>Note EMB removed<br>CLSI M62 1 <sup>st</sup> ed. 2018 |                          |    |           |

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## Antimicrobial Agents and Breakpoints for Testing Slowly Growing NTM other than MAC (cont'd)

| Antimicrobial           | MIC ( $\mu\text{g/mL}$ ) |       |             |
|-------------------------|--------------------------|-------|-------------|
|                         | S                        | I     | R           |
| Doxycycline/Minocycline | $\leq 1$                 | 2 - 4 | $\geq 8$    |
| Linezolid               | $\leq 8$                 | 16    | $\geq 32$   |
| Moxifloxacin            | $\leq 1$                 | 2     | $\geq 4$    |
| Rifabutin               | $\leq 2$                 | –     | $\geq 4$    |
| <b>TMP-SMX</b>          | $\leq 2/38$              | –     | $\geq 4/76$ |

CLSI M62 1<sup>st</sup> ed. 2018

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## AST of Other slowly growing NTM

- Includes Primary and Secondary agents as for RMP<sup>R</sup>
  - *M. kansasii*
    - *M. simiae*
    - *M. malmoense*
    - *M. xenopi*
    - Too few isolates to recommend specific method of AST

CLSI M24 3<sup>rd</sup> ed., 2018.

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## Fastidious Species of NTM

### No current standardized AST method

#### *M. haemophilum*

Requires hemin/iron compounds

Agar disk elution/"X" strips

Broth microdilution/ferric ammonium citrate

Extended incubation 2-3 weeks 28-30°C

Usually S to AMK, RMP, SXT, CLARI, LZD, R to EMB, V to DOXY/MINO, CIP/MOXI

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## Fastidious Species of NTM

### No current standardized AST method

#### *M. genavense*

Requires Mycobactin J supplementation

Extended incubation  $\geq$  6 weeks

Treatment multidrug ~ MAC

#### *M. ulcerans*

Extended incubation 4-6 weeks

Clarithromycin useful for treatment

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# Antimicrobial Susceptibility

## Testing (AST) of RGM

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### AST OF RGM CLSI Reporting: RGM MICs

- Amikacin with *M. abscessus* complex
- If MIC  $\geq 64$   $\mu\text{g/mL}$  – repeat/confirm
- Ciprofloxacin / Levofloxacin MICs are interchangeable but both are less active *in vitro* than moxifloxacin
- Sulfamethoxazole/TMP-SMX MICs are read at 80% inhibition

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## AST OF RGM CLSI Reporting: RGM MICs (cont'd)

- Doxycycline / Minocycline MICs are interchangeable
- Imipenem with *M. fortuitum* group  
If MIC >8 µg/mL – repeat / confirm  
Report MIC with *M. abscessus/chelonae*
- Tobramycin with *M. chelonae*  
If MIC >4 µg/mL – repeat / confirm ID

CLSI M24 3<sup>rd</sup> ed., 2018

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## Erythromycin methylase (*erm*) gene

- The major mechanism of macrolide resistance in *M. abscessus* is a chromosomal inducible *erm* gene [*erm* (41)]
- Phenotypic detection of inducible macrolide resistance in the presence of the drug requires extended incubation (up to 14 days)

Nash, et al, AAC, 2009; Brown-Elliott, et al., JCM 2015.

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## MACROLIDE RESISTANCE IN RGM

- rRNA erythromycin methylase genes
  - Confers inducible macrolide resistance
    - erm*(38) *M. smegmatis* group
    - erm*(39) *M. fortuitum* group
    - erm*(40) *M. mageritense*/*M. wolinskyi* group
    - erm* (41) *M. abscessus*
    - No *erm* gene in *M. chelonae*,  
*M. senegalense*, *M. peregrinum*
  - 23S rRNA mutation for macrolide resistance
- (Resistance at 3 days)

Nash, et al., Antimicrob. Agents Chemother. 2009.

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## *M. abscessus* Taxonomy

### *M. abscessus* complex

#### subsp. *abscessus*

- 80% of all clinical isolates (U.S.)
- 15% have inactive *erm* gene

#### subsp. *massiliense*

- 15% all clinical isolates (U.S.)
- 100% truncated (non-functional *erm* gene)

#### subsp. *bolletii*

- Rare in U.S.; Clari<sup>R</sup> (functional *erm* gene)

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**MAB30\_Erm\_Consensus**  
**ATCC19977\_erm\_Consensus**

```
GACCGGGGCCTTCTTCGTGATCTATCGAAACCAGTTGCATGCCCCGATATCTTTGGAGCA
GACCGGGGCCTTCTTCGTGATCTATCGAAACCAGTTGCATGCCCCGATATCTTTGGAGCA
*****

TGGGCATATTCATGATGGTGTGCTGCGTGTCCGGCCAACGGTTCGCGACGCCAGCGGGGC
TGGGCATATTCATGATGGTGTGCTGCGTGTCCGGCCAACGGTTCGCGACGCCAGTGGGGC
*****

M.massiliense_erm_Consensus
ATCC19977_erm_Consensus


TGGTATCAGCTCGCTGATGACTGGGCGGC - -GGATCGTTCGCCGAATCCGGTTTTCGTTCA
TGGTATCCGCTCACTGATGACTGGGCGGC GCGGATCGTTCGCCGAATCCGGTGTTCGCTCA
*****

GGGGAGTTTCGTTTGTGAATCTGGGCGCAGGGCACGGCGCGCTGACGGCACATCTGGTTGCC
GGGGAGTTTCGTTTGTGGATCTGGGCGCAGGACACGGCGCGCTGACGGCACATCTGGTTGCC
*****

GCTG-----
GCTGGTGC CAGGGTGTAGCCGTCGAGCTGCATCCGGGGCGGGGCTCGACACCTTCGTTCA
****

CGGTTTGCCGAGGAAGATGTCCGGATAGCGGAAGCGGACCTGCTCGCCTTCCGGTGGCCG
-----
CGACGGCCATTTCGSGTGGTGGCGAGCCCCGCCCTACCAAGTCACCAGCGCACTGATACGG
-----
AGTCTCTTGACGCCGGAATCCCGGCTGCTGGCTGCCGACCTGGTGTCTGCAGCGCGGGGCT
-----
GTGCACAAACATGCSAAGCGAGCACCTGTTTCGCCATTGGAGCGCTACGGGCCGGAATCACA
*****
```

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## Recommendation for Molecular Clarithromycin Susceptibility Testing

- Perform *erm* gene sequence
- If isolate has no functional *erm* gene (*M. chelonae*, *M. abscessus* subsp. *massiliense*, *M. immunogenum*, *M. mucogenicum*, *M. peregrinum*, *M. senegalense*), 14d incubation not necessary. (Macrolide S)
- If isolate has functional *erm* gene, extended incubation not needed. (Macrolide R)

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## Recommendation for Extended Clarithromycin Susceptibility Testing

- **CLSI recommends reporting resistance upon day of occurrence (3-14d)**
- **3 day resistance implies mutational resistance (Confirm by 23S rRNA gene mutation)**

CLSI 3<sup>rd</sup> ed., 2018.

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## 23S rRNA Gene

- **Macrolide resistance at 3d**
- **“*rrl*” mutations = mutational macrolide resistance which involves single point mutation (methylation) in peptidyl transferase region (Domain V –where macrolides bind to ribosome) at adenine position 2058 (38%) or 2059 (62%) in the 23S rRNA gene.**

Wallace, et al., AAC 1996; 40:1676-1681.

Nash, et al., AAC, 2009.

Brown-Elliott, et al., JCM, 2015.

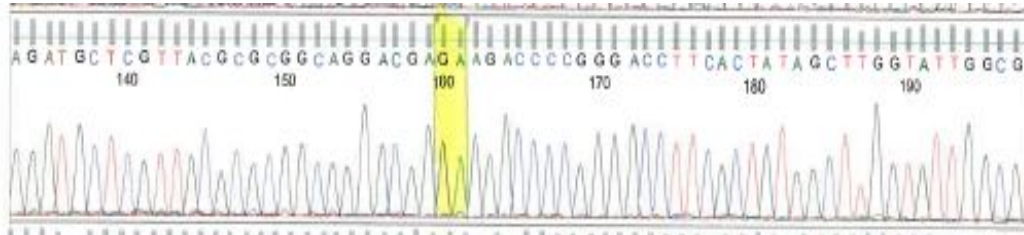
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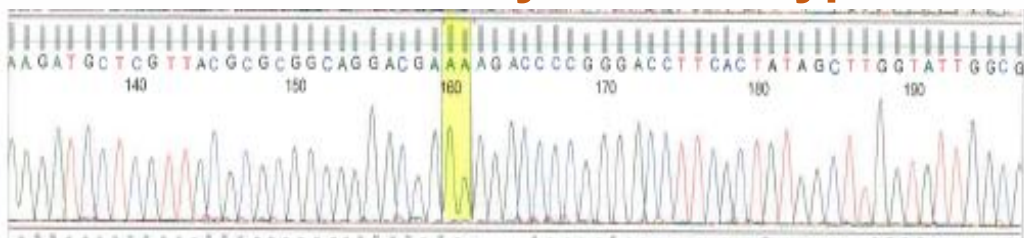
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## Clarithromycin Mutation A – G in 23S



## Clarithromycin Wild Type



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| Broth Microdilution MIC Breakpoints (µg/mL) for RGM |  |              |           |
|---|--|--------------|-----------|
| Antimicrobial                                       | Susceptible                            | Intermediate | Resistant |
| Amikacin  | ≤16                                    | 32           | ≥64       |
| Cefoxitin   | ≤16                                    | 32-64        | ≥128      |
| Cipro/Levofloxacin                                  | ≤1                                     | 2            | ≥4        |
| Clarithromycin                                      | ≤2                                     | 4            | ≥8        |
| Doxy/Minocycline                                    | ≤1                                     | 2 - 4        | ≥8        |
| Imipenem/Meropenem                                  | ≤4                                     | 8 - 16       | ≥32       |
| Linezolid   | ≤8                                     | 16           | ≥32       |
| Moxifloxacin  | ≤1                                     | 2            | ≥4        |
| TMP-SMX   | ≤2/38                                  | –            | ≥4/76     |
| Tobramycin  | ≤2                                     | 4            | ≥8        |
| CLSI M62 1 <sup>st</sup> ed., 2018                  | Tigecycline added without breakpoints. |              |           |

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## Tigecycline

- **First glycylycycline used for NTM**
- **No tigecycline breakpoints established**
- **Almost all RGM  $MIC_{50} \leq 0.12 \mu\text{g/mL}$ ;  $MIC_{90} \leq 0.25 \mu\text{g/mL}$  including Doxycycline/ Minocycline – resistant isolates**
- **Slowly growing NTM generally resistant**

Wallace, Brown-Elliott, et al., AAC, 2002.

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## CLSI: Caveats for Reporting MICs of NTM

- **If results of an MIC for an organism are not as expected for that species, the MIC should be repeated.**
- **If repeat results are still in the unexpected range, the isolate should be sent to a qualified reference lab for re-testing.**

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## Susceptibility Testing Caveats (cont'd)

- **If a laboratory does not handle a sufficient number of isolates to maintain proficiency, referral to a qualified reference laboratory is recommended.**

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