Phenotypic and molecular characterization of quinolone resistance in *Mycobacterium abscessus* subsp. *bolletii* recovered from postsurgical infections

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Several outbreaks of infections caused by rapidly growing mycobacteria (RGM) were reported in many Brazilian states (2032 notified cases) from 2004 to 2010. Most of the confirmed cases were mainly associated with *Mycobacterium massiliense* (recently renamed as *Mycobacterium abscessus* subsp. *bolletii*) BRA100 clone, recovered from patients who had undergone invasive procedures in which medical instruments had not been properly sterilized and/or disinfected. Since quinolones have been an option for the treatment of general RGM infections and have been suggested for therapeutic schemes for these outbreaks, we evaluated the *in vitro* activities of all generations of quinolones for clinical and reference RGM by broth microdilution, and analysed the peptide sequences of the quinolone resistance determining regions (QRDRs) of GyrA and GyrB after DNA sequencing followed by amino acid translation. Fifty-four isolates of *M. abscessus* subsp. *bolletii*, including clone BRA100, recovered in different states of Brazil, and 19 reference strains of RGM species were characterized. All 54 *M. abscessus* subsp. *bolletii* isolates were resistant to all generations of quinolones and showed the same amino acids in the QRDRs, including the Ala-83 in GyrA, and Arg-447 and Asp-464 in GyrB, described as being responsible for an intrinsic low level of resistance to quinolones in mycobacteria. However, other RGM species showed distinct susceptibilities to this class of antimicrobials and patterns of mutations contrary to what has been traditionally defined, suggesting that other mechanisms of resistance, different from *gyrA* or *gyrB* mutations, may also be involved in resistance to high levels of quinolones.

INTRODUCTION

Rapidly growing mycobacteria (RGM) are common in the natural environment, especially in water sources, and may contaminate medical solutions and equipment (Brown-Elliott & Wallace, 2002). RGM have emerged as important human pathogens, and have been responsible for an
increasing number of health-care-associated infections (Brown-Elliott & Wallace, 2002; Cardoso et al., 2008; De Groote & Huitt, 2006; Duarte et al., 2009; Phillips & von Reyn, 2001; Viana-Niero et al., 2008; Wallace et al., 1998).

The species *Mycobacterium massiliense* was first described in 2004 (Adékambi et al., 2004) and it has been responsible for several outbreaks of wound infections related to medical procedures in many states of Brazil (Cardoso et al., 2008; Duarte et al., 2009; Viana-Niero et al., 2008). A taxonomic note has been recently published by Leão et al. (2011) reclassifying *Mycobacterium massiliense* and *Mycobacterium bolletii* as belonging to the same subspecies of *M. abscessus*, namely *Mycobacterium abscessus* subsp. *bolletii* as suggested by Sampaio (2010). This taxonomic note also reclassifies the previous *Mycobacterium abscessus* as *M. abscessus* subsp. *abscessus*.

The largest epidemiological event associated with RGM in Brazil occurred between 2006 and 2007, when 1051 notified possible cases of postsurgical infections were spread around 63 hospitals in the state of Rio de Janeiro. During this epidemic, isolates belonging to a single clone of *M. abscessus* subsp. *bolletii* (previously named *M. massiliense*), designated BRA100, showed highly similar patterns by PFGE to those recovered in previous outbreaks in a few Brazilian states (Duarte et al., 2009). Randomly selected isolates showed resistance to ciprofloxacin (a second-generation fluoroquinolone), cefoxitin and doxycycline (Duarte et al., 2009). Furthermore, moxifloxacin (a fourth-generation fluoroquinolone with strong activity against *Mycobacterium fortuitum* group (Brown-Elliott & Hooper, 1989; Li et al., 2004; Yew et al., 1994)). Since topoisomerase IV has in strains with acquired resistance to quinolones in mycobacteria (Cambau et al., 1994; Von Groll et al., 2009; Guillemin et al., 1995, 1998; Revel et al., 1994; Takiff et al., 1994; Wang et al., 2007) and seem to play a key role in the drug–enzyme interaction. Preliminary studies reported intrinsic resistance to quinolones in mycobacterial species due to the presence of the residues Ala-83 in *GyrA*, and Arg-447 and Asn-464 in *GyrB* (Guillemin et al., 1998), which differ from the residues Ser-83 in *GyrA*, and Lys-447 and Ser-464 in *GyrB*, found in more susceptible species such as *E. coli* (Yoshida et al., 1990, 1991).

Due to the lack of data on the susceptibility of *M. abscessus* subsp. *bolletii* and some other RGM species to drugs, the aims of this study were to perform the phenotypic and molecular characterization of quinolone susceptibility of clinical strains of *M. abscessus* subsp. *bolletii* and other RGM species by determining the MIC of six quinolones (comprising all quinolone generations), including moxiﬂoxacin, and to correlate it with amino acid variations in the QRDRs of *GyrA* and *GyrB*.

**METHODS**


**Quinolone susceptibility testing.** The susceptibility of all isolates to six quinolones, nalidixic acid (first generation), ciprofloxacin, ofloxacin and levofloxacin (second generation),sparfloxacin (third generation) and moxifloxacin (fourth generation) (all from Sigma-Aldrich) was determined by broth microdilution as recommended by the Clinical Laboratory Standards Institute (CLSI) (CLSI, 2011).
**Quinolone resistance in rapidly growing mycobacteria**

**Table 1.** Interpretative criteria for MICs for *Enterobacteriaceae*, *Staphylococcus* spp. and *Streptococcus pneumoniae* (CLSI, 2010)

<table>
<thead>
<tr>
<th>Antimicrobial agent</th>
<th>MIC (µg ml⁻¹)</th>
<th>Enterobacteriaceae</th>
<th>Staphylococcus spp.</th>
<th>Streptococcus pneumoniae</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>S*</td>
<td>I</td>
<td>R</td>
<td>S</td>
</tr>
<tr>
<td>Nalidixic acid</td>
<td>≤ 16</td>
<td>–</td>
<td>≥ 32</td>
<td>–</td>
</tr>
<tr>
<td>Ofloxacin</td>
<td>≤ 2</td>
<td>4</td>
<td>≥ 8</td>
<td>≤ 1</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>≤ 1</td>
<td>2</td>
<td>≥ 4</td>
<td>≤ 1</td>
</tr>
<tr>
<td>Levofloxacin</td>
<td>≤ 2</td>
<td>4</td>
<td>≥ 8</td>
<td>≤ 1</td>
</tr>
<tr>
<td>Sparfloxacin</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>≤ 0.5</td>
</tr>
<tr>
<td>Moxifloxacin</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>≤ 0.5</td>
</tr>
</tbody>
</table>

*S, susceptible; I, intermediate; R, resistant.

**Table 2.** MIC patterns of six quinolones for 54 *M. abscessus* subsp. *bolletii* clinical isolates

<table>
<thead>
<tr>
<th>Antimicrobial agent</th>
<th>MIC (µg ml⁻¹)</th>
<th>Range</th>
<th>Mode*</th>
<th>MIC₉₀ †</th>
<th>MIC₉₀ ‡</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nalidixic acid</td>
<td>–</td>
<td>&gt;2048</td>
<td></td>
<td>&gt;2048</td>
<td>&gt;2048</td>
</tr>
<tr>
<td>Ofloxacin</td>
<td>&gt;128–32</td>
<td>128</td>
<td>128</td>
<td>&gt;128</td>
<td>&gt;128</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>&gt;32–8</td>
<td>16</td>
<td>16</td>
<td>&gt;32</td>
<td>&gt;32</td>
</tr>
<tr>
<td>Levofloxacin</td>
<td>&gt;128–16</td>
<td>64</td>
<td>64</td>
<td>&gt;128</td>
<td>&gt;128</td>
</tr>
<tr>
<td>Sparfloxacin</td>
<td>&gt;128–32</td>
<td>128</td>
<td>128</td>
<td>&gt;128</td>
<td>&gt;128</td>
</tr>
<tr>
<td>Moxifloxacin</td>
<td>32–8</td>
<td>16</td>
<td>16</td>
<td>32</td>
<td>32</td>
</tr>
</tbody>
</table>

*The value that occurred most frequently among the isolates tested.
†The MIC capable of preventing the growth of 50% of the isolates.
‡The MIC capable of preventing the growth of 90% of the isolates.

**Sequence analysis.** The sequences obtained were analysed with BioEdit Sequence Alignment Editor version 7.0.5.1 and compared with those deposited in the GenBank database by using BLAST (http://www.ncbi.nlm.nih.gov/BLAST). The phylogenetic tree was constructed using MEGA version 4.1. *M. tuberculosis* strain ATCC 25618 (H37Rv) was included as reference for sequence alignment and phylogenetic analysis.

**RESULTS**

**Quinolone susceptibility testing**

All 52 clinical isolates showed >85% similarity among the patterns obtained by PFGE, and were named as belonging to *M. abscessus* subsp. *bolletii* BRA100 clone based on the criteria of Duarte et al. (2009). These isolates, as well as the two non-clonal ones (obtained from sputa) showed high but not identical MICs for all quinolones tested (range from 8 to >2048 µg ml⁻¹). The highest MICs were for nalidixic acid (Tables 2 and 3).

The quinolone susceptibility testing among reference strains showed variable susceptibility patterns. Considering the
Table 3. Correlation between the MICs of quinolones against 19 reference strains of RGM and the amino acid residue at position 83 in the QRDR in the A subunit of DNA gyrase

<table>
<thead>
<tr>
<th>Species</th>
<th>Representative strain</th>
<th>MIC (µg ml⁻¹)*</th>
<th>Amino acid 83† in Gyra QRDR</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>NAL</td>
<td>OFX</td>
</tr>
<tr>
<td>Susceptible‡</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>M. aichense</em></td>
<td>ATCC 27280</td>
<td>16</td>
<td>1</td>
</tr>
<tr>
<td><em>M. aurum</em></td>
<td>ATCC 23366</td>
<td>4</td>
<td>≤0.25</td>
</tr>
<tr>
<td><em>M. chelonae</em></td>
<td>ATCC 35752</td>
<td>256</td>
<td>1</td>
</tr>
<tr>
<td><em>M. chitae</em></td>
<td>ATCC 19627</td>
<td>1024</td>
<td>2</td>
</tr>
<tr>
<td><em>M. chubuense</em></td>
<td>ATCC 27278</td>
<td>4</td>
<td>≤0.25</td>
</tr>
<tr>
<td><em>M. flavescens</em></td>
<td>ATCC 14474</td>
<td>2</td>
<td>≤0.25</td>
</tr>
<tr>
<td><em>M. fortuitum</em></td>
<td>ATCC 6841</td>
<td>64</td>
<td>≤0.25</td>
</tr>
<tr>
<td><em>M. neoaurum</em></td>
<td>ATCC 25795</td>
<td>2</td>
<td>≤0.25</td>
</tr>
<tr>
<td><em>M. parafortuitum</em></td>
<td>ATCC 19686</td>
<td>16</td>
<td>≤0.25</td>
</tr>
<tr>
<td><em>M. phlei</em></td>
<td>ATCC 11758</td>
<td>256</td>
<td>0.25</td>
</tr>
<tr>
<td><em>M. porcinum</em></td>
<td>ATCC 33776</td>
<td>&gt;2048</td>
<td>1</td>
</tr>
<tr>
<td><em>M. rhodesiae</em></td>
<td>ATCC 27024</td>
<td>32</td>
<td>≤0.25</td>
</tr>
<tr>
<td><em>M. smegmatis</em></td>
<td>ATCC 14468</td>
<td>512</td>
<td>1</td>
</tr>
<tr>
<td><em>M. vaccae</em></td>
<td>ATCC 15483</td>
<td>128</td>
<td>0.5</td>
</tr>
<tr>
<td>Resistant†</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>M. abscessus</em> subsp.</td>
<td>ATCC 19977</td>
<td>&gt;2048</td>
<td>&gt;128</td>
</tr>
<tr>
<td><em>M. abscessus</em> subsp.</td>
<td>CCUG 48898</td>
<td>&gt;2048</td>
<td>128</td>
</tr>
<tr>
<td><em>M. chelonae</em></td>
<td>ATCC 14472</td>
<td>512</td>
<td>32</td>
</tr>
<tr>
<td><em>M. gadium</em></td>
<td>ATCC 27726</td>
<td>&gt;2048</td>
<td>64</td>
</tr>
<tr>
<td><em>M. agri</em></td>
<td>ATCC 27406</td>
<td>&gt;2048</td>
<td>32</td>
</tr>
</tbody>
</table>

*NAL, nalidixic acid; OFX, ofloxacin; CIP, ciprofloxacin; LVX, levofloxacin; SPX, sparflloxacin; MOX, moxifloxacin.
†Numbering system used for *E. coli*.
‡Based on MIC breakpoints for ciprofloxacin.

MIC interpretations for ciprofloxacin, the RGM fell into two groups: susceptible and resistant (Table 3). The susceptible group comprised *M. aichense* ATCC 27280, *M. aurum* ATCC 23366, *M. chelonae* ATCC 35752, *M. chitae* ATCC 19627, *M. chubuense* ATCC 27278, *M. flavescens* ATCC 14474, *M. fortuitum* ATCC 6841, *M. neoaurum* ATCC 25795, *M. parafortuitum* ATCC 19686, *M. phlei* ATCC 11758, *M. porcinum* ATCC 33776, *M. rhodesiae* ATCC 27024, *M. smegmatis* ATCC 14468 and *M. vaccae* ATCC 15483. The resistant group comprised *M. abscessus* subsp. *abscessus* ATCC 19977, *M. abscessus* subsp. *bolletii* CCUG 48898, *M. agri* ATCC 27406 and *M. chelonae* ATCC 14472. The strain for which the MIC was highest was *M. abscessus* subsp. *abscessus* ATCC 19977, and the lowest MIC was for *M. neoaurum* ATCC 25725 (Table 3). The reference strain CCUG 48898 of *M. abscessus* subsp. *bolletii* showed resistance to high levels of all quinolones, similar to the clinical isolates.

Nucleotide sequences of the *gyrA* and *gyrB* QRDRs

The nucleotide sequences of *gyrA* and *gyrB* QRDR differed among the mycobacterial species (Fig. 1); however in *gyrA* they were identical for all clinical isolates of *M. abscessus* subsp. *bolletii* and the reference strain CCUG 48898. The homology analysis of the *gyrA* nucleotide sequences is shown in Fig. 2.

The nucleotide sequences of the *gyrB* QRDR of *M. abscessus* subsp. *bolletii* showed four different patterns. In pattern 1 (P1), consisting of 50 BRA100 isolates and the two non-clonal ones, sequences (GU831599) were identical and showed 95.7 % homology to the CCUG 48898 strain (HQ24105). Sequences in pattern 2 (P2, HQ285758), consisting of two BRA100 isolates from Rio de Janeiro, were identical to the CCUG 48898 strain. Patterns 3 (P3, one BRA100 isolate from Rio de Janeiro, HQ285759) and 4 (P4, one BRA100 isolate isolated from Goiás, HQ285760) showed, respectively, 99.1 and 97.4 % homology to the CCUG 48898 strain (Fig. 3).

Peptide sequences of the *GyrA* and *GyrB* QRDRs

The peptide sequences of the *GyrA* and *GyrB* QRDRs obtained for RGM were aligned with the peptide sequences of *M. tuberculosis*, *E. coli* and *Staphylococcus aureus*, using
**Fig. 1.** Alignment of the nucleotide sequences of the QRDRs of *gyrA* and *gyrB* from species of RGM. Sequences extend from nucleotides 220 to 339 for *gyrA* and from nucleotides 1414 to 1530 for *gyrB*, in the numbering system used for *M. tuberculosis*. Sequences of *M. tuberculosis* were used as the reference and dots represent identical nucleotides. *M. chelonae* 1 represents ATCC 35752, *M. chelonae* 2 represents ATCC 14472; *M. abscessus* has been recently renamed as *M. abscessus* subsp. *abscessus*, and *M. massiliense* as *M. abscessus* subsp. *bolletii*.
the numbering system of the DNA gyrase of *E. coli* (Fig. 4). In all RGM strains, the peptide sequences were identical for the GyrB QRDR and showed Arg-447 and Asn-464, the same residues as found in *Staphylococcus aureus* and *Streptococcus pneumoniae*.

The peptide sequences of the GyrA QRDR were identical for all isolates of *M. abscessus* subsp. *abscessus*, and *M. massiliense* as *M. abscessus* subsp. *bolletii*. The numbers at the nodes are bootstrap values from 1000 resamplings.

**DISCUSSION**

Over the past few years, RGM have played an important role as emerging health-care-associated pathogens (Brown-Elliott & Wallace, 2002; De Groote & Huitt, 2006; Phillips & von Reyn, 2001; Wallace et al., 1998). An epidemic such as the one that occurred recently in different states of Brazil (see Introduction), had never been described before worldwide and it has been considered as an epidemiological emergency. Since RGM have been rising as a significant health problem, it is essential to evaluate their susceptibility patterns to current antimycobacterial drugs...
and to describe mechanisms of resistance to antimicrobial agents in order to improve treatment and drug choice.

In a previous study (Duarte et al., 2009) resistance to ciprofloxacin was observed in some *M. abscessus* subsp. *bolletii* isolates recovered from postsurgical infections; however, the susceptibility of these strains to quinolones of other generations remained unknown until this present study. In the present study, most of the epidemic isolates were recovered from all hospitals with confirmed cases in the state of Rio de Janeiro, accounting for around 32% of the total of isolates obtained (*n* = 148), and additional representative strains from another two states with cases confirmed. During the characterization, these isolates exhibited clonal clustering by PFGE and were named as clone BRA100 (Duarte et al., 2009; Leão et al., 2010). Knowledge about potential emergence of *M. abscessus* subsp. *bolletii* and its antimicrobial resistance profile may contribute to systematic recovery of new isolates from different clinical sources and regions and improvement of their characterization.

The MIC results for nalidixic acid, ofloxacin, ciprofloxacin, levofloxacin, sparflaxcin and moxifloxacin demonstrated that quinolones of all generations were not inhibitory against any isolate of *M. abscessus* subsp. *bolletii*, including non-BRA100 isolates. The MIC results were similar to those found in previous studies (Guillemin et al., 1995, 1998), and previously unknown quinolone susceptibility patterns of other reference strains were also characterized in the present study. Quinolones are widely used in Brazil for treatment of urinary tract, respiratory, gall bladder, skin and gonococcal infections, and also used prophylactically for urinary or general surgery. Additionally, moxifloxacin has been described as a possible alternative for treatment of tuberculosis, and *Mycobacterium avium* and *Bacteroides fragilis* infections. Incorrect prescription of these drugs in routine medical practice and their prophylactic use for gall-bladder surgery may occur. No data on prescriptions of quinolones for these purposes were available in this study.

It is important to mention that the CLSI have breakpoints for just two quinolones, ciprofloxacin and moxifloxacin, and the recommendations have been described only for *M. fortuitum* group (*M. fortuitum*, *M. peregrinum* and *M. fortuitum* third biovariant complex), *M. chelonae*, *M. abscessus* subsp. *abscessus*, *M. mucogenicum* and *M. smegmatis* group (*M. smegmatis*, *M. goodi* and *M. wolinskyi*). It was shown in this work that the breakpoints for the other
quinolones described in the CLSI M100-S20 document for E. coli, Staphylococcus aureus and Streptococcus pneumoniae (CLSI, 2010) were useful for determining the susceptibility pattern in mycobacterial species when compared to molecular results, suggesting a good applicability of these criteria to RGM. Since the previous CLSI M-24-A document for antimicrobial susceptibility testing in mycobacteria, published in 2003, new antimicrobial agents, including new generations of quinolones and additional mycobacterial species have been reported up to the newest version, published in 2011 (CLSI, 2011). So there is a need for continuous updating of this document, and information obtained in this study may be useful. In our study the susceptibility patterns for all generations of quinolones were precisely determined and reproducible for all RGM evaluated by using cation-adjusted Mueller–Hinton broth as recommended by CLSI.

The homology analysis demonstrated the high similarity between M. abscessus subsp. abscessus and M. abscessus subsp. bolletii.

**Fig. 4.** Alignment of the peptide sequences of the QRDRs of GyrA and GyrB from species of RGM and from E. coli, Staphylococcus aureus and Streptococcus pneumoniae. Dots represent amino acids identical to those in M. tuberculosis. The GyrA QRDR extends from amino acid residues 67 to 106, and the GyrB QRDR extends from amino acid residues 426 to 464, in the numbering system used for E. coli. M. chelonae 1 represents ATCC 35752, M. chelonae 2 represents ATCC 14472; M. abscessus has been recently renamed as M. abscessus subsp. abscessus, and M. massiliense as M. abscessus subsp. bolletii.
abscessus for both gyrA and gyrB, but the RGM strains showed a different pattern for each tree. It is important to note that in gyrA, the sequences for clonal and non-clonal isolates were identical, whereas in gyrB, the clonal isolates had four different patterns (P1, P2, P3 and P4), even when comparing only the isolates belonging to the BRA100 clone. P2 was identical to the reference sequence of M. abscessus subsp. bolletii CCUG 48898, which may represent an intra- or inter-clone divergence between isolates. Possible reasons for this diversity being detected only in gyrB sequences are (i) different isolates from the same clone have suffered different evolutionary pressures, (ii) gyrB might play a different and possible minor role in the susceptibility of this species to quinolones or (iii) it represents a naturally hypervariable region of RGM genomes. Additionally, these results suggest that similar PFGE patterns of epidemiologically related isolates (BRA100, >85 % similarity) do not represent identical genome sequences, and even different phenotypic profiles may be observed in following studies evaluating distinct biological characteristics. Thus the concept of defining clonal strains for M. abscessus subsp. bolletii based only on PFGE patterns may be assumed with restrictions.

It was also observed that M. chelonae ATCC 14472 showed 100 % (gyrA) and 99 % (gyrB) homology to M. abscessus subsp. bolletii CCUG 50184 by using BLAST analysis. Furthermore, the rpoB sequence of this strain showed high similarity to M. abscessus subsp. bolletii (unpublished data). These results may suggest that this strain is in fact M. abscessus subsp. bolletii and not M. chelonae.

Considering the peptide sequences of GyrA, variation in residue 83 was found in the QRDR in the RGM species. Less susceptible species of RGM studied in this work, including M. abscessus subsp. abscessus and M. abscessus subsp. bolletii, had Ala instead of Ser in this position, the same residues as found in less susceptible species such as Staphylococcus aureus (Ito et al., 1994) and Streptococcus pneumoniae (Pan et al., 1996). However, contrary to what has been traditionally described, M. agris and M. gadium were clear exceptions, since they were resistant to quinolones yet had Ser at this locus. This suggests that the variation between Ala and Ser in residue 83 may not be the unique determinant for a resistant or susceptible phenotype. The opposite was also observed and supports this hypothesis: strains phenotypically susceptible to quinolones, such as M. phlei and M. smegmatis, had Ala as residue 83 in the GyrA QRDR. Previous authors hypothesized that the differences in the structures between Ser and Ala should be related to intrinsic resistance in some species, such as M. abscessus subsp. bolletii. It is thought that Ala cannot provide a hydrogen bond because of its lack of a hydroxyl radical, providing the resistant profile (Guillemin et al., 1995), but this does not explain the variations observed in the present study.

The peptide sequences of QRDR of GyrB were identical in all RGM tested and contained the residues Arg-447 and Asn-464, which also seem to be associated with lesser susceptibility to quinolones, compared to other bacteria. These residues differ from those found in E. coli (Lys-447 and Ser-464), a more susceptible species. Guillemin et al. (1998) argued that since Arg is bulkier than Lys and has an additional positive charge, and Asn is non-hydroxylated and bulkier than Ser, their presence could decrease the interaction between the DNA gyrase and the drug.

A recent study of gyrA and gyrB mutations in ciprofloxacin-resistant M. abscessus subsp. bolletii isolated from an outbreak in southern Brazil showed the substitution Ala-90→Val-90 (Ala-83→Val-83 using the E. coli numbering system) in the QRDR of GyrA in 88.6 % (31/35) of the isolates. This study also showed that 11.4 % (4/35) of the isolates did not show this substitution and were resistant to ciprofloxacin. The isolates from this outbreak had a PFGE profile characteristic of the BRA100 clone (Monego et al., 2011). The BRA100 isolates studied in the present work did not show the substitution Ala-83→Val-83 and they were also resistant to quinolones of all generations, not only to ciprofloxacin, suggesting that (i) the BRA100 clone as defined by PFGE criteria does not consist of isolates with the same genomic sequence, as previously discussed in our work; (ii) resistance to quinolones may involve not only mutations in QRDR of gyrA and gyrB but also other mechanisms of resistance.

Mechanisms of antimicrobial resistance besides the classic low cell wall permeability have already been described for mycobacteria and they involve porins (Danilchanka et al., 2008; Svetlikova et al., 2009; Stephan et al., 2004), efflux pumps (Li et al., 2004; Liu et al., 1996; Louw et al., 2009) and a pentapeptide MfpA, which plays a role in quinolone resistance in M. smegmatis (Montero et al., 2001). It has been recently proposed that a single mechanism which confers a low level of resistance to quinolones should not be underestimated and the combination of several mechanisms could explain the level of resistance achieved in clinical isolates (Hernández et al., 2011). This might be the explanation for the high levels of resistance observed in M. massiliense and related RGM. Those mechanisms should also be studied and associated with the MIC results in order to complete the characterization of quinolone resistance.

In conclusion, even though quinolones of different generations may be effective against some species of RGM, they should not be used to treat M. abscessus subsp. bolletii infections due to the resistance to high levels found in this subspecies. The variation between Ser and Ala at position 83 may play a role in reduced susceptibility to quinolones in mycobacteria. However, this does not explain the high levels of resistance to all generations of quinolones in M. abscessus subsp. bolletii and related species, since the presence of Ala-83 in the GyrA QRDR is not expected in some species of mycobacteria, including species susceptible to ciprofloxacin (Guillemin et al., 1995, 1998), and no other amino acid change was observed in both
genes. Other mechanisms might be present in those species to explain such resistance. The present study represents an important aid to the knowledge about mechanisms of quinolone resistance in RGM and for future review of susceptibility criteria.

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