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## Abstract

Although fluoroquinolones are considered as an alternative therapy of pulmonary Mycobacterium avium complex (MAC) disease (1), association of fluoroquinolone resistance and MAC genotypes in clinical isolates from individuals not previously treated for MAC infection has not been fully shown. A total of 154 M. avium isolates and 35 Mycobacterium intracellulare isolates were obtained from treatment-naïve patients with pulmonary MAC disease at the diagnosis of MAC infection at 8 hospitals in Japan. The susceptibility of moxifloxacin was determined by broth microdilution methods. Moxifloxacin-resistant isolates were examined for mutations of gyrA and gyrB. Variable numbers of tandem repeats (VNTR) assay was performed using 15 M. avium VNTR loci and 16 M. intracellulare VNTR loci. Moxifloxacin susceptibility was categorized as resistant and intermediate for 6.5% and 16.9% of M. avium isolates and 8.6% and 17.1% of *M. intracellulare* isolates, respectively. Although *M. avium* and *M. intracellulare* isolates had amino acid substitutions of Thr 96 and Thr 522 at the sites corresponding to Ser 95 and Gly 520 in the *M. tuberculosis* proteins GyrA and GyrB, respectively, these substitutions were observed irrespective of susceptibilities and did not confer resistance. VNTR assays showed three clusters among M. avium isolates and two clusters among *M. intracellulare* isolates. No significant differences in

moxifloxacin resistance were observed among these clusters. In conclusion, although resistance to moxifloxacin was observed in approximately one-fourth of *M. avium* and *M. intracellulare* isolates, this resistance was not associated with mutations in *gyrA* and *gyrB* or with VNTR genotypes.

 Koh WJ, Hong G, Kim SY, Jeong BH, Park HY, Jeon K, et al. Treatment of refractory *Mycobacterium avium* complex lung disease with a moxifloxacin-containing regimen. Antimicrob Agents Chemother 2013; 57: 2281-2285.