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Molecular Characterization and Antimicrobial Susceptibility of *Bordetella pertussis* Isolates in South Korea, 2024

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ABSTRACT

Background Since MRBP were first reported in China in 2011, it has spread in Asia and Europe. This study analyzes antibiotic resistance and genotypes of *B. pertussis* isolates from South Korea in 2024.

Methods Antimicrobial susceptibility testing and whole genome sequencing were performed.

Results Six (42.9%) was MRBP, all harboring the A2047G mutation. Four were *ptxP*3/*ptxA*1/*ptxC*4/*prn*150/*fhaB*1/*fim2*-1/*fim3*-1; two were prn-deficient but similar otherwise. Among eight susceptible isolates, seven were *ptxP*3/*ptxA*1/*ptxC*4/*prn*2/*fhaB*1/*fim2*-1/*fim3*-1, and one was *ptxP*1/*ptxA*1/*ptxC*1/*prn*1/*fhaB*1/*fim2*-1/*fim3*-4.

Conclusions This study shows the presence of MRBP strains in South Korea, and exhibiting an identical virulence-associated allelic profile consistent with globally circulating MRBP lineages.

INTRODUCTION

Pertussis is a highly contagious respiratory disease caused by *Bordetella pertussis*, with rising incidence despite widespread vaccination[1-2]. Macrolides are the first-line treatment, but the emergence of macrolide-resistant *B. pertussis* (MRBP) mainly associated with the A2047G mutation in the 23S rRNA gene, has raised global concern, especially with high prevalence in China[3]. This study investigates the antimicrobial susceptibility and molecular genotypes of *B. pertussis* isolates collected in South Korea in 2024 to elucidate their genetic and epidemiological features.

MATERIALS AND METHODS

Bacterial isolates In 2024, a total of 14 *B. pertussis* clinical isolates obtained in South Korea were analyzed.

Antimicrobial susceptibility testing Minimum inhibitory concentrations (MICs) were determined by E-test.

Whole genome sequencing and data analysis DNA libraries were prepared with Nextera DNA Flex and sequenced on Illumina MiSeq. Reads were assembled on CLC Genomic Workbench and analyzed for genomic features and SNPs using BIGSdb-Pasteur and CGE. cgMLST analysis was done with SeqSphere+.

RESULTS

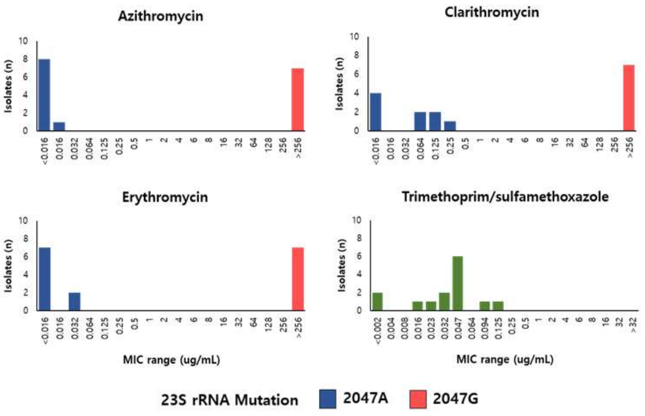

Figure 1. MIC distribution of *B. pertussis* strains isolated in South Korea in 2024

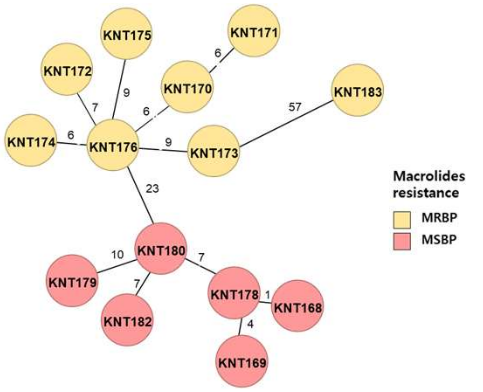

Figure 2. Minimum spanning tree(MST) of *B. pertussis* isolates based on cgMLST analysis

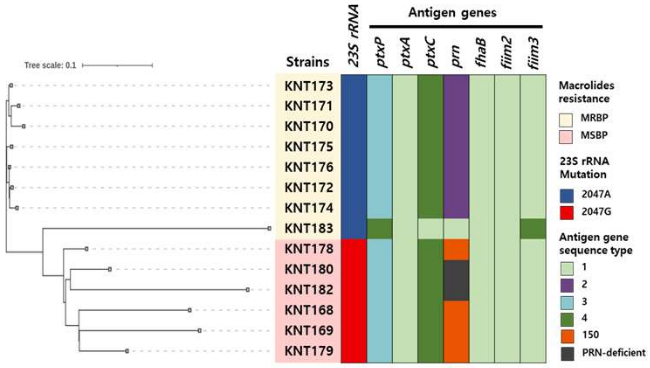

Figure 3. Phylogenetic tree based on SNP analysis and molecular characteristics of *B. pertussis* isolates

CONCLUSIONS

- This study shows the presence of MRBP strains in South Korea.
- Genetic analysis revealed that MRBP and MSBP strains possess distinct antigenic profiles.
- All resistant strains shared the *ptxP*3/*ptxA*1/*ptxC*4/fhaB1/fim2-1/fim3-1 genotype with *prn*150 or *prn*-deficiency, similar to the antigenic allelic profiles of the MRBP strain currently circulating in China suggesting potential genetic relatedness.
- Continued monitoring of antimicrobial resistance and genetic traits is essential to guide public health and vaccine strategies.

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