

Characterisation of Erythromycin-Resistant *Streptococcus pneumoniae* Isolates Causing Invasive Diseases among Chinese Children

Dear Editor,

Although some data have shown that *Streptococcus pneumoniae* were high resistance to erythromycin in some Asia countries and areas,¹ data from cases of invasive pneumococcal diseases (IPD) were rare and the characterisation of these isolates had not been well detected in the hinterland of China.

Recently, we detected the susceptibility to antimicrobial for 171 *Streptococcus pneumoniae* isolates which were collected from 11 medical centers in China from children under 14 years with invasive pneumococcal diseases² and analysed the characterisation of erythromycin-resistant isolates. To our knowledge, this is the largest collection of IPD isolates recovered and characterised in Chinese children.

Among the 171 isolates, 164 (95.9%) were resistant to erythromycin. Resistance to erythromycin was generally with high minimal inhibitory concentration (MIC) level (MIC₅₀ and MIC₉₀ ≥256 µg/ml for 162 isolates among all the 164 strains. The level of MIC didn't show significant differences in distinct geographic regions, age groups and penicillin-resistant isolates or penicillin-susceptible isolates. Meanwhile, there were 104 (63.4%) isolates carried the *ermB* gene only and 59 (36.0%) were found to harbor both *ermB* and *mefA/E* genes, which suggested that the mechanism of ribosomal methylation encoded by the *ermB* gene was the major resistance mechanism in the IPD isolates from China. It maybe responsible to the high MIC levels of erythromycin because *ermB* gene is usually associated with high-level resistance and the *mefA/E* gene is related to low level resistance. The distribution of resistant genes didn't show significant differences in distinct geographic regions. Furthermore, all the serotypes showed similar resistance levels to erythromycin. However, in Europe, erythromycin resistance was often associated with

pneumococcal serotype 14.³ This maybe the result of wide and inappropriate using of macrolide antibiotics, such as azithromycin and clarithromycin in the hinterland of China.

An interesting finding concerning the distribution of resistance determinants was the high rate of dual presence of the *ermB* and *mefA/E* genes in serogroup 19. Most of them (54/59, 91.5%) belonged to the serotype 19F and 19A and had an identical PFGE pattern (C pattern). Furthermore, 54 of these strains had an MLST profile similar to the reference strain of Taiwan^{19F}-14 clone (ST236:15-16-19-15-6-20-26). Based on the data from PFGE and MLST in this study, the serotype 19F and 19A isolates with the *ermB* and *mefA/E* genes could be the variants of the Taiwan^{19F}-14 clone. Since the Taiwan^{19F}-14 clone was originally known to have only a *mefA/E* gene, horizontal transfer of the *ermB* gene into this clone, and subsequent dissemination of this variant, could be responsible for the high rate of dual presence of the *ermB* and *mefA/E* genes in Chinese children.

This study was limited by the number of isolates in each region was relatively small and all the isolates were collected from tertiary hospitals in Chinese big cities. In that regards, there maybe some bias in isolate collection (i.e. the cultures more likely to be obtained from children who failed treatment or who have the more severe form of infections).

In summary, surveillance has showed that the erythromycin resistance rate is very high among *S.pneumoniae* causing IPD in chinese children. The major mechanism was the ribosomal methylation encoded by the *ermB* gene among most of the major serotype, furthermore, the mechanism of efflux encoded by the *mefA/E* gene mainly were detected in serogroup19. In addition, molecular studies suggested the spread of resistant strains (Taiwan^{19F}-14 clone) in the mainland of China.

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X MA
KH YAO
SJ YU
L XUE
YH YANG*

Key Laboratory of Major Diseases in Children and National Key Discipline of Pediatrics (Capital Medical University), Ministry of Education, Beijing Pediatrics Research Institute, Beijing Children's Hospital, 56# Nan Lishi Road, Beijing, China

*Correspondence to: Prof. YH YANG