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Determination of Characteristics of Erythromycin Resistant *Streptococcus pneumoniae* with Preferred PCV Usage in Iran

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Amongst 100 *Streptococcus pneumoniae* isolated from clinical cases and nasopharynx of healthy individuals, 60 erythromycin resistant strains were isolated and characterized using MLST, PFGE, transposon analysis and Quellung reaction. Most of the *S. pneumoniae* erythromycin resistant (80%) were found to be attributable to the *ermB*-edncoded ribosome methylase activity which differs from the dominant mechanism of macrolide resistance seen in North America. The most predominant transposons were; Tn1545/6003 (27%), Tn6002 (22%), Tn2009 (20%), Tn2010 (17%). Number of the clinical isolates carrying Tn2010 was more significant than the normal flora. The serotypes found were; 14 (33%), 3 (22%), 23F (15%), 19F (15%), 19A (7%), 6A (3%), 9V (3%) and 6B (2%). The most prevalent serotypes among the clinical (n=28) and normal flora (n=32) isolates were serotypes 14 (46%) and 3 (31%), respectively. The most prevalent vaccine serotypes amongst the clinical isolates and the healthy individuals were pneumococcal conjugate vaccines (PCV) 13 and PCV10, respectively. PFGE revealed 34 pulsotypes with 9 common and 25 single types. Significant number of the normal isolates belonged to CT5 and CT6. On the other hand, significant number of clinical isolates belonged to CT8 as compared to the normal flora isolates. MLST showed 2 dominant sequence types. ST3130 (23 %) and ST180 (22%) were the most predominant sequence types in the clinical and normal isolates, respectively. There was no significant difference in other sequence types between clinical and normal flora isolates. Three polyclonal complexes including Sweden15A -25, Spain23F-1 and Spain9V-3 constituted 58% of the isolates. Our results suggest that the genetic diversity and transposon distribution were high among *S. pneumoniae*, particularly in the isolates containing *erm*(B) and double antibiotic resistant genes (*erm/mef*). The results presented here could influence the change in the current vaccination practices in Iran which currently calls for vaccination with PCV7 or PCV10.

Biography

Mohammad R Pourshafie is a faculty member at the Pasteur Institute of Iran. He has published over 80 peer-reviewed manuscripts on epidemiology and genomics of enterococci, *Vibrio cholerae* and *Lactobacillus sp* and *S. pneumoniae*.

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