

RESEARCH NOTE

INVESTIGATION OF SEROTYPE 19F *wzy* VARIANT AMONG CLINICAL *STREPTOCOCCUS PNEUMONIAE* ISOLATES IN KOREA

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Abstract. Accurate identification of *Streptococcus pneumoniae* serotypes 19A and 19F is important because these serotypes are predominant in invasive pneumococcal disease and are closely associated with multi-drug resistance, especially in Asia. Although the Quellung assay is accepted as the gold standard in *S. pneumoniae* serotyping, its high cost and labor intensive procedures has led to adoption of sequential multiplex (SM)-PCR of *S. pneumoniae*. However, the existence of a 19F *wzy* variant with its close genetic similarity to 19A *wzy* has given rise to false-negative 19F and false-positive 19A serotyping. Hence, the study employed a 19F *wzy* variant-specific primer set in a PCR-based identification among 378 *S. pneumoniae* clinical isolates previously serotyped using SM-PCR and Quellung assays. Although 112 of 378 isolates showed positive results by 19Fvar primer set, no 19F *wzy* variant obtained when they were confirmed by SM-PCR and Quellung assay. Among 8 SM-PCR nontypeable serotypes, none could be confirmed as being serotype 19F *wzy* variant. Thus the reliance on the PCR using 19Fvar primer set to detect *S. pneumoniae* 19F *wzy* variant is subject to high frequency of false positive results and should be confirmed by the Quellung assay. Based on these results, *S. pneumoniae* 19F *wzy* variant was not detected yet in this study from Korea.

Keywords: *Streptococcus pneumoniae* 19F *wzy* variant, Quellung assay, sequential multiplex-PCR, Korea

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