

# INVASIVE *STREPTOCOCCUS PNEUMONIAE* SEROTYPE 19A IN THAILAND (2008-2018)

Piriyaporn Chongtrakool<sup>1</sup>, Unchalee Puangprasart<sup>1</sup>, Wanatpreeya Phongsamart<sup>2</sup>,  
Chanwit Tribuddharat<sup>1</sup>, Chalerm Sri Pummangura<sup>3</sup> and Somporn Srifuengfung<sup>3</sup>

<sup>1</sup>Department of Microbiology, <sup>2</sup>Department of Pediatrics, Faculty of Medicine Siriraj Hospital, Mahidol University; <sup>3</sup>Faculty of Pharmacy, Siam University, Bangkok, Thailand

**Abstract.** Following introduction of a 7-valent pneumococcal polysaccharide-protein conjugate vaccine (PCV7), incidences of invasive pneumococcal disease caused by *Streptococcus pneumoniae* serotype 19A non-susceptible penicillin dramatically increase worldwide. In Thailand, as molecular characterization of invasive *S. pneumoniae* serotype 19A is sparse, we determined multilocus sequence types (MLSTs) and antibiogram profile of invasive disease serotype 19A isolated from 21 hospitals during 2008-2018. *S. pneumoniae* ( $n = 62$ ) demonstrated twenty different STs, grouped into three main clonal complexes (CCs), namely, CC63 (36%), CC230 (21%) and CC320 (43%), with the most predominant MLST being ST320 ( $n = 25$ ), followed by ST2930 ( $n = 9$ ), ST230 ( $n = 7$ ), ST63 ( $n = 3$ ), ST95 and ST8346 ( $n = 2$  each); there were also seven isolates having novel STs (14415, 14391, 14392, 14389, 14390, 14413, and 14414). Based on criteria for meningitis, 93 and 52% of isolates were non-susceptible to penicillin and cefotaxime/ceftriaxone, respectively while 30 and 8% of non-meningitis isolates were non-susceptible, respectively. Non-susceptibility to meropenem and erythromycin constituted 72% of the isolates while 100% were susceptible to levofloxacin, ofloxacin and vancomycin. The predominant ST320 and ST2930 isolates were multidrug resistant (*ie*, resistant to at least three classes of antimicrobial) and were disseminated among the study hospitals during the survey period. Hence, control and prevention of infection by highly antimicrobial-resistant *S. pneumoniae* serotype 19A should be a major health care concern.

**Keywords:** *Streptococcus pneumoniae* serotype 19A, antibiogram profile, clonal cluster, multilocus sequence type, Thailand

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Correspondence: Somporn Srifuengfung, Faculty of Pharmacy, Siam University, 38 Petchkasem Road, Phasicharoen District, Bangkok 10160, Thailand  
Tel/Fax: +66 (0) 2868 6665 E-mail: somporn.sri@mahidol.ac.th