

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

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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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