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Study of *Streptococcus pneumoniae* serotype 19A blood isolates from Thailand by enterobacterial repetitive intergenic consensus (ERIC)-PCR typing

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ABSTRACT: *Streptococcus pneumoniae* serotype 19A is frequently isolated worldwide. In this study, the clonal relationships among 62 isolates from different patients from 21 hospitals between 2008 and 2018 were characterized using enterobacterial repetitive intergenic consensus-polymerase chain reaction (ERIC-PCR). The different band patterns that appeared upon agarose gel electrophoresis were used to construct an unweighted pair group method with an arithmetic mean (UPGMA) dendrogram. There were 23 different ERIC types (E1–E23). The most prevalent type was E9, accounting for 19.36% of all isolates, followed by E6 at 16.13%, E5 at 11.30%, and 13 ERIC types present in only one isolate or at 1.61% each. Using an additional study to determine the clonal relationships, we compared our ERIC-PCR results to the corresponding multilocus sequence types (MLSTs) from our recent study with the same 62 *S. pneumoniae* serotype 19A isolates. The results showed there were 20 different MLST types and that ERIC-PCR was comparable to MLST as a valuable complementary tool for the investigation of *S. pneumoniae* serotype 19A isolates. Furthermore, ERIC-PCR is very fast, affordable, and easy to perform compared to MLST. However, there is less concordance between these two methods. These results suggest a high diversity of different ERIC-PCR and MLST patterns. Overall, the combination of results from both methods can add greater discrimination and complementary information for the differentiation of *S. pneumoniae* strains in Thailand.

KEYWORDS: *Streptococcus pneumoniae*, serotype19A, ERIC-PCR, multilocus sequence typing

INTRODUCTION

Streptococcus pneumoniae is a highly virulent pathogen that can cause pneumonia, bacteremia, sepsis, and meningitis. It causes millions of deaths worldwide and has a significant morbidity rate, particularly in the elderly and young children [1]. Invasive pneumococcal disease (IPD) is when *S. pneumoniae* invades sterile sites, such as blood, pleural fluid, cerebrospinal fluid, joint fluid, tissues, and organs [1, 2]. The Centers for Disease Control and Prevention (CDC) in the US has reported an annual incidence of IPD of 10.6/100,000 people. The CDC noted that IPD cases occur more in adults than in children, and that bacteremia was present in 20% of total IPD cases [3]. In Latin America and the Caribbean, *S. pneumoniae* causes 12,000–18,000 deaths, along with 4000, 1229, and 327,000 cases of meningitis, sepsis, and pneumonia yearly and involves patients < 5 years of age [4]. At present, 98 serotypes of *S. pneumoniae* have been reported, depending on the polysaccharide composition of its bacterial capsule, which is the most important pneumococcal virulence factor of its antiphagocytic activity [5]. The decline in IPD found in one study, following the introduction of the 7-valent pneumococcal conjugate vaccination (PCV7), was tempered by the emergence of non-vaccine serotypes, particularly 19A [6]. Serotype 19A has been a subject of concern in some regions since PCV7 implementation is due to increased prevalence and drug resistance [7]. However, a previous report suggested that in addition to the vaccine, areas where PCV7 was unattainable or was scarcely used also showed an increase in *S. pneumoniae* serotype 19A prior to PCV7 implementation [8]. The recognition that serotype 19A is a predominant serotype associated with IPD and that *S. pneumoniae* serotype 19A clinical isolates have high rates of multiple drug resistance makes *S. pneumoniae* serotype 19A interesting in the field of epidemiology and of great clinical importance [9]. Furthermore, the increase in serotype 19A IPD in several countries following the implementation of PCV-7 or PCV-10 has made it the most common serotype identified in recent years [10], and this highlights the need for the continued surveillance of serotype 19A [9].

Several genetic characterizations or molecular typing can be used to discriminate different isolates of *S. pneumoniae* within the same serotypes, such as pulsed-field gel electrophoresis, restriction fragment length polymorphism, amplified fragment length polymorphism, penicillin binding protein fingerprinting, and MLST [10]. The principle of MLST is the system-