

## Emm (M Protein Gene) Sequences of Invasive Group A Streptococci Isolates from Thai Patients at Chulalongkorn University Hospital from 1995 -1999

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**Objective:** Previous study of the incidence and pattern of invasive group A streptococci (GAS) at Chulalongkorn University Hospital (CUH) demonstrated an increase in incidence and a wide variety of clinical features. In this study, we are interested in analyzing the variability of *emm* gene which encode a major virulence factor, M protein, from these invasive GAS isolates.

**Methods:** The study involved 41 invasive GAS infections in the patients admitted to CUH from January 1, 1995 to December 31, 1999. Strains were confirmed as GAS by latex agglutination grouping. The *emm* genes were amplified by PCR and subjected to direct sequencing method according to CDC protocol.

**Results:** Of the 41 invasive GAS isolates analyzed, 39 *emm* genes can be amplified with 24 different *emm* sequences. Ten of the 24 *emm* types were standard *emm* types *emm1*, *emm11*, *emm22*, *emm23*, *emm25*, *emm35*, *emm49*, *emm58*, *emm61*, *emm68*; with one provisional *emm* types *pt3875*; and two were previously identified *emm* sequence types *TR2612* and *cmuj76*. The other nine *emm* sequences have similar sequences to GAS strains *STBSA29*, *Sp11014/vt15*, *SS1448*, *SS1444*, *STNS1*, *NS5*, *2034.92*, *6949-99*, *STI4935*; however, the name of *emm* types has never been previously assigned for these sequences. Lastly, 2 novel *emm* sequence types were discovered in this study from strain NSRT1 and NSRT2 that have some homology to *emm43* and *emm60*, respectively. Interestingly, the *emm* types that were commonly found in this invasive GAS infection include *emm22* (4 isolates), *emm1* (4 isolates), *emm25* (3 isolates), *emm61* (3 isolates), *emm* from NSRT1 (3 isolates), *emm68* (2 isolates), and *emm* from STBSA29 (2 isolates).

**Conclusions:** A variety of *emm* sequences have been reported in this study including the identification of 2 novel *emm* types. The *emm* gene sequencing (*emm* typing) is an effective tool to characterize the variability and the prevalent of invasive GAS isolated.