CHAPTER VII

CONCLUSION

Emm gene is a virulent gene that encoded M protein found in GAS, GCS, and GGS. In this study, we are interested in the variation of *emm* gene in GCS and GGS from Thai patients and also compared the sequences of *emm* gene between non-invasive and invasive specimens. Sixty GGS clinical isolates and 52 GCS clinical isolates obtained from patient admitted to King Chulalongkorn Memorial Hospital between 1995 to 2000 were included in this study. These specimens were divided into two group (non-invasive and invasive) by using the different site of infections. Strains were confirmed as GCS and GGS by co-agglutination grouping. The *emm* genes were amplified by PCR and subjected to direct sequencing method according to CDC protocol.

All of 60-*emm* gene from GGS isolates were amplified and sequenced. A variety of *emm* sequences (28 types, 47%) have been reported in this study including the identification of 6 (18%) *emm variant* types and 10 (26%) novel *emm* types. The common *emm* types of GGS isolates include *STC6979* (7 isolates,12%) and *STC5345* (6 isolates, 10%). As for GCS, only 24 out of 52-*emm* gene can be amplified and sequenced. Twelve (50%) different *emm* types including 7 (38%) novel *emm* types were identified in GCS. The most common *emm* types is *ST245* (9 isolates, 42.8%). In GCS, some isolates can not be amplified by PCR method from CDC protocol. It is possible that *emm* gene of GCS has polymorphism at primer site. Different sets of primers (MF2 and MR1) were used to prove this problem. However, MF2 and MR1 still can not amplify *emm* gene from those GCS isolates. Another most likely hypothesis is that some GCS may not have *emm* gene.

This study demonstrates the diversity and unique population of GGS and GCS isolates in Thailand. However, it is also possible that the unique *emm* sequence types is due to the limited information in *emm* types from GGS and GCS. When the *emm* types

of this study were compared to the collection of CDC, GenBank database, and the Schnitzler' s study; interestingly, some *emm* sequence types of GGS isolates were similar to *emm* types of GAS (*emm3.1*, *emm23*, and *emm100.1*) and some *emm* sequences types of GCS isolates were similar to *emm* types of GGS isolates (e.g., *H46A* type). These finding confirm the evidence of horizontal gene transfer of *emm* genes among GAS, GCS, and GGS.

Different *emm* types seem to be associated with invasive compared to non-invasive groups. However, these differences are not statistically significant. The lack of association might be because the sample size is not large enough.

In conclusion, M protein (*emm*) typing is a useful tool for conducting epidemiological studies of streptococcal infections, particularly in an area where severe streptococcal infections are commonly found. This information of the *emm* gene from GCS and GGS in Thai patients that provides the addition result to the *emm* database of GAS will be useful in vaccine development to *Streptococcus* in Thailand.

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