IX. SUMMARY

This study describes a new method designed for analysis of *emm* genes. The principle of the method is based on the polymorphism of the genes. PCR and restriction endonuclease digestions generated diverse patterns of the genes of interest. The results were as follows.

1) The group of GAS with different N-terminal DNA sequences of *emm* genes showed distinctive *Mbo*I digestion patterns of the PCR products and divergent chromosomal DNA.

2) Almost all of the GAS pairs having high homology of the *emm* genes (88.89%) showed identical *Mbo*I digestion patterns. Only 11.81% of them had distinctive *Mbo*I digestion patterns. These results may indicate the subgroup of the same type of *emm* genes.

3) All of the M-typable and M-nontypable GAS investigated in this study could be typed by this method. The method is relatively easy to interpret and may be useful for typing a large number of GAS isolates.

The combination of this method with the traditional serotyping or other DNA typing may be useful for epidemiological study of GAS infection in highly endemic areas .