

## CHAPTER VII

### CONCLUSION

The present study revealed that the genotypes *cagA* positive, *vacA* s1, m2 and *iceA2* were predominated in *H. pylori* Thai strains. The presence of genes *cagA*, *vacA* and *iceA* or their combinations do not have a predictive value as risk markers for the development of peptic ulcer in Thai patients. However, combination of *vacA* s1a and mixed *iceA* genotype may be regarded as marker for predicting the peptic ulcer disease in Thai setting if the mixed *iceA* genotype proven to be existed.

The result of this study supports geographic differences among *H. pylori* strains and suggests the role of other variables such as other genes, host and environmental factor in clinical outcome of *H. pylori* infection.



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