CHAPTER 7

CONCLUSION

In conclusion, in order to investigate the allele frequency and genotype distribution of *CYP2A13* polymorphisms in a Thai population of 336 unrelated healthy subjects, the six SNPs , four SNPs in coding region (74G>A in exon 1, 578C>T in exon 2, 1662G>C in exon 3 and 3375C>T in exon 5) and other two SNPs in non coding 3'-untranslated region (7520C>G and 7571G>C), were detected through PCR-based analysis i.e. PCR-RFLP; mASA; and tetra-primer PCR assay. The most frequent of these variants were 3375C>T and 7571G>C. The most common haplotype observed in Thai subjects were 7520G; 74A, 3375T, and 7571C; and 74A and 3375T which corresponded to**1H* or **3, *2B,* and **2A* alleles of the *CYP2A13* gene, respectively. In general, the results in this study are in agreement with those in Asian racial groups from the previous studies. The present study confirmed that the *CYP2A13* genetic polymorphisms exist in Thai population.

These findings provided data for further studies to clarify that the *CYP2A13* polymorphisms might constitute a genetic background contributing to ethnic differences in the susceptibility to some tobacco-related cancer. Because these genetic polymorphisms are medically significant, genotyping could help clinicians to optimization of therapy or identification of person at risk of lung carcinogenesis. Knowledge of the polymorphic status of *CYP2A13* gene in individual patients might be useful in anticipating dosage and therapeutic efficiency or adverse drug effects before clinical trials.