CHAPTER V

CONCLUSIONS

In this study, we investigated the prevalence of mutations at codon 12 and codon 13 of K-*ras* gene in ovarian cancer tissue specimens of Thai patients. The methods involved amplification of the DNA specimen by amplified created restriction site (ACRS) and restriction fragment length polymorphism (RFLP). The samples in which mutations were detected were further confirmed by DNA sequencing. Of all 82 ovarian cancer samples, 14 samples were found to have mutation at codon 12 and 1 sample was found to have mutation at codon 13 of K-*ras* gene. The mutations were found predominantly in mucinous ovarian cancer samples (45.45%: 10 of 22), more than nonmucinous ovarian tumors (8.33%: 5 of 60). The mutations also correlated with the tumors of low malignant potential (52.17%: 12 of 23) than malignant ovarian tumors (7.69%: 3 of 39).

Of the 14 cases that had the mutation at codon 12 of the K-ras gene, the high frequency of nucleotide change was detected in the second position of codon 12, which was changed from GGT to GAT (5 cases), to GTT (4 cases), or to GCT (3 cases), while the mutation at the first position of codon 12, which was changed from GGT to CGT, was found in 2 samples. For the only case that mutation occurred at codon 13, the nucleotide substitution was detected in the second position of codon 13, which was changed from GGC to GAC.

In this study, an initial database of the K-*ras* mutation in Thai ovarian cancer may use for the studies in the mechanism of ovarian tumorigenesis in the future.