CHAPTER 6

CONCLUSION

In our study, three genetic assays, consisted of chromosome aberration and micronucleus tests, and single cell gel electrophoresis test, were employed to assess chromosomal and DNA damage in peripheral blood lymphocytes of two human populations. They are populations from Saraphi and Chom Thong, the areas in Chiang Mai, Thailand, with the highest and lowest of lung cancer incidences respectively. The population residing in Saraphi revealed a significantly lower average frequency of chromosome aberrations, but significantly higher average frequency of micronuclei, in their cultured lymphocytes. A significantly higher of DNA damage in non-stimulated peripheral blood, measured by tail length, was also detected from Saraphi population. However, when the DNA damage was measured by tail intensity and tail moment, no statistically significant differences was seen. No difference was measured when the stimulated peripheral blood with and without DNA repair inhibitor were investigated.

In addition, an evaluation of potential confounding factors, including age, gender, pesticide exposure, smoking habit, alcohol drinking, and chewing of fermented tea leaves or betel nut, were analyzed. The analysis indicated that smoking and chewing habits elevated the frequency of chromosomal aberrations, while gender affected micronucleus frequency. However, there was no effect of any confounding factor on DNA damage.

Despite the conflicting results obtained from these three short-term assays, the corresponding results of the basal levels of micronucleus frequency and DNA damage which was higher in Saraphi population, the area with high incidence of lung cancer were detected. It might be concluded, though not so certain, that Saraphi population might exposed to heavier environmental pollutants than those in Chom Thong. The conflicting result of chromosome aberration and the others two assays may be attributed to the mechanism of the test and/or the adaptive response of the subjects' cells. Moreover, some unrecognized lifestyles and confounding factors that are unequally distributed in the target and the reference population should be taken into account.

It is evident that health risk could not be assessed, based on only potential exposure of the toxic agents, which was detected by various biomarkers. The identification of hazardous substances, the quantitative analysis between dose response and effect in human would be a necessity. In order to achieve the precise health risk assessment, the additional information about assays using biomarkers of effect and/or biomarkers of susceptibility, for example, polymorphism or mutation of genes responsible for activation or detoxification of genotoxic agents and DNA repair, are recommended.