SUMMARY AND CONCLUSION
CHAPTER-5

5.1: SUMMARY AND CONCLUSIONS

In light of the projected increases in the prevalence of oral cancer, in addition to the morbidity and mortality associated with the disease, the importance of the prevention or early detection of oral cancer is evident, especially in those at increased risk for the disease. As the development of oral cancer is dependent on both genetic and environmental factors, the identification of those genes conferring an increased risk would aid in the identification of individuals with a heightened susceptibility for the disease. Equally important is the determination of the environmental factors that may attenuate the genetic susceptibility of the disease. The purpose of the present study was to evaluate the association of the detoxification gene polymorphisms with oral cancer in an effort to expand upon the existing literature examining the \textit{CYP1A1}, \textit{CYP2E1}, \textit{EPHX1} and \textit{NAT2} genes as potential candidate genes in the development of oral cancer.

5.1.1: Effect of Smoking

Thirty four (34.4\%) of oral cancer patients in the study reported smoking but in the control group only 23 (17.4\%) subjects admitted to have a smoking habit. The distribution of
smokers was significantly different between cases and controls (p=0.001) with OR (CI) 2.485 (1.375-4.512).

5.1.2: CYP1A1 and oral cancer

The CYP1A1 gene Thr461Asn site is not polymorphic in the present study. The genotypes or haplotypes of IVS1-728G>A and Ile462Val are not associated with oral cancer.

5.1.3: CYP2E1 and oral cancer

The (CYP2E1_-1295G>C (dbSNP rs3813867) and CYP2E1_-1055C>T (dbSNP rs2031920) SNPs found in the CYP2E1 gene co-inherited in the Indian population. The genotype or allele frequencies of these SNPs were not statistically significant between controls and oral cancer. The pairwise LD values between these markers revealed that one SNP can act as a surrogate for another.

5.1.4: EPHX1 and oral cancer

The EPHX1 gene polymorphisms have shown similar minor allele frequencies in controls and cases and were not associated with oral cancer either at genotype or haplotype level. Of the 3 studied polymorphisms, 2 were in strong LD and form 1 haplotype block, but that haplotype are not associated with oral cancer.
5.1.5: NAT2 and oral cancer

The NAT2 gene functional SNPs (rs1799929, rs1799930 and rs1799931) is not associated with oral cancer either at genotype, haplotype and deduced acetylator phenotypes. But the overall acetylator phenotypes showed statistically significant association, in particular rapid acetylator genotypes, to oral cancer risk.

5.1.5: Limitations to this study

There are several potential limitations to this study. First, we ascertained cases and controls from the hospital which will question genetic homogeneity and allow unmeasured confounding factors of population stratification. Second, our relatively small total sample size may have influenced the ability to identify an association between oral cancer and detoxification gene polymorphisms. As we could not find the association at genotype and haplotype level we presume that the limited sample size decreases the possibility of observing moderate effects. Because of these limitations, additional studies in different populations are necessary to clarify the role of the detoxification genes in causing oral cancer.