

CHAPTER VI

CONCLUSION AND SUGGESTION

6.1 CONCLUSION

In summary, CNVs of smaller size affecting miRNA genes do occur in germline DNAs from CRC patients. Some of the CNVs in miRNAs are shown to be polymorphic however many has not been reported, especially in CRC patients. Custom oligo-aCGH has been useful in detecting these small CNVs affecting miRNAs although further optimization needs to be done in order to use the array to its best. Nevertheless, miR-646 was found to be duplicated in one patient and miR-770 was deleted in another patient. These CNVs could not be detected in healthy controls, making them good candidates for their involvement in CRC predisposition. These results can not represent all the familial CRC cases as the cohort study being used is too small as well as the validation is still ongoing. However it is a good starting point in finding the CNVs affecting miRNAs in familial CRC and understanding its functions.

6.2 SUGGESTIONS

To understand about CNVs affecting miRNAs in CRC predisposition more in depth, a bigger cohort of patients will be needed. More patients will give us a broader overview about CNVs found whether it's pathogenic or indeed polymorphic CNVs. For the best use of the array, more validation of all candidates CNVs is needed to enabling us in setting the threshold for the array. Proceeding further miR-770 needs to be screened in more healthy control and also

designing PCR primers in detecting deletions is needed. Once we ascertain its uniqueness, databases and software can be used to predict the target of miR-770. Following this we can acquire the information whether the target of miR-770 has been validated and the involvement of it in CRC. Next, sequencing of the CNVs to acquire the unique sequence of the CNVs affecting the miRs needs to be performed not only for miR-646 and miR-770 but also for the future interest of a certain miR. This will facilitate a better picture of the CNVs.

The results of this study will enable the early diagnosis of familial colorectal cancer hence can be used as prevention measurement. This will also in turn help in the genetic counseling for the patients and relatives. Furthermore this research will provide some insight information about possible treatment for colorectal cancer based on the defect on their genetic sequence.