CHAPTER VI

CONCLUSIONS AND FUTURE DIRECTIONS

VI. 1. CONCLUSIONS

From the result of this study we can conclude that:

1. Three mutations in *CRB1* (c. 3914 C>T, p.P1305L); *RPE65* (c.730 G>A, p.G244S) and *RP1* (c.1012 C>T, p.R338X) were found in three different families by using this approach and one mutation in *CRB1* (c. 3914 C>T, p.P1305L) was found in one family from the Indonesian RP known mutations screening. Mutations in *RP1* and *RPE65* genes were novel mutations, whereas the *CRB1* mutation has been described in the previous study in Indonesian population.
2. Type of inheritance: arRP : 17.9 %
   Sporadic : 82.1 %

   The mode of inheritance of unsolved cases (which genetic defects has not been identified in this study) are still remain undetermined and classified as sporadic cases.

VI. 2. FUTURE DIRECTIONS

1. It is very important for the other relatives (non affected person) from the family to participate to narrow the homozygous regions for candidate genes selection. Therefore, sample of relatives and parents (including non affected) have to be obtained from RP families.
2. Screening of the RP known mutations in Indonesian families was succeeded to find a causative mutation of one family in this cohort. This approach is relatively cost-effective and simple to perform. Therefore, screening of all identified mutations in Indonesian cohort is useful before performing other methods.
3. Functional studies are required to prove pathogeneicity of each mutations.
4. The first Indonesian patient series was analyzed by means of homozygosity mapping two years ago with approximately 25 genes were reported. In the mean time, the numbers of identified arRP genes are increasing to 39 genes. Hence, reanalyzing homozygosity mapping data of this cohort with the recently identified RP genes is needed to find the genetic defects in the remaining unsolved cases.
5. Thus far, only a few data are available about non syndromic RP in Indonesian population, especially about causative genes. Further studies are needed to provide more data of prevalence rate of Indonesian RP and the genetic defects responsible for the disease.

6. Early interventions to slow the disease progression are needed. Life style modification is essential, such as minimize contact with the UV light, consumption of fruits and vegetables which rich of antioxidants, not smoking and alcohol consumption.
7. Next generation sequencing (NGS) applications have proven their potential in the novel disease gene identification for both homozygous and compound heterozygous mutations. Nonetheless, costs of NGS remain considerable, and the availability of other family members' samples is important to confirm the variants found in the NGS data. Therefore, selection is needed to include the families that suitable for this genotyping approach. Proband has to display a clear RP phenotype with multiple affected family members. Availibility of parents and siblings samples is also important in order to confirm the variants found in the NGS data.