

## CHAPTER VI

### CONCLUSION

In summary, a total of 358 differentially expressed circRNAs (DECs) were identified in YHV-infected shrimp through whole-transcriptome analysis. To validate these findings, qRT-PCR was applied to confirm the expression profiles of the identified DECs. The results obtained from circRNA-Seq and qRT-PCR were found to be consistent. The characteristics of circRNAs were further confirmed through RNase R treatment, PCR, and Sanger sequencing. The discovery of circRNAs in YHV-infected shrimp adds valuable insights to the shrimp genome, and these circRNAs hold promise as potential targets for preventing pathogen infections.