CHAPTER VII

CONCLUSION

For the genetic information, *gyr*A gene was amplified by PCR. The PCR products were used to detect mutation by DNA sequencing and heteroduplex formation. The results of the DNA sequencing procedure show that *gyr*A mutation was detected in 18/21 (85.71%) isolates, whereas 20 control isolates, fluoroquinolone-susceptible *M. tuberculosis*, show no mutation of *gyr*A gene. The 3/21 (14.29%) isolates lacked mutation in QRDR of *gyr*A. The results from this study indicated that *gyr*A gene mutation associated with ciprofloxacin-resistance in *M. tuberculosis* and the results displayed cross-resistance to both ciprofloxacin and ofloxacin. For evaluation PCR-HDF technique, it could not detect the differentiation between susceptible strain H37Rv and resistant strains.