

CHAPTER 5

CONCLUSION

The present study has investigated for the first time mtDNA D-loop sequences in Thai native pigs and Thai wild boars. The D-loop region begins at position 15434 and nucleotide sequence lengths of 1264 to 1324 bp were found depending on the length of the variable number tandem repeat (VNTR). The sequence alignment has revealed nucleotide variations at 54 from 1047 positions (including gap), representing 5.16% of the total sequence analyzed (1044 bp). Thai native pigs and Thai wild boars showed a highly variable region of 33 polymorphic sites compared with *Sus scrofa* (representing 3.15%). Within groups comparisons displayed 19 polymorphic sites, representing a variation of 1.85%. A total of 32 mtDNA haplotypes (14 Thai, 9 Asian and 9 European haplotypes) was found, which can be determined in two major groups. One was the European group and the other one was the Asian group.

The results propose that Thai native pigs and other Asian breeds may go back to a closely related common ancestor. There are similar in their mtDNA sequence but also distinctly different from the European breeds. The mtDNA D-loop analysis proved to be a valuable tool for revealing genetic relationships between and genetic diversity among the different Thai pig breeds.

Based on these results, we intend to continue with a large-scale investigation of Thai native pigs in other parts of Thailand. The genetic information from this study will be a benefit for conservation purposes and utilization of Thai indigenous pigs as an important genetic resource in the future.