

CHAPTER 6 CONCLUSION

This study provides not only the first large-scale genetic profiles of recent Thai people across Thailand, but also insights into the patterns of past demographic events in mainland Southeast Asia. The highly admixed genetic patterns of Thai individuals suggest historical gene flow patterns across the lowland of mainland Southeast Asia. Thai individuals have a high percentage of shared genetic components and close affinity with Chinese people, more so with those in the Southern part of China. This coincides with the expansion of Tai people from the Southern part of China into the lowland area that is now Thailand. However, genetic evidences show that recent Thai people are not made up entirely of one genetic source from ancestral Tai people from up north. Recent Thai individuals across Thailand also have another large genetic component shared with Iban people, who have close genetic relationship with indigenous Thai Ayutthaya people, whose genetic characters closely match those of indigenous Mon people. The relationship among these three indigenous people is brought together by the close relationship between recent Thai and Khmer people. This genetic finding provide a support for Tai-Austroasiatic assimilation in mainland Southeast Asia, reinforcing existing ethnolinguistic findings of overlapping characteristics in Tai and Khmer languages. Autosomal polymorphism studies which include a higher number of recent Khmer individuals and individuals from Myanmar, Laos and island Southeast Asia could shed more light into the pattern of inter-mixing genetic history of people in Thailand as well as other parts of mainland Southeast Asia.

Discreet substructure and high degree of genetic variations among Thai individuals address the need for careful subsampling in future genetic studies in mainland Southeast Asia. Despite the overall similar genetic admixture components, there are still discreet genetic substructures across the four geographical regions of Thailand, resulting from various genetic admixture component ratios. Within the same region, the genetic ratios also relatively vary among individual. Detailed subsampling could enhance the results of population genetic studies and improve the accuracy and usefulness of case-control studies in mainland Southeast Asia.