Chapter 5

Conclusion and Recommendation

5.1 Conclusion

1. All selected chicken microsatellite-flanking PCR primers can use to amplified microsatellite DNA from the Red Junglefowl's genomic DNA. five of six markers shown polymorphism which allele number of 9, 12, 8, 10 and 8 with number allele for HUJ1, HUJ2, HUJ7, LEI73 and LEI92 in 20 sampling respectively. Otherwise, AD37 locus were not shown a polymorphism, only two observed allele were found. Hence, many chicken microsatellite markers are possible to use for investigation of microsatellite variability of the Red Junglefowl.

2. Analysis of geographic heterogeneity using the marker chain "approximation to exact test" shown nin significant different between northern (n = 8) and southern (Chumphon province, n = 11) at HUJ1 (P = 0.103), HUJ2 (P = 0.313), HUJ7 (P = 0.065) and LEI92 (P = 0.465) locus whereas significant differnet in these locate was found out LEI73 (P = 0.013) locus. Comformity with Hardy-Weinberg expectation was found at almost loci (HUJ1, HUJ2, HUJ7 and LEI92) in northern locate. Unlike, only HUJ2 and LEI92 loci in southern locate (Chumphon province) conformed this expectation.

5.2 Recommendation

In order to determine genetic variation of the Red Junglefowl, chicken microsatellite markers is likely to be possible markers. For more precise-investigation, sample should collected as much as possible. Due to DNA extraction and microsatellite amplification, blood stain collection take advantage over feather samples. Genomic DNA extraction of blood stain appears to be easier and yield better quality of DNA template than that of feather. Optimal PCR condition for amplification of blood stain extracts is uniquely fitted to reference condition. Unlikely amplification from feather extract was difficult to obtain and diverse conritions were required. Consequently, condition optimization for feather extracts may take a lot of labor and cost. Blood stain sampling are recommend.