

## Chapter 5

### Conclusion and Recommendations

#### Conclusion

This study confirms the anatomical phylogeny which separate one subspecies from another on the basis of earlobe color.

Morphometric analysis of 5 characters gives no significant differences (4 out of 5), but there is one parameter, a beak length, that shows the difference between 2 populations.

DNA sequence analysis from partial D-loop sequencing (225 bp) separated one group from another using statistical analysis. In this principle, it is also found that there is a difference in some DNA sequences between the two groups.

The final conclusion would say that there are two subspecies of Red Junglefowl in Thailand using DNA analysis.

The DNA sequence analysis shows that *Gallus gallus spadiceus* samples have higher divergence in their nucleotide sequence than that of *G. g. gallus*: 15 sites versus 5 sites. Using the assumption that mutations accumulate through time of evolution, it is possible that *G. g. gallus* might have evolved from *G. g. spadiceus*.

In the genetic distance tree, specimen number G9 falls into the same group with another subspecies, which might be evidence of genetic hybridization with *G. g. spadiceus* but this needs confirmation by nuclear DNA profile.

The most parsimonious tree showed two distinctive groups with unclear polytomies, which are S84 and S85, G1, G2, G8 and G9. These samples show common characters in the observed 225 base pairs sequence even though their

morphology is different. The samples S84 and S85 that showed 100% homology might have common ancestor.

From the point of view of conservation genetics, the animal number G8 and G9 may not be appropriate to use as a parent stock for the *G. g. gallus* lineage because their DNA profile was closely related to their *G. g. spadiceus* counterparts. All other specimen would be good future breeding stock. Heterozygosity should be preserved through careful breeding management.

### **Recommendation**

In the further, the study of population genetics will be needed for the evaluation of genetic diversity as well as the status of the natural population in these two subspecies. Further data is still unclear in terms of animal morphology. Pure genetic stocks should be protected for the future as an important source of genetic diversity.

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