
Thesis Advisors: Asst. Prof. Dr. Monchai Duangjinda, Assoc. Prof. Banyat Laupaiboon

**ABSTRACT**

The first objective of this study was to classify the genetic similarity between 4 lines of Thai native chickens, Luang Hang Khao (LK), Pradoo Hang Dam (PD), Dang (DG), and Chee (CH). Phenotypic data (beak, feather and shank color) \(N = 288\) and molecular data (microsatellites) \(N = 353\) were used in the analyses. Genomic DNA was isolated from whole blood sampling from the Department of Livestock Development Research Center. Fifteen microsatellites with 73 alleles were typed for each individual. Dice’s similarity coefficients between animals were estimated. The result from cluster analysis and principal component plot from phenotypic data showed that Thai native chicken can be classified into 4 groups. The cluster analysis and principal component plot from microsatellites data showed that genetics between each line of Thai native chickens were hardly to differentiate. However, the analysis of Nei’s genetic distance showed the relatedness between LK and PD, and between DG and CH. This study also found that heterozygosity indices of LK, PD, DG and CH were 0.315, 0.365, 0.331 and 0.371, respectively. The subpopulation effects was slightly occurred \(F_{st} = 0.088\).

The second objective was to detect the DNA markers for specific characters for LK, PD, DG, and CH. The associations of microsatellites alleles with the specific lines were analyzed by logistic regression. The significant alleles was found only in LK (ADL268.4, MCW0081.1 and MCW0034.3), ประดู่ทรงตํา (ADL268.1, MCW0081.3, MCW0034.3, MCW295.3, MCW0037.1, MCW183.2, MCW183.3 and ADL122.2) and Chee (ADL268.6, MCW0081.4, MCW295.2, MCW295.5, MCW0037.4, LEI0166.5, MCW183.4 and MCW0104.1) with corrected prediction probability greater than 0.85.