

GENETIC DIVERSITY OF 12 CHINESE LOCAL CHICKEN BREEDS**C. L. Ji¹, G. H. Chen¹, M. Q. Wang², S. Weigend³**¹ College of Animal Science and Technology, Yangzhou University, Yangzhou, P. R. China;² Chemical Biology and Physics College, Yantai University, Yantai, 264005, P.R. China;³ Institute for Animal Breeding, Federal Agricultural Research Centre, Mariensee, 31535 Neustadt, Germany

China has a wide variety of indigenous chicken breeds, but little is known about their genetic differentiation. Assessment of genetic differences of these important genetic resources is an important prerequisite to establish efficient conservation measures.

In this study, genetic diversity of 12 Chinese indigenous chicken breeds were evaluated at the molecular level. In total, 448 individuals from the 12 Chinese breeds including Luyuan chicken (LY), Gushi chicken (GS), Tibetan chicken (TC), Baier chicken (BE), Xianju chicken (XJ), Chahua chicken (CH), Dagu chicken (DG), Beijing Fatty chicken (BF), Langshan chicken (LS), Henan Game chicken (HG), Taihe Silkies (TS) and Xiaoshan chicken (XS), were genotyped at 29 microsatellite loci. The F -statistics indices (WRIGHT, 1978), F_{IT} , F_{ST} , and F_{IS} were estimated using FSTAT program (GOUDET, 2002) to quantify the genetic variation within and among populations. A phylogenetic tree was constructed based on the Reynolds' genetic distance and the Neighbor-Joining method (FELSENSTEIN, 1995). A Bayesian approach for deducing population structure from multi-locus data, as implemented in the software package *structure* (PRITCHARD et al. 2000), were used to assess the relationship of the chicken breeds under study.

Genetic differentiation (F_{ST}) among breeds was, on average, 0.167 indicating that about 17% of the total genetic variation corresponded to differences between breeds, whereas the remaining 83% resulted from differences among individuals. All loci contributed to this differentiation significantly. The phylogenetic tree discovered two main branches; the light-body weight chicken breeds (TC, CH, BE, GS, XJ, and TS), and heavy-body type chicken breeds (LY, XS, BF, DG, LS, and HG).

Consistent clustering of breeds was obtained by *structure* program. At $K=2$, two main groups, the light-body type chickens and the heavy one, were found. For the six light populations, CH and TC separated first from remaining populations, and then did TS, GS, BE one by one along with a increasing number of k clusters. TC always appeared as a mixture population. The second set of breeds, the heavy-body weight populations, split first into two groups, one comprised LY, XS, and BF, and the other contained DG, HG, LS. Later, BF and LS formed separate clusters. In contrast, XS and LY fell together for any K value suggesting genetic exchange between these two populations. Solutions were consistent across ten runs for light group and heavy one, with all similarity coefficients above 0.97, except for $K=3$.

Key words: chicken, microsatellite, genetic differentiation, population structure

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