# GENETIC STRUCTURE AND DIVERSITY OF
# 12 CHINESE INDIGENOUS CHICKEN BREEDS

## Ji, C. L.,[1] Chen, G. H.,[1] Wang, M. Q.,[2] Weigend, S.[3†]

[1]College of Animal Science and Technology, Yangzhou University, Yangzhou, 225009, P. R. China; [2]Chemcial Biology and Physics College, Yantai University, Yantai, 264005, P.R. China; [3]Institute for Animal Breeding, Federal Agricultural Research Centre, Mariensee, 31535 Neustadt, Germany

[†] Presenting author: Steffen Weigend, Institute for Animal Breeding, Federal Agricultural Research Centre Mariensee, Hoeltystr. 10, 31535 Neustadt, Germany
steffen.weigend@fal.de

**Summary**
Genetic structure and diversity of 12 Chinese indigenous chicken breeds were evaluated using 29 microsatellite loci. Considerable breed differentiation were observed. About 17% of the total genetic variation originated from between breed differences. Two main clusters, heavy-body sized breeds and light ones, were found with both of the two methods, the Neighbor-joining -method based on the Reynolds' distance and the *structure* program.

**Key words**
Chicken, microsatellite, genetic differentiation, genetic structure

**Introduction**
With its long history of animal husbandry and diversified geographical conditions, China has a wide variety of indigenous poultry resources. Most of them are local and fancy breeds characterized by medium or low performance and often maintained in small populations. However, as a result of the introduction of modern commercial chicken breeds and the limitation for conservation measures, some populations have decreased rapidly in population sizes. In this study, we typed 12 Chinese indigenous chicken breeds at 29 microsatellite loci to assess their genetic structure and diversity. The results may be useful to understand genetic differentiation of these important local chicken genetic resources.

**Materials and methods**
448 individuals from 12 Chinese indigenous chicken 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 with 29 microsatellite markers. The $F$-statistics indices [1], $F_{IT}$, $F_{ST}$, and $F_{IS}$ were estimated using FSTAT program [2] to quantify the genetic variation within and among populations. The Neighbor-Joining method [3] based on the Reynolds' distance and the *structure* program [4] implemented a Bayesian approach for deducing population structure from multi-locus data were used to assess the relationship of chicken breeds, respectively. Similarity coefficients were computed for an ordered pair of *structure* runs with the same number of assumed clusters, using the program *simcoeff2.perl* [5].

**Results and discussion**
In our study, on average, the genetic differentiation ($F_{ST}$) among breeds was 0.167, a very high value and extremely significant(p<0.001), which suggested that about 17% of the total

genetic variation corresponded to differences of breeds and the remaining 83% was the result of differences among individuals. All loci contributed to this differentiation significantly. Using Reynolds' genetic distance and the Neighbor-joining method, a phylogenetic tree was reconstructed for 12 Chinese indigenous chicken breeds. Tree topology resulted in two groups. Light-body sized chicken breeds, including TC, CH, BE, GS, XJ, and TS, formed a branch; the heavy-body type, LY, XS, BF, DG, LS, and HG formed another one.

Consistent clustering result of breeds was obtained by *structure* program (Figure 1). For total data, two groups were acquired (K=2), light-body type chickens and heavy one. For the six light populations, CH and TC separated from remaining populations of this set, and then did TS, GS, BE one by one along with the number of clusters k increasing. TC always appear as a mixture population. At K=2, heavy-body populations split into two groups, one contained LY, XS, and BF, the other contained DG, HG, LS. And at K=3, BF formed separate cluster. At K=4, LS comprised the cluster. And for any K value, XS and LY always fell together. These two population could not be separated, even when k equalled 6. Solutions were consistent across ten runs for light group and heavy one, with all similarity coefficients (Table 1) above 0.97, except for K=3.

**Figure 1**: Estimated population structure. From total data, ten *structure* runs at k=2 produced nearly identical individual membership coefficients, with pair-wise similarity coefficients above 0.93, two major groups appeared, light-body type populations and heavy type one. We subdivided total data into two groups, and then run *structure* ten times from k=2 to 6 with light type data and heavy type data, respectively. The figure shown for a given k is based on the highest probability run at that k.
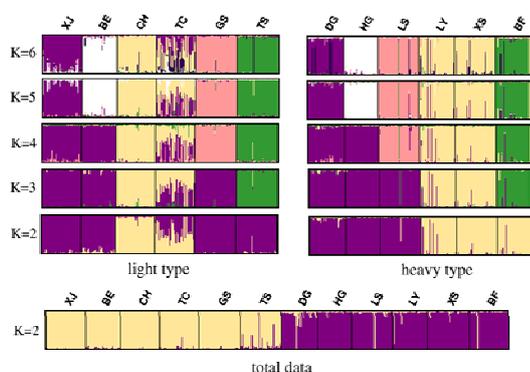


**Table 1** Average similarity coefficients for total data, light type data and heavy data

|            | K=2   | K=3   | K=4   | K=5   | K=6   | K=7   | K=8   |
|------------|-------|-------|-------|-------|-------|-------|-------|
| Total data | 0.930 | 0.184 | 0.261 | 0.209 | 0.239 | 0.513 | 0.505 |
| Heavy type | 0.997 | 0.516 | 0.997 | 0.996 | 0.972 |       |       |
| Light type | 0.998 | 0.636 | 0.996 | 0.994 | 0.976 |       |       |

In conclusion, we assess the variation within and among populations in 12 Chinese indigenous chicken breeds. Three major points were acquired: (1) two main groups, light-type group and heavy one, were acquired in 12 Chinese chicken breeds; (2) Relative large genetic exchange exists between Xiaoshan chicken and Luyuan chicken, and Tibetan chicken appeared as a mixture population; (3) Structure program clustered the analysed populations well, and specified that Tibetan chicken appeared as a mixture population, and such information can not be found from the methods based on genetic distance.

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