Available online at www.sciencedirect.com
ScienceDirect
Journal of Integrative Agriculture
2014, 13(4): 849-857
April 2014
RESEARCH ARTICLE

Analysis of the Genetic Diversity and Origin of Some Chinese Domestic Duck Breeds

ZHANG Yang[1], CHEN Yang[2], ZHEN Ting[1], HUANG Zheng-yang[1], CHEN Chang-yi[1, 2], LI Xin-yu[1, 2], DUAN Xiu-jun[3], DONG Biao[3], XU Qi[1] and CHEN Guo-hong[1]

[1] *College of Animal Science and Technology, Yangzhou University, Yangzhou 225009, P.R.China*
[2] *College of Animal Science and Technology, Jiangxi Agricultural University, Nanchang 330045, P.R.China*
[3] *Vocational and Technical College of Jiangsu Animal Husbandry and Veterinary College, Taizhou 225300, P.R.China*

Abstract

Twelve fluorescence-labeled microsatellite markers were used to analyze the genetic diversity of 12 domestic duck breeds and 2 wild duck breeds to determine the relationship and origin of Chinese domestic duck breeds. Gene frequency, effective number of alleles (N_e), expected heterozygosity (H_e), polymorphism information contents (PIC), inbreeding coefficient in population (F_{is}), standard genetic distance (D_S), and genetic distance (D_A) were calculated by FSTAT and distance and phylogenetic analysis after the dates which were output from the Microsatellite-Toolkit software. Genetic distances between 12 domestic duck breeds and 2 wild duck breeds were analyzed by variance analysis. Unweighted pair group method with arithmetic mean (UPGMA) and phylogenetic trees used for cluster analysis were structured. The results indicated that 11 loci had medium- or high-level genetic diversity among the 12 loci, which could be efficiently used in the detection of the genetic parameters of each population. The values of H_e were 0.5414 to 0.7343, those of PIC proved similar, and those of F_{is} were 0.1101 to 0.3381 among all populations. All breeds were clustered into three groups by UPGMA phylogenetic trees. Banzui duck was clustered into a separate group. Differences of the D_A were analysed by *t*-test. The results showed that difference in D_A between the 12 domestic duck breeds and Lvtou duck and the Banzui duck were very significant ($P<0.01$), indicating that these 12 domestic duck breeds originated from Lvtou wild duck, but not Banzui duck.

Key words: wild duck, Chinese domestic duck, origin, microsatellite DNA marker, cluster analysis

INTRODUCTION

Taxonomically, Chinese domestic ducks representing waterfowls belong to the Anseriformes, Anatidae, sub-family *Anas platyrhynchos* domestic. Two academic views (Monadism and Dualism) exist regarding the origin and evolution of Chinese domestic ducks (Chang 2009). Some scholars believe that Chinese domestic ducks originated from Lvtou wild duck (wild mallards *A. platyrhynchos*), whereas others argue that Chinese domestic ducks originated from wild mallards (*A. platyrhynchos*) and Banzui duck (spot-billed *Anas zonorhyncha*), or domesticated from hybrids of *A. platyrhynchos* and *A. zonorhyncha*. China is a country with a vast territory, various geographical, ecological, and climatic conditions, and a variety of people with different habits and customs. With long-term natural selection and artificial selection, Chinese domestic duck breeds with different characteristics evolved in the environment (Chen 2004). The local variety with very ample genetic diversity is the basis for future fowl varietal improvement and adaptation to production condition changes (West *et al.* 1989).

Received 1 November, 2012 Accepted 28 January, 2013
ZHANG Yang, E-mail: zhangyang19860808@126.com; Correspondence CHEN Guo-hong, E-mail: ghchen@yzu.edu.cn

doi: 10.1016/S2095-3119(13)60447-5

Locality factors, such as natural geography isolation, artificial selection, and introduction, cause the lack of marketability of some Chinese domestic duck breed performances and even the most cherished genetic resources (Editorial Board of the Situation of Livestock and Poultry in China 2004; Wang 2006). Therefore, studying the genetic diversity of domestic duck breeds and determining their genetic structures and origin are necessary to formulate reasonable strategies for conservation and breeding, exploitation, and utilization (Zhang 2007; Li 2009). The microsatellite marker is a new molecular marker that is widely applied (Crooijmans *et al.* 1999; Romanov *et al.* 1999) in the construction of genetic linkage maps of poultry, localization of quantitative trait loci (Zhang 2006), research of molecular diversity (Tang *et al.* 2007), and pedigree identity (Machugh *et al.* 1994; Crooijmans *et al.* 1996) because it has many merits, such as high polymorphism, co-dominance in genetics and adherence to Mendel genetic law, convenient detection and good repetition, and wide distribution in the genome (Ellegren *et al.* 1992; Johansson *et al.* 1992). The diversity and origin of some Chinese domestic ducks have been studied based on molecular markers (Yan *et al.* 2005; Li *et al*. 2007; Zhang *et al*. 2007; He *et al*. 2008). However, no consensus has been reached about the origin of Chinese domestic ducks.

In this paper, we investigated the genetic diversity of 12 Chinese domestic duck breeds and 2 wild duck breeds on the molecular level to reveal the current situation of their genetic diversity. Cluster analysis was used based on genetic distances to discuss the genetic relationship among domestic duck breeds and the relationship between 2 wild duck and domestic duck breeds. Our data provided theoretical basis for proper evaluation, protection and utilization, origin, and evolution of Chinese domestic ducks.

RESULTS

Genomic DNA extraction of ducks

Absorbed light curve and concentration of the extracted blood genome DNA were measured by a NanoDrop ND-1 000 concentration analyzer after dissolved by Tris-ethylenediaminetetraacetic acid (EDTA) solution overnight. The curve was smooth and OD_{260}/OD_{280} was between 1.8 and 2.0. Thus, the quality of the extracted DNA samples can completely satisfy the requirements of amplification for microsatellite loci.

Genetic parameters of each microsatellite locus

Effective number of alleles (N_e) was used to assay the effect of alleles in each population and to reflect the genetic variation expressed by inverse homozygosity. Polymorphic information content (PIC) reflecting the abundance of microsatellite loci is a good index for genetic diversity evaluation. Heterozygosity (H_e) refers to the frequency of heterozygotes that indicate the heterozygous level of alleles on the same locus; it is one of the indices used to assay the genetic variation of each population (Crooijmans *et al*. 1995). The calculated results of the genetic parameters (Table 1) were obtained with the Microsatellite-Toolkit and distance and phylogenetic analysis (Dispan) software.

Table 1 Indices of the genetics of 12 microsatellite loci in 14 duck breeds

Loci	No.	N_e	PIC	H_e	F_{is}
AY493256	14	6.8475	0.7516	0.7851	0.1036
CMO11	12	2.6830	0.4509	0.5343	0.1577
APH01	16	2.4819	0.4910	0.5619	0.2825
APL2	43	9.0766	0.7945	0.8189	0.1572
AJ515884	14	4.5955	0.6904	0.7310	0.1936
AJ272579	12	3.0959	0.5068	0.5814	0.1401
AJ515887	16	6.1941	0.6122	0.6535	0.1473
AY493313	8	2.8030	0.4932	0.5371	0.3023
AJ272578	11	1.4592	0.2373	0.2716	0.0693
AJ272577	11	2.6877	0.4396	0.4954	0.386
AJ515893	17	2.9687	0.5076	0.5715	0.5434
AY493289	12	3.1629	0.6074	0.6459	0.2091
Mean	15.5	4.0047	0.5485	0.5989	0.2243

N_e, effective number of alleles; PIC, polymorphism information contents; H_e, expected heterozygosity; F_{is}, inbreeding coefficient in population.

As shown in Table 1, the allele number of the 12 microsatellite loci was the highest (43) on APL2, whereas the lowest (8) was on AY493313. The average number of all loci was 15.5, with effective number of alleles varying from 1.4592 to 9.0766. Effective number of alleles of all loci exceeded 2, except AJ272578. PIC of the 12 loci was the highest