Livestock Science 184 (2016) 85–91

Contents lists available at ScienceDirect

Livestock Science

journal homepage: www.elsevier.com/locate/livsci

Monitoring of genetic diversity in Taiwan conserved chickens assessed by pedigree and molecular data

Manh-Hung Pham [a,b,*], Xuan-Hoan Tran [c], Cécile Berthouly-Salazar [d], Michèle Tixier-Boichard [e], Chih-Feng Chen [a,f], Yen-Pai Lee [a]

[a] Department of Animal Science, National Chung-Hsing University, Taichung 40227, Taiwan
[b] Faculty of Animal Science, Vietnam National University of Agriculture, Trau Quy Town, Gia Lam District, Ha Noi City, VietNam
[c] Key Laboratory of Animal Cell Technology, National Institute of Animal Sciences, Tu Liem, Hanoi, VietNam
[d] Institut de Recherche pour le Développement, UMR Diversité, Adaptation et Développement des Plantes (DIADE), Avenue Agropolis, BP 64501, 34394 Montpellier Cedex 5, France
[e] INRA/AgroParisTech, UMR1313 Génétique Animale et Biologie Intégrative, Jouy-en-Josas, France
[f] Research Center for Integrative and Evolutionary Galliformes Genomics (iEGG), National Chung-Hsing University, Taichung 40227, Taiwan

ARTICLE INFO

Article history:
Received 9 August 2015
Received in revised form
27 December 2015
Accepted 29 December 2015

Keywords:
Conservation priorities
Effective population sizes
Inbreeding
Molecular data
Pedigree information

ABSTRACT

Local chicken breeds face high risks of extinction. A conservation program has been set up for eight Taiwan conserved chicken populations (TCP). The research presented here aims at estimating effective population size (N_e) and conservation priorities of TCP populations using pedigree and molecular data. Genome diversity was assessed by genotyping 22 microsatellite markers in 45–50 animals per breed. Results from the pedigree-based analysis showed that most N_e values ranged between 50 and 100 except the Shek-Ki breed which exhibited the smallest value (46) so that most breeds could be considered as safe from a conservation point of view. The change in inbreeding per generation varied between 0.7% to 1.9% depending on breeds. N_e values estimated from molecular-based analysis were generally lower than those estimated from pedigree-based analysis, suggesting a loss of diversity between the onset of the conservation program (from 1983 to 1995) and the start of pedigree recording in 2002. According to N_e values, the TCP populations do not appear to be at a high risk, but mating plans by a rotation mating system should be designed in order to limit the increase in inbreeding. Regarding the conservation strategy within the TCP, the Shek-Ki and Hua-Tung breeds showed the highest priority for conservation in terms of genetic risk status and contributions to total diversity across pedigree- and molecular-based approaches. In conclusion, this study of TCP populations shows how different types of data can be combined to define conservation priorities considering risk, diversity, or utility of local chicken breeds.

1. Introduction

Local chicken breeds play an important role in Taiwan due to the traditional cuisine and culture. Local chicken breeds may carry disease-resistant genes and show high abilities to adapt to alternative farming systems, such as organic, which will particularly improve animal welfare and food safety (Fanatico et al., 2009; Pham et al., 2012) as well as adaptation to harsh environmental conditions (Tixier-Boichard et al., 2009). Phenotypic data and pedigree information have proven to be useful for characterization and management of genetic diversity (Boichard et al., 1997; Tixier-Boichard et al., 2009; Lenstra et al., 2012). Unfortunately, phenotypic data and pedigree records of local chickens are rarely documented in reality (Tixier-Boichard et al., 2009). Therefore, molecular markers are used to monitor the loss of genetic diversity of populations and set priorities for conservation (Boettcher et al., 2010).

FAO (2014) reported that 21.3 percent of chicken breeds in the world were classified as being at risk of extinction, highlighting the importance to assess genetic diversity and the current population status. This percentage might be higher than that because of a large number of populations with an unknown status in developing countries. Basically, there are three strategies for setting priorities in conservation such as the maximum-risk strategy, the maximum-diversity strategy as well as the maximum-utility strategy (Bennewitz et al., 2007).

The maximum-risk strategy is based on the numbers of

* Corresponding author at: Faculty of Animal Science, Vietnam National University of Agriculture, Trau Quy Town, Gia Lam District, Ha Noi City, VietNam.
E-mail addresses: phammanhhung@vnua.edu.vn (M.-H. Pham), hoantranvcn@yahoo.com (X.-H. Tran), c.berthouly@gmail.com (C. Berthouly-Salazar), michele.boichard@jouy.inra.fr (M. Tixier-Boichard), cfchen@dragon.nchu.edu.tw (C.-F. Chen), yplee@mail.nchu.edu.tw (Y.-P. Lee).

http://dx.doi.org/10.1016/j.livsci.2015.12.013
1871-1413/

breeding animals (FAO, 2000), inbreeding rate (EAAP, 1998; Meuwissen, 2009) and recommended effective population size (N_e) (Meuwissen, 2009). The N_e measures the number of breeding individuals in an idealized population in equilibrium that would show a similar trend in inbreeding as the population under study, it is one of the most pivotal parameters in both evolutionary biology and conservation of genetic diversity (Waples and Do, 2010; Goyache et al., 2011; Leroy et al., 2013). This parameter is considered as one of the major criteria for monitoring risk status in livestock populations because it accounts for inbreeding and loss of genetic diversity through random genetic drift (Falconer and Mackay, 1996; Meuwissen, 2009). Leroy et al. (2013) showed that estimates of effective population size varied according to the within-breed genetic structure, for different species (i.e. cattle, dog, horse and sheep).

The maximum-diversity strategy defines that a breed is selected for conservation when it contributes significantly to the overall genetic diversity weighted by both the between- and within-breed diversity. Breeds can be ranked according to their contribution either to the actual or to the predicted future diversity (Bennewitz et al., 2007). For instance, Zanetti et al. (2010) set up conservation priorities for five Italian local chicken breeds undergoing *in situ* conservation using 20 microsatellites. In the case of Vietnamese domestic chickens, Pham et al. (2013a) showed that black H'mong, Lien Minh and Luong Phuong were ranked with the highest priorities for conservation according to Caballero and Toro (2002), and Petit et al. (1998) approaches, taking into account within- and between-breeds components of diversity.

When possible, pedigree information and molecular data should be combined for decision making of conservation priorities (Zanetti et al., 2010). Pedigree-based and molecular-based estimates of genetic diversity may be more or less correlated depending on the pedigree completeness and the number of markers (Toro et al., 2006) as illustrated in Iberian pigs with correlations between pedigree inbreeding and marker homozygosity ranging from 0.69 with 49 microsatellites (Toro et al., 2002) to 0.92 with 60 K SNPs (Silió et al., 2010). Furthermore, perfect correlations between approaches cannot be reached because pedigree-based estimates do not take into account Mendelian sampling, and it is known that full-sibs would share between 45% and 55% of their genes rather than exactly 50% in a traditional relationship matrix (VanRaden and Tooker, 2007). An additional difference between pedigree- and molecular-based analyses is the definition of the founder population, which depends on the depth of pedigree for pedigree-based analysis, the more complete the pedigree, the more ancient the founder population (Falconer and Mackay, 1996). Consequently, pedigree- and molecular-based analysis is using different information, as pedigree-based analysis reflects only diversity due to relatively recent ancestry, depending on the population history (Toro et al., 2006; Engelsma et al., 2012).

The purposes of this study were (i) to assess genetic diversity with pedigree-based estimates and molecular-based estimates for eight populations kept under a conservation program in Taiwan since 1982, and (ii) to monitor trends in genetic diversity and to make recommendations for conservation strategy.

2. Material and methods

2.1. Data

Conservation of native chickens in Taiwan started from 1982, when native chickens were collected around the islands and conserved at National Chung-Hsing University (NCHU) experimental farm. Eight Taiwan conserved chicken populations (TCP: B strain, L2 strain, Hsin-Yi, Hua-Tung, Ju-Chi, Nagoya, Quemoy and Shek-Ki) have been conserved at NCHU experimental farm since then (Lee, 2006). The L2 and B strains were selected by NCHU from the same Taiwan native chicken population (Lee, 2006). Both strains were closed populations since their establishment in 1983, while B strain was a male line and a L2 female line for crossing to produce commercial meat-type chicken. Since then, they have been selected for 24 and 26 generations, respectively, and have been extensively used in research as well as in production (Chao and Lee, 2001; Chen et al., 2007; Pham et al., 2013b). A small number of parents were used to set up the first generation for eight populations between 1984 and 1995 (Table 1). The management of conserved chicken populations followed a routine procedure (Chao and Lee, 2001). Chicks were raised in floor pens until 16 week of age, when they were transferred to individual wire floored cages. Artificial insemination was individually used for the female chickens with sire known and dam known. On the average, the generation interval of TCP populations was one generation per year (Table 2). For the present study, pedigree information recorded between 2002 (starting with ancestors in 2001) and 2008 were used to estimate the effective population size with different methods. The pedigree information included a total of 4283 individuals and the numbers of founders at the onset of pedigree recording are shown in Table 2. In addition, samples from 383 individuals (i.e. 288 individuals from six TCP born in 2003 and 95 individuals from B and L2 strains born in 2008) were genotyped and part of the data was previously published (Berthouly et al., 2008; Chang et al., 2012; Pham et al., 2013b). Briefly, an average of 48 individuals per population was genotyped for 22 microsatellites among FAO (2011) recommended markers. These

Table 1
Pedigree information in the first generation of the eight populations when conservation program started.

Population	First generation				
	Year	Sire	Dam	N_{es}	ΔF
B strain (BS)	1984	6	20	18.5	2.71
L2 strain (LS)	1984	5	28	17.0	2.95
Hsin-Yi (HY)	1984	7	15	19.1	2.62
Hua-Tung (HT)	1990	2	4	5.3	9.38
Ju-Chi (JC)	1986	12	38	36.5	1.37
Nagoya (NG)	1989	9	22	25.5	1.96
Quemoy (KM)	1995	1	4	3.2	15.63
Shek-Ki (KT)	1989	6	19	18.2	2.74

N_{es}, effective population size based on number of sires and dams; and ΔF, rate of hypothetical inbreeding (in percentage) for a population with such an effective population size.

Table 2
Number of founders at the onset of pedigree recording and average number of male and female in the 2002–2008 periods for the eight populations.

Population	Founders in 2001				2002–2008 generations				
	Sire	Dam	N_{es}	ΔF	N_m	N_f	N_{es}	ΔF	g_{2008}
B strain	5	35	17.5	2.86	11.2	76.8	39.1	1.28	6
L2 strain	16	328	61.0	0.82	20.8	194.2	75.2	0.67	5
Hsin-Yi	22	30	50.8	0.98	17.6	34.1	46.4	1.08	6
Hua-Tung	19	40	51.5	0.97	17.7	37.4	48.1	1.04	6
Ju-Chi	19	36	49.7	1.01	20.1	40.4	53.8	0.93	6
Nagoya	21	39	54.6	0.92	17.7	43.4	50.3	0.99	6
Quemoy	25	44	63.8	0.78	16.7	43.1	48.2	1.04	6
Shek-Ki	16	35	43.9	1.14	13.6	32.6	38.3	1.30	6

N_{es}, effective population size based on number of founder animals; ΔF, rate of hypothetical inbreeding (in percentage) expected for a population with N_{es}; N_m, average number of male; N_f, average number of female; N_{es}, effective population size based on number of breeding animals; and ΔF, rate of hypothetical inbreeding (in percentage) expected for a population with N_{es} across the 2002–2008 generations; g_{2008}, number of generations known for the last generations.