Mitochondrial DNA Diversity of Korean Ogol Chicken

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ABSTRACT

한국재래오골계는 천연기념물로 등록이 되어 있어 세계의 중요한 유전자원 중 하나이다. 현재 한국에서 사육되어 있는 오골계의 유전적 특성을 규명하기 위하여 미토콘드리아 DNA의 변이를 이용하여 계통 분석을 실시하였다. 총 31 마리의 한국재래오골계가 이 분석에 이용되었으며 10개의 haplotypes이 관찰되었다. NJ 방법으로 만들어진 계통도 분석을 통하여 이미 닭에서 알려진 A부터 C의 lineage를 포함하는 것으로 보아 한국 재래오골계는 아직도 높은 유전적 다형성을 유지하고 있음을 알 수 있었다. 이 연구 결과는 한국재래오골계의 육종 및 보존 계획을 세우는데 유용하게 이용될 수 있을 것으로 사료된다.

▶ **Key words** : phylogenetic analysis, Korean Ogol chicken, mitochondrial DNA (mtDNA), D-loop

INTRODUCTION

The displacement loop (D-loop) is the major control region for mtDNA expression. The mtDNA polymorphism, especially the D-loop region, has been largely applied to investigate the structure of populations, about the origins and nature of the domestication process, phylogenetic relationships between chicken populations (Niu et al., 2002; Liu et al., 2004; Liu et al., 2006). The Korean Ogol chicken has been registered as a natural monument (registration number 265) and the conservation program has been being carried out for this breed. In this study, the current phylogenetic status and genetic diversities of Korean Ogol chicken has been investigated in order to understand the genetic basis of this breed and ultimately contribute to make better breeding and conservation strategies.

MATERIALS AND METHODS

Blood samples of 31 Korean Ogol chicken chickens were collected from National Livestock Research Institute (NLRI) in Korea. Genomic DNAs were extracted according to the manufacturer's protocol using Magextractor (Toyobo Ltd, Japan). Partial mitochondrial D-loop region was amplified directly from the genomic DNA by polymerase chain reaction (PCR). The primer pair, described by Niu et al. (2002), was used to amplify first 510 bp segment of the D-loop hypervariable region. Sequencing reaction was performed by using Big Dye Terminator Cycle Sequencing Ready Reaction Kit (v 3.0) and electrophoresis was done by a 3100 DNA sequencer (Applied Biosystems, CA, USA). The sequences were

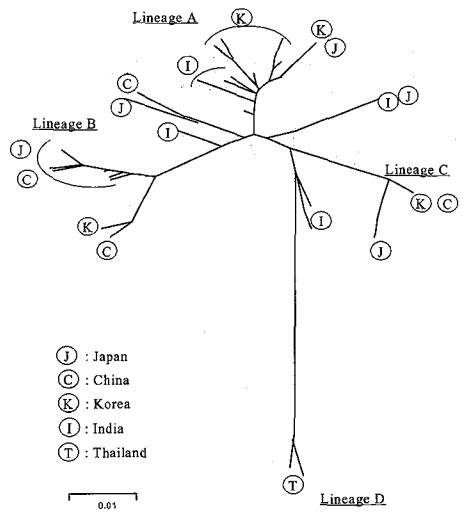

Fig1. Unrooted neighbor-joining tree constructed from Japan, China, Korea, Thailand and Indian native chicken populations. Different letters are used to denote respective country.

aligned by ClustalW program (Thompson et al., 1994). Genetic distances and phylogenetic analyses were performed using MEGA software ver. 3.1 (Kumar *et al.*, 2004) and AMOVA was performed by Arlequin ver. 3.01 (Excoffier *et al.*, 2006). We included published mtDNA sequence data in our analyses from domestic chicken populations of Japan, China, India and Thailand. The nucleotide sequences of Korean Ogol chicken have been deposited in GenBank under accession numbers from DQ629864 to DQ629894.

RESULTS AND DISCUSSION

Mitochondrial sequences analyses from 31 Korean Ogol chicken represented 10 different haplotypes and 25 variable base substitutions were determined. OG 6 and OG 8 were found to be two major haplotypes represented each 6 times, whereas OG 7 represented 5 times; OG 2, OG 3 and OG 9 represented 3 times; OG 1 occurred twice and 3 haplotypes are unique. No deletion or insertion was detected in our sequences. The average percentage of polymorphic sites was 4.9 for 510 bp of 31 DNA sequences of Korean Ogol chicken. The transition versus transversion rate was 16% indicating a heavy bias towards the transition substitution. Variance components estimation with AMOVA indicated that 67% of the variability was due to differentiation within chicken population ($P < 0.001$).

The highest sequence divergence value (0.054) was observed between China and Thailand chicken populations and the lowest value (0.014) displayed in between Korea and India. Mean sequence divergence values in between populations ranged from 0.014 to 0.018 among the countries of Japan, China, Korea and India, that indicates Korean Ogol chicken population was more closely related with 4 Asian countries than Thailand. Considering within population, Korean Ogol chicken showed higher sequence divergence value (0.014) than Chinese, Indian and Thai domestic chicken populations (0.009-0.010). This supports the existence of more genetic variability in Korean Ogol chicken than the three Asian countries except Japanese chicken population (0.018). The un-rooted tree indicates that Japanese, Korean and Indian chicken belong to the three major chicken lineages (A to C) representing these populations has the highest mtDNA sequence diversity in the Asian chicken populations investigated (Fig 1). Here, it is noted that

the present Korean Ogol chicken breed shared 3 common maternal lineages. Lineage A contained 7 haplotypes of Korean Ogol chicken and that represented 54.8% (17/31) of the total samples whereas, lineage B and C represented 16.1 % and 29.0 % of the total samples. The haplotypes of Korean Ogol chicken are concentrated mainly in specific regions of mt lineage A indicates they were inbred within Korean peninsula for a long time.

In this study, we found that the Korean Ogol chicken still maintains genetic variability to some extent within the small population. In order to maintain this genetic variation for this valuable breed, appropriate conservation breeding program is ultimately needed. However, more detailed molecular studies are required in near future.

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