ABSTRACT

Indonesia as an archipelagic country has a variety of local sheep. The most familiar Indonesian local sheep are Indonesian Fat Tail sheep (IFT), Indonesian Thin Tail sheep (ITT), and Garut sheep. However, there are not many of genetic studies to classify Indonesian local sheep. The genetic study is necessary in order to determine the identity, genetic relationship, and diversity over local sheep population. Furthermore, it can be used as the basis for management in livestock. Popular marker used to analyses the genetic relationship are mitochondrial DNA (mtDNA) and Y chromosome. The aim of this study is to determine phylogeny and origin of the maternal and paternal lineage in Garut sheep of fighting type (GAF), Garut sheep of mutton type (GAM), and Indonesian Fat Tail sheep (IFT). The high level of genetic diversity is found in analysis of the 427 bp of the mitochondrial DNA control region sequences from GAF, GAM, and IFT population. Whereas analysis of the 732 bp SRY gene sequences is found no variation. The genetic distance within population based on mtDNA analysis on GAF, GAM, and IFT are 0.0370, 0.0424 and 0.0105, respectively. In a total, 28 mtDNA haplotype was confirmed but single haplotype is found in SRY. That mtDNA haplotype is divided into two main groups, i.e. type A (10 haplotype) and type B (18 haplotype). Type A is commonly found and distributed in sheep breed population over Asian mainland whereas type B is in Europe.

Keywords: phylogeny, genetic diversity, Indonesian local sheep, mitochondrial DNA, SRY gene, Garut sheep, Fat Tail sheep
SUMMARY

Naturally, Indonesia has no indigenous species of sheep. They are domestic sheep (*Ovis aries*) which were introduced by human to Indonesia archipelago for particular purpose. The origin of domestic sheep has been suggested from domestication of wild species/subspecies of sheep (*O. vignei, O. musimon musimon* and *O. musimon orientalis*). The domestication event is widely accepted begin in the Near and Middle East between 9000 to 5000 BC.

Indonesia is an archipelagic country consist of thousands island with varies local climates, geographics, and cultures. Those characteristic gives a chance for the formation of local sheep that have adapted to its condition. The most familiar Indonesian local sheep are Indonesian Fat Tail sheep (IFT), Indonesian Thin Tail sheep (ITT), and Garut sheep. Garut sheep is unique because of its phenotype character, functions, and values. Garut sheep is product of cultural selection, i.e. fighting contest.

Genetic characterization of Indonesian local sheep has been less conducted. Accordingly, this research was conducted to determine phylogeny and the origin of the maternal and paternal lineage in Garut sheep of fighting type (GAF), Garut sheep of mutton type (GAM), and Indonesian Fat Tail sheep (IFT) in Indonesia. Mitochondrial DNA (mtDNA) control region (dloop) is used to determine maternal lineage, while SRY gene is used to determine paternal lineage. The research was conducted from July 2009 through January 2010 at the division of Animal Behaviour and Biological Function, Laboratory of Zoology, Department of Biology, Faculty of Mathematics and Sciences, Bogor Agricultural University. Genomic DNA was obtained from whole blood of 25 Garut sheep of fighting type, 11 Garut sheep of mutton type, and 20 Indonesian Fat Tail sheep. All samples were collected from sheep husbandries in Garut, Bandung, and Bogor.

DNA extraction was conducted according to Sambrook’s standard protocol with some modifications. A total 56 rams and ewes were amplified and sequenced for mtDNA control region. But, only 25 rams were amplified and sequenced for SRY gene. For mtDNA control region, the primer were 15388F [5'-GCCCCACTATCAACACCCAAAG-3'] and CD744R [5'-AATGGGCGATTTTAGATGAGATGGC-3'] that generate 823 bp visualized on 6% polyacrylamide gel electrophoresis. Its amplicon were then amplified using CR653-rev [5'-GAAGAAAGAACCAGATGCCT-3' ] for sequenced. For SRY gene, the primer were AF130 [5'-GGTAAAAGTGCAGAAGAGAGTGAT-3'] and AF132 [5'-TCTAGAGCCACCTTTC GTCTTC-3'] that generate 1150 bp visualized on 6% polyacrylamide gel electrophoresis.

The length of the corresponding mitochondrial DNA sequence data is 427 bp, while the SRY gene is 754 bp. Both of them were analyzed separately to determine the phylogeny, genetic distances, and its diversity.

A high diversity is showed in mtDNA control region. The genetic distance within populations are 0.0105 (IFT), 0.0370 (GAF), and 0.0424 (GAM). The genetic distances between population are relatively similar (GAF/GAM = 0.0377; GAF/IFT = 0.0386; GAM/IFT = 0.0395). Average diversity overall populations are 0.0345. A total of 28 mtDNA haplotypes were identified. A phylogenetic tree was constructed using a neighbor joining method and two main clades were confirmed. They are type A (Asian) and type B (European) based on GenBank sequence data. Type A consists of 10 haplotypes from both type of Garut sheep population, while type B consists of 18 haplotypes from Garut sheep and IFT populations. A network using median joining method agrees with the phylogenetic tree.

The analysis of SRY gene nucleotide sequences shows a different case with mitochondrial DNA. There is no diversity found in SRY gene in three population samples.

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