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Asian Journal of Animal and Veterinary Advances



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Research Article

Molecular Phylogenetic of Hutan Sumatera Goat (Sumatran Serow) and Domestic Goat (*Capra hircus*) in Indonesia Based on Analysis Mitochondrial Cytochrome b Gene

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Abstract

Background: Hutan Sumatera goat (Sumatran serow) is one of wildlife that is quite similar to the domestic goats and have never been investigated at the molecular level. Indonesian society believes that Hutan Sumatera goat belongs to the group of the genus *Capra*, therefore, this animal is called a wild goat or forest goat. Hutan Sumatera goat has been categorized as an endangered species in the IUCN as red list. **Materials and Methods:** The genomic DNA of Sumatran serow and Indonesian goat were isolated by gSYNC DNA Mini Kit (Geneaid) and cytochrome b gene was amplified using PCR method with a pair of primer. Cytochrome b gene region was amplified completely from all samples with a length 1140 bp. **Results:** Alignment results show that there are many nucleotide differences between Hutan Sumatera goat and Indonesian domestic goats. Translation nucleotide results indicate that there are 11 different amino acids between Hutan Sumatera goat and domestic goats except with JAW (12 amino acids) and GS (10 amino acids). The percentage of A+T and G+C on Hutan Sumatera goat is 56.4 and 43.6%, whereas the Indonesian domestic goat is 58.6 and 41.4%. Using the restriction enzyme *Bam*HI results in differences fragments between Hutan Sumatera goats and domestic goats. In the Cyt b gene Hutan Sumatera goat was cut on site 561 bp to produce two DNA bands, while in the domestic goat there is no cutting of DNA fragments at the site. **Conclusion:** The genetic distance between Hutan Sumatera goats ranged from 0.001-0.004, while the Hutan Sumatera goat to domestic goat ranged from 0.001-0.118. Based on a phylogenetic tree analysis, Hutan Sumatera goat form a group with genus *Capricornis*. This suggests that goat Hutan Sumatera goat is a part of the genus *Capricornis*.

Key words: Goat, genetic distance, mtDNA cytochrome b, phylogenetic, sumatran serow

Received: December 10, 2015

Accepted: March 31, 2016

Published: May 15, 2016

Editor: Dr. Kuldeep Dhama, Principal Scientist, Division of Pathology, Indian Veterinary Research Institute (IVRI), Izatnagar, Uttar Pradesh, India

Citation: Suhendra Pakpahan, Wayan Tunas Artama, Rini Widayanti and I. Gede Suparta, 2016. Molecular phylogenetic of Hutan Sumatera goat (sumatran serow) and domestic goat (*Capra hircus*) in Indonesia based on analysis mitochondrial cytochrome b gene. Asian J. Anim. Vet. Adv., 11: 331-340.

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Competing Interest: The authors have declared that no competing interest exists.

Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Indonesia is one country that has huge biological resources. Many species of animals and plants are not yet known and not well identified. Hutan Sumatera goat (Sumatran serow) is one of the wildlife that is quite similar phenotype to the domestic goats and has never been characterized. Indonesian society believe that this animal belong to the group of the genus *Capra*, so that this animal is called a wild goat or forest goat. This animal is already very rare because of the occurrence of deforestation and illegal poaching^{1,2}.

Capricornis has several subspecies is *C. crispus* (Japanese serow, restricted to Japan), *C. milneedwardsii* (Chinese serow, but also occurring in Southeast Asian countries), *C. rubidus* (Red serow, restricted to Myanmar), *C. sumateraensis* (Sumatera serow, in Indonesia, Malaysia and Southern Thailand), *C. swinhoei* (Formosan serow, restricted to Taiwan, Province of China), *C. thar* (Himalayan serow, along the Himalayan range). It spread only in Asia, covering India, Southern China, Burma, Thailand, Malaysia and Indonesia³. Hutan Sumatera goats located in Indonesia are a subspecies where its spread is only found in the mountains and highlands of Sumatera, namely in Mount Kerinci, Padang Highlands, Mount Talaman, Tapanuli, Mount Leuser, the area North side of the river Alas, lake Gunung Tujuh and Lampung⁴.

Hutan Sumatera goat has been categorized as an endangered species in the IUCN as red list. Many studies of morphology and ecology have raised debate about the taxonomy serow. Studies show that the serow chromosomes of chromosome arm number (NF) are 60, but the karyotype of the Sumatera serow (*C. sumateraensis*), the Japanese serow (*C. crispus*) and the Formosan serow (*C. swinhoei*) showed a diploid number of $2n = 48^5$, 50^6 and 50^7 .

Mitochondrial DNA (mtDNA) is a genetic marker that is very important because it is passed down the maternal without recombination and has a high mutation rate. Because of these genetic features, mtDNA becomes genetic markers that are very useful for studying the origins, genetic diversity and divergence of the two species having a close relationship⁸⁻¹⁰. Mitochondrial cytochrome b gene sequence has been used previously in studies of the molecular phylogenetic group Bovidae and other mammals¹¹⁻¹⁴.

The purpose of this study is to clarify the status of Hutan Sumatera goat species (*C. sumateraensis*) and determine the phylogenetic position of Hutan Sumatera goat with domestic goat in Indonesia and other Capricornis obtained from GenBank, based on cytochrome b gene sequences. The results of this study provide information about phylogenetic relationships between Hutan Sumatera goat and domestic goat breeds in Indonesia.

MATERIALS AND METHODS

Sample collection: This study used blood and hair follicle from individuals and Hutan Sumatera goat samples collected from the forests of North Sumatera (Fig. 1), where the animal had died due to illegal poaching by local people. Nine subpopulations of domestic goat breeds in Indonesia (Fig. 2), namely: Samosir goat (SAM), Muara goat (MUR), Gunung Sumatera (GS) goat, Peranakan Etawah (PE), Jawarandu goat (JAW) and Kacang goat (KC), Lakor goat (LAK), Gembrong goat (GEM), Marica goat (MAR). The samples of goat with purposive sampling method determine first the district native goat production centers (Fig. 1), then the specified districts and villages.

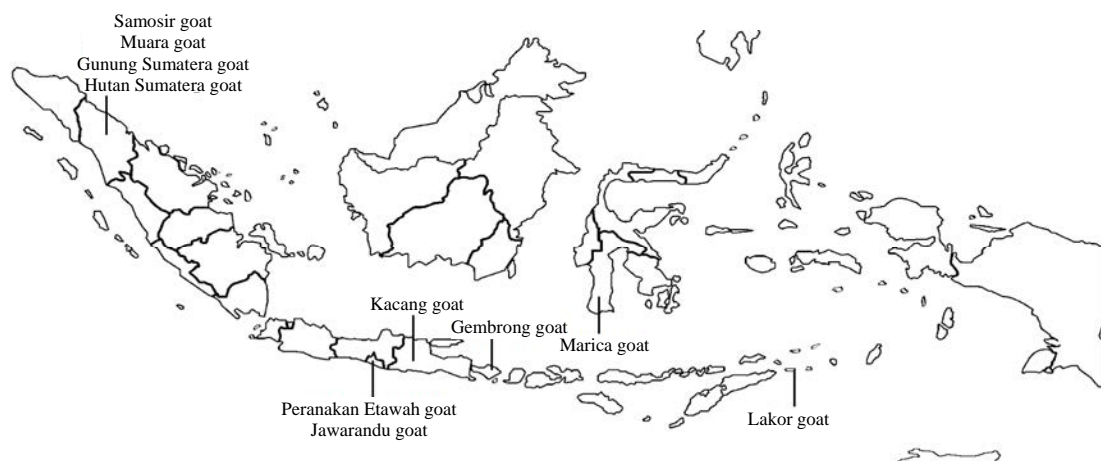


Fig. 1: Location of sampling Hutan Sumatera goat and domestic goats in Indonesia



Fig. 2(a-j): Morphology of Hutan Sumatera goat and domestic goat breeds in Indonesia, (a) Hutan Sumatera goat, (b) Gunung Sumatera goat, (c) Samosir goat, (d) Muara goat, (e) Marica goat, (f) Kacang goat, (g) Gembrong goat, (h) Peranakan Etawah goat, (i) Jawarandu goat and (j) Lakor goat^{15,16}

Molecular techniques: The blood and hair follicle samples were isolated using the gSYNC™ DNA Mini Kit (Geneaid). The primers used to amplify Cyt b was as follows: SCF:- 5'GGAATCTAACCATGACCAAT-3' and SCR:- 5'GCTTCTCCTTGAGTCTTAG-3'¹⁷. The PCR conditions were:

The DNA template 3 µL, Kapa 2G Ready Mix 25 µL, each forward and reverse primer 1 µL (10 pmol) and ddH₂O in a total of 50 µL. The PCR amplification was conducted using a Infinigen Thermal Cycler according to the program, an initial denaturation at 94°C for 6 min, Followed by 35 cycles,

each consisting of 30 sec denaturation at 94°C, 45 sec primers annealing at 47°C, 90 sec elongation at 72°C, then a final 5 min elongation at 72°C and storage at 4°C. The PCR product was visualized using 1% agarose gel (5 µL PCR products added with 2 µL of loading dye). Electrophoresis was run on 100 V condition for 40 min and the amplification result could be seen on the UV light. The purified PCR products were sequenced directly by 1st BASE Sequencing INT (Singapore).

Data analysis: Long amplification products Cyt b gene sequence was 1140 bp for each individual and analyzed using MEGA software version 6.0¹⁸. The Cyt b gene sequences in this study aligned with other Cyt b sequences of *Capra* from GenBank using Clustal W contained in the MEGA program. Analysis of genetic variation seen by differences in the nucleotide sequences of the cytochrome b gene. Genetic distances were analyzed by the method of Kimura two parameters¹⁹. Phylogenetic tree (Neighbor-joining tree) was built on Cyt b nucleotide sequences with repetition 1000x bootstrap test²⁰ and Kimura 2-parameter method²¹.

Furthermore, to give a more complete information, several Cyt b gene sequences of domestic and wild goats were downloaded from GenBank and used as a comparator to Hutan Sumatera goat and domestic goats in order to see the genetic distance and estimates its origin. The access codes in GeneBank are as follows: *Capra hircus* (AB736144), *C. aegagrus* (AB110593), *C. falconeri* (D84202), *Capricornis crispus* (D32191), *Capricornis milneedwardsii maritimus* (EF558665), *Capricornis sumateraensis* (DQ459334), *Capricornis swinhoei* (EF558665).

RESULTS

Complete cytochrome b sequences of Hutan Sumatera goat:

Cytochrome b gene region was amplified completely from all samples with a length 1140 bp. Alignment results show that there are many nucleotide differences (126 sites) between the Hutan Sumatera goat and domestic goat breeds in Indonesia (Fig. 3). In this study Goat Sumatra consists of 3 haplotypes, while the domestic goats consist of 6 haplotypes. Among domestic goat breeds have similar nucleotide of Cyt b. It shows that the Hutan Sumatera goat has different ancestors (different genus) from domestic goat breeds of Indonesia.

Aligned amino acid from translation products of the entire nucleotide sequences of Cyt b (1140 bp) was obtained 380 amino acids. Translation results indicate that there were 10-12 differences of amino acids between Hutan Sumatera goat and domestic goats (Table 1). Amino acid of Hutan

Table 1: Differences of amino acids in Hutan Sumatera goat with Indonesian domestic goats based on cytochrome b sequences

	1	6	9	2	9	1	3	5	0	2	6	6
Breed	7	0	8	2	0	5	8	7	2	4	5	8
HS 1	A	T	V	T	M	T	T	T	A	L	L	V
HS 2
HS 3
SAM	.	M	I	A	T	A	V	I	V	M	M	A
MUR	.	M	I	A	T	A	V	I	V	M	M	A
PE	.	M	I	A	T	A	V	I	V	M	M	A
JAW	P	M	I	A	T	A	V	I	V	M	M	A
KAC	.	M	I	A	T	A	V	I	V	M	M	A
LAK	.	M	I	A	T	A	V	I	V	M	M	A
GEM	.	M	I	A	T	A	V	I	V	M	M	A
MAR	.	M	I	A	T	A	V	I	V	M	M	A
GS	.	M	I	A	T	.	V	I	V	M	M	A

Dots indicate identities to Hutan Sumatera goat 1 (HS 1) sequence at the top

Table 2: Composition of nucleotide bases per sample

Breed	T	C	A	G	Total
HS 1	24.7	30.7	31.8	12.8	1140.0
HS 2	24.6	31.0	31.7	12.8	1140.0
HS 3	24.6	30.8	31.8	12.8	1140.0
SAM	26.8	28.2	31.8	13.2	1140.0
MUR	26.8	28.2	31.8	13.2	1140.0
PE	26.8	28.2	31.8	13.2	1140.0
JAW	26.8	28.2	31.8	13.1	1140.0
KAC	26.8	28.2	31.8	13.2	1140.0
LAK	26.8	28.2	31.8	13.2	1140.0
GEM	26.8	28.2	31.8	13.2	1140.0
MAR	26.8	28.2	31.8	13.2	1140.0
GS	26.8	28.2	31.9	13.1	1140.0

Sumatera goats (HS 1, HS 2, HS 3) is 100% similar, while the domestic goats was compared to Hutan Sumatera goats there are 12 different amino acids. On the sequence 17th, there is a difference only in JAW goat (A-P).

Nucleotide composition shows an average difference of each nucleotide base. On Hutan Sumatera goat average percentage of nucleotide bases of T, C, A and G are 24.6, 30.8, 31.8 and 12.8%, respectively, while the Indonesian domestic goats are 26.8, 28.2, 31.8 and 13.2%, respectively (Table 2). The percentage of A+T and G+C in Hutan Sumatera goats are 56.4 and 43.6%, while the Indonesian domestic goats are 58.6 and 41.4%. It shows that the composition of the A+T of mtDNA Cyt b is higher in both types of species.

Application of PCR-RFLP technique: The PCR-RFLP is a DNA fragment specific amplification using a primer pair specific/universal resulting fragments in question. Amplification of the target area using SCF primer: 5'-GGAATCTAACCATGACCAAT-3' and SCR: -5'GCTTCTCTCTTGAGTCTTAG-3' generate target throughout 1287 bp.

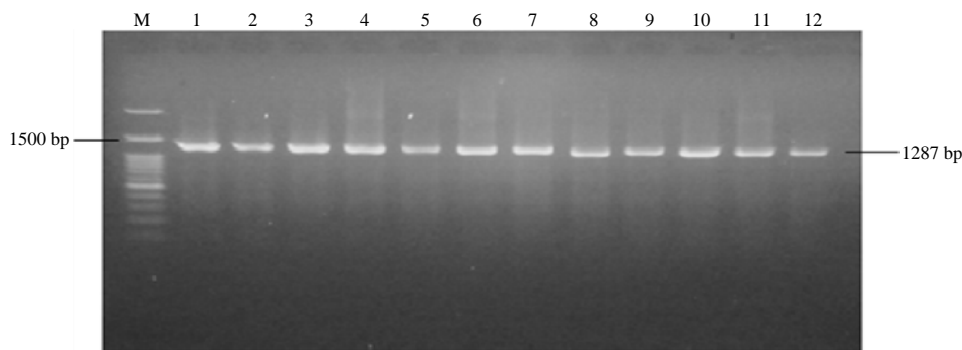


Fig. 4: Electrophoresis of Cyt b amplification from 12 samples in size of 1287 bp. Lane M: DNA marker ladder. Lane 1-12 are the PCR products. Lane 1: HS 1, Lane 2: HS 2, Lane 3: HS 3, Lane 4: SAM, Lane 5: MUR, Lane 6: PE, Lane 7: JAW, Lane 8: KAC, Lane 9: LAK, Lane 10: GEM, Lane 11: MAR and Lane 12: GS

BamHI

accatgccgcgtgaaccagcaaccgctgggcaaggatcctcttctcgctccgggccattaattgtgggggt base pairs
 tggtagggcgaccttggctgttgggagccggtcctaggagagaagagcgaggcccggttaattaacaccccca 526 to 600

Fig. 5: Site is cut by *Bam*HI enzymes in Cyt B Hutan Sumatera goat

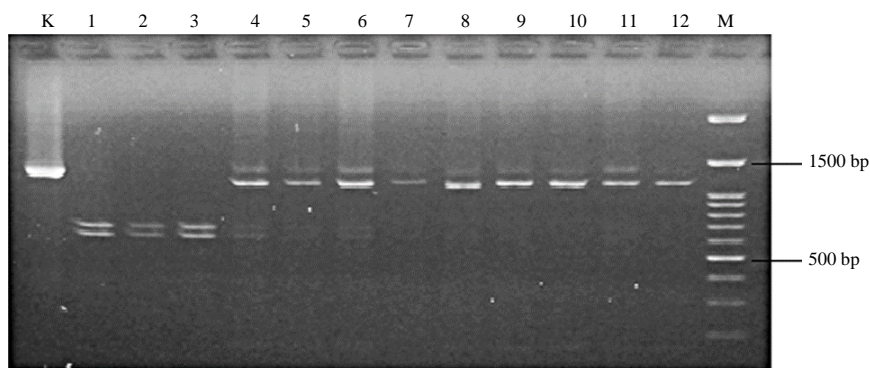


Fig. 6: Electrophoresis of PCR products digested by *Bam*H1 enzyme roomates. Lane M: Marker DNA ladder. Control (K). Lane 1: HS 1, Lane 2: HS 2, Lane 3: HS 3, Lane 4: SAM, Lane 5: MUR, Lane 6: PE, Lane 7: JAW, Lane 8: KAC, Lane 9: LAK, Lane 10: GEM, Lane 11: MAR and Lane 12: GS

goat ranged from 0.001-0.004 (Fig. 7), while the genetic distance of Hutan Sumatera goat to domestic goat ranged from 0.001-0.118. Some domestic goat Indonesia has a very close genetic distance once as Kacang with Lakor, Gembrong with Kacang, Kacang with Marica. Highest genetic distance between Hutan Sumatera goat and Gunung Sumatera goat is 0.118.

Based on mtDNA Cyt b sequences, Hutan Sumatera goat (Sumatran serow) has a genetic distance which is quite close to the *Capricornis sumatraensis* species is 0.012. This provides evidence that Hutan Sumatera goat has a very close relationship to *C. sumatraensis*. The farthest genetic distance

between Hutan Sumatera goat and some members of the genus *Capricornis* is against *Capricornis crispus* 0.054, in which *C. crispus* is found in the three main islands of Japan, i.e., Honshu, Shikoku and Kyushu²⁴.

Phylogenetic relationships between Hutan Sumatera goat and Indonesian domestic goat: Phylogenetic tree was constructed using Neighbor Joining (NJ) method from Kimura 2-parameter method. All Cyt b sequences of Hutan Sumatera goat and nine subpopulations domestic goat and some genus *Capricornis* were analyzed using Kimura 2-parameter method²¹.

Breed	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	
HS 1																				
HS 2	0.004																			
HS 3	0.001	0.004																		
SAM	0.112	0.110	0.111																	
MUR	0.114	0.112	0.113	0.002																
PE	0.114	0.112	0.113	0.002	0.002															
JAW	0.113	0.111	0.112	0.001	0.003	0.003														
KAC	0.113	0.111	0.112	0.001	0.001	0.001	0.002													
LAK	0.113	0.111	0.112	0.001	0.001	0.001	0.002	0.000												
GEM	0.113	0.111	0.112	0.001	0.001	0.001	0.002	0.000	0.000											
MAR	0.113	0.111	0.112	0.001	0.001	0.001	0.002	0.000	0.000	0.000										
GS	0.118	0.116	0.117	0.006	0.006	0.006	0.007	0.005	0.005	0.005	0.005									
<i>Capricornis milneedwardsii</i>	0.114	0.017	0.015	0.118	0.120	0.120	0.119	0.119	0.119	0.119	0.119	0.123								
<i>Capricornis sumatrensis</i>	0.012	0.014	0.012	0.118	0.120	0.120	0.119	0.119	0.119	0.119	0.119	0.123	0.003							
<i>Capricornis swinhoei</i>	0.035	0.040	0.036	0.113	0.115	0.116	0.114	0.114	0.114	0.114	0.114	0.121	0.041	0.038						
<i>Capricornis crispus</i>	0.054	0.055	0.055	0.114	0.116	0.117	0.115	0.115	0.115	0.115	0.115	0.118	0.056	0.055	0.062					
<i>Capra falconeri</i>	0.108	0.106	0.107	0.048	0.048	0.048	0.049	0.047	0.047	0.047	0.047	0.043	0.112	0.111	0.108	0.109				
<i>Capra hircus</i>	0.109	0.109	0.110	0.044	0.044	0.044	0.045	0.043	0.043	0.043	0.043	0.039	0.116	0.115	0.107	0.115	0.020			
<i>Capra aegagrus</i>	0.109	0.109	0.110	0.036	0.036	0.036	0.037	0.035	0.035	0.035	0.035	0.034	0.118	0.117	0.113	0.114	0.040	0.027		

Fig. 7: Pairwise distances of mitochondrial cytochrome b gene of the Hutan Sumatera goats (Sumatran serow) and Indonesian domestic goats using the Kimura 2-parameter models

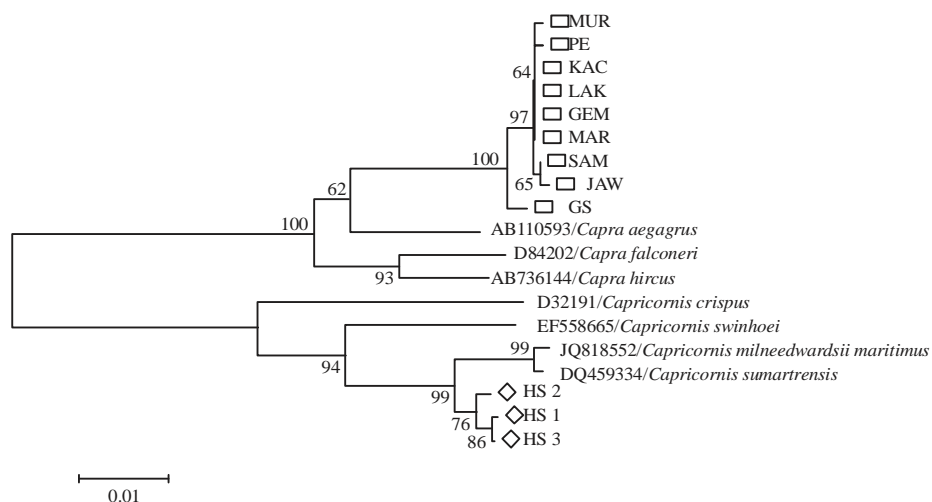


Fig. 8: Phylogenetic tree (neighbor-joining analysis(NJ)) of the Hutan Sumatera goat with domestic goat breeds and some species of genus Caprinae from GenBank based on mtDNA cytochrome b sequences and neighbor-joining analysis. The scale indicates numbers of nucleotide substitution per site. Numbers above branches are for percent supports in 1,000 bootstrap replications

Hutan Sumatera goat species are separated clearly from Indonesian domestic goats as well as other *Capra* species. Hutan Sumatera goat forms a group with genus *Capricornis* and *Naemorhaedus* (Fig. 8 and 9). This suggests to Bechstein in 1799 that Hutan Sumatera goat is part of the genus *Capricornis*. Hutan Sumatera goat subspecies differ with *Capricornis sumatrensis* (from GenBank) supported bootstrap value of 99%. Indonesian domestic goats form a group together with several species *Capra* from GenBank.

Evolutionary relationships of taxa: The evolutionary history was inferred using the Neighbor-Joining method²⁵. The optimal tree with the sum of branch length = 0.22499083 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches²⁰. The tree is drawn to scale with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Kimura 2-parameter method²¹ and are in the units of the

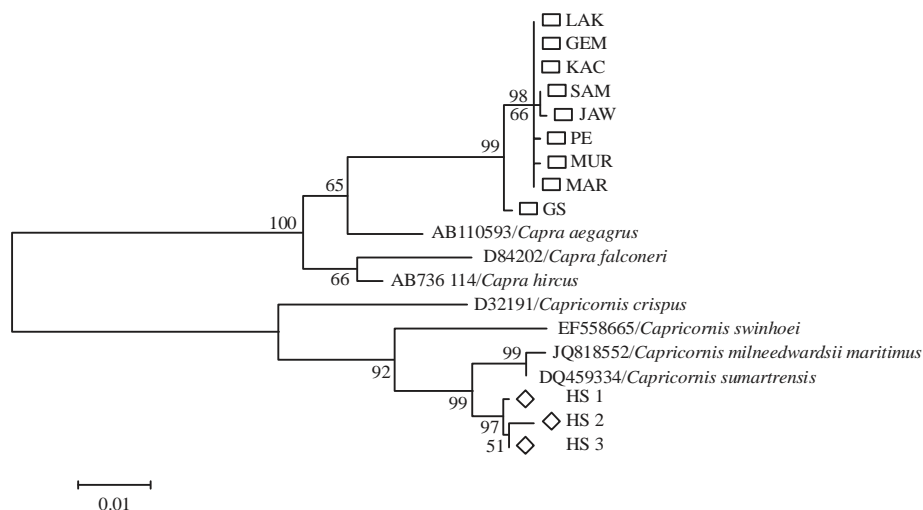


Fig. 9: Phylogenetic tree (maximum-likelihood analysis (ML)) of the Hutan Sumatera goat with domestic goat breeds and some species of genus Caprinae from GenBank based on mtDNA cytochrome b sequences and neighbor-joining analysis. The scale indicates numbers of nucleotide substitution per site. Numbers above branches are for percent supports in 1,000 bootstrap replications

No. of base substitutions per site. The analysis involved 19 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 1140 positions in the final dataset. Evolutionary analyses were conducted in MEGA6¹⁸.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Kimura 2-parameter model²¹. The tree with the highest log likelihood (-2954.4799) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the No. of substitutions per site. The analysis involved 19 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 1140 positions in the final dataset. Evolutionary analyses were conducted in MEGA6¹⁸.

DISCUSSION

Habitat and population of Hutan Sumatera goat (*Capricornis sumateraensis*): Mountains and forests along Sumatera island are the habitat of Hutan Sumatera goat. These

animals live in the wild and usually take shelter in the rocks of the mountains. Forest destruction and poaching makes the population oppressed. Government has made the protection of these animals with the Wild Animal Protection Regulations 1931 No. 266 enacted since, 1931. The habitat Hutan Sumatera goat this time, the remaining is Mount Kerinci, Padang Highlands, Mount Talaman, Tapanuli, Mount Leuser, Mamas river, especially areas valley and the area north side of the river Alas, lake Gunung Tujuh and Lampung (KSDA Extension Directorate). Hutan Sumatera goat population is until now unknown but according to the International Union for the Conservation of Nature and Natural Resources (IUCN) has been categorized as vulnerable (VU). These animals are very difficult to be identified and monitored as these animals have a keen sense of smell and hearing³.

Phylogenetic relationship of Hutan Sumatera goat: The present study on Hutan Sumatera goat (Sumatran serow) phylogenetics emphasizes the importance of accurate information on the taxonomic status of Sumatran serow, because the No. of Sumatran serow in nature is very small, this study is only to clarify the phylogenetic status among Hutan Sumatera goat and domestic goat in Indonesia. Never there has been study on Sumatran serow molecularly. Until now, phylogenetic status of Hutan Sumatera goat is not clear.

Phylogenetic relationships and genetic variation among 9 Indonesian goat breeds had have been analyzed using cytochrome b gene sequences. The relationship between sub-population of Indonesian goats are very close¹⁷.

According to phylogenetic tree analysis using Cyt b gene sequences to the conclusion that the Hutan Sumatera goat forms separate groups to Indonesian domestic goats. Hutan Sumatra goat phenotypically similar to the Indonesian domestic goat (*Capra hircus*). Male and female of Hutan Sumatera goat have a pair of curved, narrow and sharp pointed horns and long ear which are longer than the size of the horns. Sumateran goat has a gland that look like a rounded bulge around the eyes and has rather dense body hairs, coarse and black²⁶.

A single concordant topology was obtained from all analyses (NJ and ML). Species of the genus *Capricornis* are clearly separated from the others with 100% bootstrap value. Hutan Sumatera goat is a member of the genus *Capricornis* where the genus comprises several species, namely *Capricornis crispus*, *milneedwardsii*, *rubidus*, *sumatraensis*, *swinhoe* and *thar*.

According to study by Min *et al.*²⁴ on genetic distance *C. crispus* and *C. sumatraensis* shows that the genetic distance is 0.109. While in this study, the genetic distance between the Sumatran serow with *C. crispus* was 0.054. This may be possible due to differences in sampling sites so that there is a genetic variation.

Conservation in Indonesia: One of the main causes of the decline of species in Indonesia is over-exploitation, although, there are some estimates, the illegal trade in Indonesian flora and fauna is estimated to reach tens of millions dollars per year, reflecting the huge losses of the Indonesian economy and the devastating loss of cultural heritage and environment of Indonesia. Although, the existing legal and regulatory framework that is comprehensive and derivatives designed to prevent losses, poachers, traders, shippers and buyers wildlife can still avoid these regulations²⁷. Hunting of Hutan Sumatera goat in the beginning is to get the food source but eventually develop up to an economic community to get the skin as wall hangings and horns. Hutan Sumatera goat horns trusted people can neutralize toxins and treat some diseases. The existence of special properties of Hutan Sumatera goat horns, making the hunt intensified, so that the Hutan Sumatera goat population is diminishing and rare to the point at the moment²⁸.

The success of the legal trade in animal products will depend on the ability to identify specimens that belong to protected species of animals and how many products are traded legally can affect wildlife populations of the region. Utilization of molecular tools in the field of ecology to preserve the existence of wildlife and prohibits traffic wildlife products²⁹. With the discovery of these results, it can be used

a genetic marker in identifying Hutan Sumatera goat samples of poaching result. The PCR technology that is increasingly sophisticated and inexpensive, then this can be realized in identifying.

Pursuant to the Law on Forestry No. 41/1999, Conservation Forest is a forest area with a specific characteristic with the main function for conservation of biodiversity and their ecosystem. Such a forest area is divided into three categories, namely Sanctuary Reserve Area, Nature Conservation Area and Game Hunting Park Sanctuary Reserve Area is a forest with specific characteristic with its main function is to preserve wildlife and plant species and their ecosystem and serve as life supporting system. Forests as providers of the highest biodiversity not only save natural resources such as wood, but also has an important role in many aspects of life. Until the year 2013, 54 units of organizations and implementing partners have done conservation project, while the captive unit of plants and wildlife to 2013 has 776 units. Based on recalculation of land cover, forest conditions around 33.6% is forested. The forest area of Sumatra island consists of forest conservation covering an area of 4.73 million ha, protected forest covering an area of 5.85 million ha and production forest covering an area of 16.68 million ha³⁰.

CONCLUSION

Genetic distance among Hutan Sumatera goats ranged from 0.001-0.004, while between Hutan Sumatera goat with goat domestic ranged from 0.001-0.118. On Hutan Sumatera goat average percentage of nucleotide bases of T, C, A and G, respectively 24.6, 30.8, 31.8 and 12.8%, while the Indonesian domestic goat is 26.8, 28.2, 31.8 and 13.2%. By using PCR-RFLP method, the Cyt b gene of Hutan Sumatera goats are cut on site to produce two 561 bp DNA band of sheep domestication while there is no cutting of DNA fragments at the site. Hutan Sumatera goat species are separated clearly from Indonesian domestic goats as well as other *Capricornis* species. Hutan Sumatera goat genus form a group with *Capricornis*.

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