Biologia
https://doi.org/10.1007/s11756-022-01234-0

ORIGINAL ARTICLE

Andaman local goat: mitochondrial genome characterization and lineage analysis

Arun Kumar De[1] · Jai Sunder[1] · Ramachandran Muthiyan[1] · Sneha Sawhney[1] · Perumal Ponraj[1] · Eaknath Bhanudasrao Chakurkar[1] · Debasis Bhattacharya[1]

Received: 24 June 2022 / Accepted: 30 September 2022

Abstract

Andaman local goat (ALG) is an endemic goat germplasm of Andaman and Nicobar Islands, notable for its adaptability to the hot and humid climate of these islands. Due to lack of a proper breeding plan and indiscriminate crossbreeding, the breed is under threat and its population is on a declining trend. Designing and implementation of a proper breeding plan necessitates the genetic characterization of the breed. Moreover, origin, evolution and phylogeography of the breed is still not well understood. Therefore, the present study deals with next generation sequencing based whole mitochondrial genome characterization of Andaman local goat and its evolutionary relationship with different goat breeds all over the world. The mitogenome was 16,640 bp in length containing 13 protein coding genes (PCGs), 22 transfer RNAs (tRNAs), 2 ribosomal RNA subunits (rRNAs) and a non-coding region. Nucleotide composition and AT-GC skewness indicated that the mitogenome had a biasedness towards A + T over G + C. Incomplete or truncated stop codon was detected in *ND1*, *ND2*, *COX3*, *ND3* and *ND4*. Presence of 16 intergenic spacer regions of length ranging from1 bp to 7 bp and 8 overlapping regions ranging from 1 to 40 bp were also detected. Phylogenetic analysis indicated that ALG is included under haplogroup or lineage A of *Capra*. Moreover, evolutionary analysis revealed that ALG formed a separate cluster and was phylogenetically close to some Chinese goat breeds and Jamnapari goat breed of Bangladesh. The findings of the study throw light on the evolution of the breed and will be vital for sketching a suitable breeding programme for the conservation of the breed.

Keywords Andaman local goat · Mitogenome · Evolution · Andaman and Nicobar Islands · Conservation

Abbreviations

ALG	Andaman local goat
D-loop	Displacement loop
FAO	Food and Agriculture Organization
HVR-1	Hypervariable region 1
Lat.	Latitude
Lon.	Longitude
NJ	Neighbor-joining
mtDNA	Mitochondrial DNA
PCGs	Protein coding genes
rRNAs	Ribosomal RNA subunits
RSCU	Relative synonymous codon usage
SNPs	Single nucleotide polymorphisms
tRNAs	Transfer RNAs

✉ Debasis Bhattacharya
debasis63@rediffmail.com

Arun Kumar De
biotech.cari@gmail.com

[1] Animal Science Division, ICAR-Central Island Agricultural Research Institute, Port Blair, Andaman and Nicobar Islands 744101, India

Introduction

Domestic goats are considered as assets for resource poor and marginal farmers due to their immense contribution to nutritional and livelihood security (Kumar et al. 2010; MacHugh and Bradley 2001; Lohani and Bhandari 2021). Goats possess the unique ability to adapt to a range of environments and climatic conditions ranging from humid tropical region to hot dry region to high altitude cold hypoxic regions (Berihulay et al. 2019); therefore, they are distributed throughout the world. Moreover, goats are considered to be very much resilient to impending climate change due to their remarkable ability to cope with different environmental stressors and adversities (Nair et al. 2021). As per Domestic

Published online: 20 October 2022

Animal Diversity Information System (DAD-IS) of Food and Agriculture Organization (FAO), about 1200 breeds of domestic goat have been described (http://dad.fao.org).

Domestication process of goat is very much well studied and it is believed that goats were domesticated through pray pathway, in which wild animals were hunt and brought to human periphery for meat purpose (Larson and Burger 2013; Zeder 2012). Archaeological data suggested that domestication of goats initiated in the Fertile Crescent around ~ 11,000 years ago (Zeder and Hesse 2000). Wild bezoar (*Capra aegagrus*) is considered as the progenitor of domestic goat (Alberto et al. 2018; Naderi et al. 2008; Zeder 2008). However, gene flow from other *Capra* species played a significant role in shaping the genetic structure of domestic goats (Zheng et al. 2020). Following domestication, goats spread globally and varied selection pressure and gene flow led to genetic and phenotypic alterations and evolution of different breeds (Ahmad et al. 2020). As per the latest information, domestic goats are classified into six highly divergent lineages or haplogroups based on the hypervariable segment of mitochondrial DNA (mtDNA) control region; A, B, C (Luikart et al. 2001), D (Sultana et al. 2003), F (Sardina et al. 2006) G (Naderi et al. 2007). Lineage A is present throughout the world whereas other lineages are concentrated in different regions (Chen et al. 2005; Luikart et al. 2001; Naderi et al. 2007). Therefore, lineage analysis of ALG will be of great interest and throw light on the origin of the breed.

Mitochondrial DNA is a very popular genetic marker for phylogenetic analysis, molecular diversity study and in evolution related analysis of species (Galtier et al. 2009; Kemp et al. 2017; Moray et al. 2014). Based on the literature, it has been found that most researchers focus on a particular region of mtDNA, most commonly control region, *cytochrome B* or *cytochrome oxidase I* for phylogenetic studies (Avise et al. 1987; Farias et al. 2001; Harrison 1989). *Cytochrome B* and *cytochrome oxidase I* were used to analyse the genetic diversity, phylogeny and origin of several goat breeds like Kacang and Senduro goats of East Java (Suyadi et al. 2022), Samosir goat, Muara goat, Gunung Sumatera goat, Perenakan Etawah goat, Jawarandu goat, Lakor goat, Gembrong goat and Marica goat of Indonesia (Pakpahan et al. 2016), Black Bengal and Jamunapari goats of Bangladesh (Chowdhury et al. 2019), 13 Chinese indigenous goat breeds (Chen et al. 2006) and Lakor goats from the Southwest Maluku Regency of Indonesia (Rumanta et al. 2020). Mitochondrial rRNA genes are being used for species identification (Ramadan 2011; Yang et al. 2014) as well as molecular characterization of livestock species (Mahmoodi et al. 2018; Saikia et al. 2016). Phylogenetic trees based on these single markers sometimes suffer from low resolution or contradictory topologies (Sasaki et al. 2005). To overcome this problem, mitogenome analysis is in vogue in recent times as it provides better resolution and precision relative to single region-based markers (Duchêne et al. 2011). In the present study, we investigated the mitogenome structure of Andaman local goat and used it to understand the migration route and evolution of the breed.

Andaman local goat is an endemic goat germplasm of Andaman and Nicobar Islands (Sunder et al. 2019) with an estimated population of 52,000 in 2019 (20th Livestock Census, Department of Animal Husbandry and Dairying, India). Although, the breed is well adapted to the local microenvironment and notable for its ability to sustain in harsh climatic condition of Andaman and Nicobar Islands (Sunder et al. 2019), a rapid decreasing trend in its population has been recorded; its population has been decreased from 64,200 to 2003 to 52,000 in 2019 (20th Livestock Census, Department of Animal Husbandry and Dairying, India; Sunder et al. 2019) making the breed very vulnerable. Meagre information on the origin, evolution, migration route and phylogeography of Andaman local goat is available. Therefore, the present study deals with mitogenome characterization of Andaman local goat and its evolutionary relationship with different goat breeds all over the world, which is helpful to understand the origin, migration route and phylogeography of the goat breed.

Materials and methods

Sample collection and DNA extraction

A pure Andaman local goat kept at the goat farm of ICAR-Central Island Agricultural Research Institute, Port Blair (Lat. 6° to 14° North and Lon. 92° to 94° East) was sampled. 10 mL of blood sample was drawn from the external jugular vein. Isolation of total genomic DNA was done by using a commercial DNA isolation kit (DNeasy Blood and Tissue Kit, Qiagen). Quality of the isolated DNA was assessed using a Nanodrop spectrophotometer and quantity was measured with a Qubit fluorometer using a commercial kit (dsDNA high-sensitivity kit, Invitrogen).

Mitogenome sequencing

Enrichment of mitochondrial DNA from total genomic DNA was carried out by following the protocol of NEBNext Microbiome DNA enrichment kit, Illumina. Further, Nextera XT DNA Library Preparation protocol, Illumina was followed for preparation of DNA library. Then the DNA libraries were sequenced on Illumina Nextseq platform (150×2 chemistry). The Illumina paired end raw reads were quality checked using FastQC v 0.11.8 program (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/). Illumina raw reads were processed using TrimGalore v 0.4.4 program (http://www.bioinformatics.babraham.ac.uk/projects/trim_galore/) to trim low-quality bases, barcode and adapter sequences with cut-off q30 with 99.9% base call accuracy and minimum read

length of 20. Further, Picard 2.18 algorithm (https://github.com/broadinstitute/picard) was used to remove overleaping reads from total reads. A total of 11,404,103 raw reads and 10,849,883 high quality processed reads were generated. The processed reads were aligned to the reference mitochondrial genome sequence of *Capra hircus* (GenBank: NC_005044). SPADES v.3.15.4 program ($ spades.py -1 input_R1.fastq.gz -2 illumina_R2.fastq.gz –careful –cov-cutoff auto –o output) was used for read assembly and Bwa v 0.7.17 (Li and Durbin 2009) program was used for reads alignment and mapping. A total of 9664 reads aligned to the reference sequence with coverage of 92.2184% at 20 X read depth. Variations (single nucleotide polymorphisms, SNPs) to the reference were reported with Samtools v 1.2 (Li et al. 2009) and Bcftools v 1.2 (Li 2011). Gaps, translocations or reversals were not identified. Protein coding genes (PCGs), rRNAs and non-coding region were identified by Basic Local Alignment Search Tool (BLAST) searches and tRNAs were identified by tRNAscan-SE (Lowe and Chan 2016). Graphical representation of the organization of Andaman local goat mitochondrial genome was prepared using OGDRAW (http://ogdraw.mpimp-golm.mpg.de/) (Greiner et al. 2019).

Table 1 The organization and characterization of complete mitogenome of Andaman local goat

Gene	Stand	Location	Size	T/U%	C%	A%	G%	AT%	Start Codon	Stop Codon	Anticodon	Intergenic Nucleotides
D-loop	H	1.1212	1212	29.21	25.41	31.35	14.03	60.56	-	-	-	0
tRNA-Phe	H	1213–1280	68	23.53	19.12	38.24	19.12	61.76	-	-	GAA	0
12 S rRNA	H	1281–2234	954	21.70	23.69	36.58	18.03	58.28	-	-	-	2
tRNA-Val	H	2237–2303	67	29.85	19.40	38.81	11.94	68.66	-	-	TAC	0
16 S rRNA	H	2304–3869	1566	24.46	20.75	37.80	16.99	62.26	-	-	-	6
tRNA-Leu1	H	3876–3950	75	28.00	22.67	32.00	17.33	60.00	-	-	TAA	2
ND1	H	3953–4908	956	26.78	29.71	32.11	11.40	58.89	ATG	TA- (*)	-	0
tRNA-Ile	H	4909–4977	69	33.33	11.59	39.13	15.94	72.46	-	-	GAT	-3
tRNA-Gln	H	4975–5046	72	25.00	29.17	37.50	8.33	62.50	-	-	TTG	2
tRNA-Met	H	5049–5117	69	28.99	24.64	27.54	18.84	56.52	-	-	CAT	0
ND2	H	5118–6159	1042	26.58	28.21	37.04	8.16	63.63	ATA	T–(*)	-	0
tRNA-Trp	H	6160–6226	67	26.87	19.40	37.31	16.42	64.18	-	-	TCA	1
tRNA-Ala	L	6228–6296	69	39.13	10.14	28.99	21.74	68.12	-	-	TGC	1
tRNA-Asn	L	6298–6370	73	30.14	16.44	24.66	28.77	54.79	-	-	GTT	2
rep_origin	H	6373–6408	36	5.56	30.56	33.33	30.56	38.89	-	-	-	-6
tRNA-Cys	L	6403–6470	68	27.94	19.12	32.35	20.59	60.29	-	-	GCA	0
tRNA-Tyr	L	6471–6538	68	27.94	16.18	35.29	20.59	63.24	-	-	GTA	1
COX1	H	6540–8084	1545	29.32	25.50	29.13	16.05	58.45	ATG	TAA	-	-3
tRNA-Ser1	L	8082–8150	69	30.43	17.39	24.64	27.54	55.07	-	-	TGA	7
tRNA-Asp	H	8158–8225	68	27.94	17.65	36.76	17.65	64.71	-	-	GTC	1
COX2	H	8227–8910	684	27.92	23.54	35.38	13.16	63.30	ATG	TAA	-	3
tRNA-Lys	H	8914–8980	67	28.36	19.40	34.33	17.91	62.69	-	-	TTT	1
ATP8	H	8982–9179	198	27.78	25.25	39.39	7.58	67.17	ATG	TAA	-	-40
ATP6	H	9140–9820	681	27.46	29.37	32.60	10.57	60.06	ATG	TAA	-	-1
COX3	H	9820–10,603	784	29.59	29.21	26.91	14.29	56.51	ATG	T–(*)	-	0
tRNA-Gly	H	10,604–10,672	69	30.43	20.29	34.78	14.49	65.22	-	-	TCC	0
ND3	H	10,673–11,018	346	27.46	29.77	31.50	11.27	58.96	ATA	T–(*)	-	1
tRNA-Arg	H	11,020–11,088	69	37.68	10.14	40.58	11.59	78.26	-	-	TCG	0
ND4L	H	11,089–11,385	297	30.30	26.26	32.32	11.11	62.63	ATG	TAA	-	-7
ND4	H	11,379–12,756	1378	27.65	29.83	32.29	10.23	59.94	ATG	T–(*)	-	0
tRNA-His	H	12,757–12,826	70	32.86	15.71	41.43	10.00	74.29	-	-	GTG	0
tRNA-Ser2	H	12,827–12,886	60	30.00	21.67	33.33	15.00	63.33	-	-	GCT	1
tRNA-Leu2	H	12,888–12,957	70	28.57	14.29	38.57	18.57	67.14	-	-	TAG	0
ND5	H	12,958–14,778	1821	26.91	28.94	33.50	10.65	60.41	ATA	TAA	-	-17
ND6	L	14,762–15,289	528	42.42	7.20	21.59	28.79	64.02	ATG	TAA	-	0
tRNA-Glu	L	15,290–15,359	70	41.43	10.00	24.29	24.29	65.71	-	-	TTC	3
CYTB	H	15,363–16,502	1140	26.32	28.77	32.28	12.63	58.60	ATG	AGA	-	3
tRNA-Thr	H	16,506–16,575	70	25.71	21.43	34.29	18.57	60.00	-	-	TGT	-1
tRNA-Pro	L	16,575–16,640	66	34.85	13.64	24.24	27.27	59.09	-	-	TGG	-

*indicates abbreviated stop codon, rep_origin indicates origin of L-stand replication

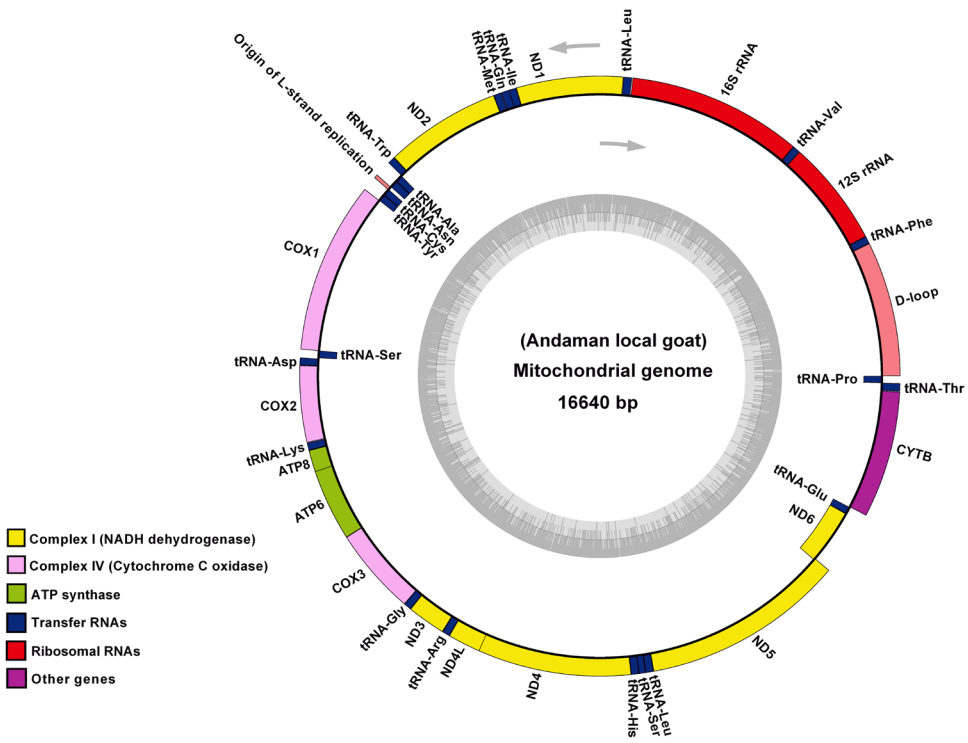

Fig. 1 Complete mitochondrial genome organization of Andaman local goat. The graph was drawn in OGDRAW (http://ogdraw.mpimp-golm.mpg.de/) (Greiner et al. 2019)

Bioinformatics analysis

Nucleotide composition was analysed by Geneious Prime v. 2021 (https://www.geneious.com) and predicted amino acid composition of protein coding genes (PCGs) was analysed in MEGA X (Kumar et al. 2018). AT- and GC- skew of PCGs were calculated based on nucleotide composition of PCGs as described by Perna and Kocher 1995. For calculation of AT-/GC- skew, the following formulas were used.

$$\mathrm{AT-skew} = (\mathrm{A}-\mathrm{T})/(\mathrm{A}+\mathrm{T}) \text{ and } \mathrm{GC-skew} = (\mathrm{G}-\mathrm{C})/(\mathrm{G}+\mathrm{C})$$

Relative Synonymous Codon Usage (RSCU) was assessed in MEGA X (Kumar et al. 2018). For RSCU analysis, coding regions were extracted from the genome and concatenated. Sequence alignment was done in MEGA X (Kumar et al. 2018) using MUSCLE (Edgar 2004) tool. Haplogroup assignment of ALG was carried out based on its phylogenetic relationship with six standard *Capra* haplogroups. For haplogroup assignment we used (i) mtDNA D-loop hypervariable region 1 (HVR-1) sequence information (Naderi et al. 2007) and (ii) concatenated nucleotide sequence information of complete D-loop, *16 S rRNA* and *cytochrome B* gene. Sequence information of six standard *Capra* haplogroups used in the present study is presented in Table S1. Evolutionary relationship of ALG with different goat breeds all over the world was assessed based on concatenated nucleotide sequence information of 13 PCGs. For this purpose, representative goat mitogenome sequences were retrieved from NCBI (Table S1). Phylogenetic trees were constructed in MEGA X (Kumar et al. 2018) using the Neighbor-Joining method (Saitou and Nei 1987) with Tamura-Nei model (Tamura and Nei 1993) and 1000 bootstrap replications were applied. Bayesian phylogenetic relationship was inferred in BEAST v1.10.4 (Suchard et al. 2018) and network tree was constructed in PopART ver. 1.7 (Leigh and Bryant 2015).

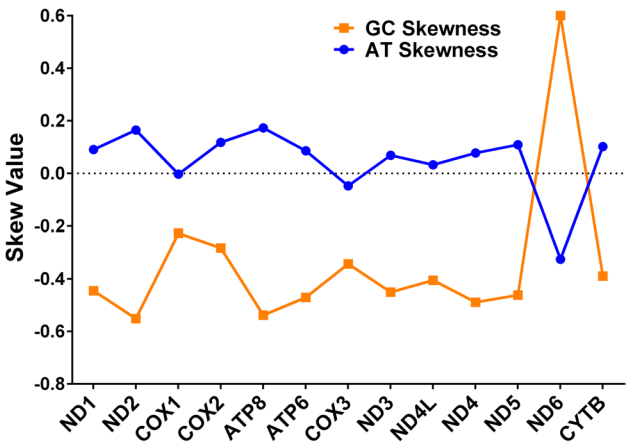

Fig. 2 AT- and GC- skew of all the 13 protein-coding genes of Andaman local goat mitogenome

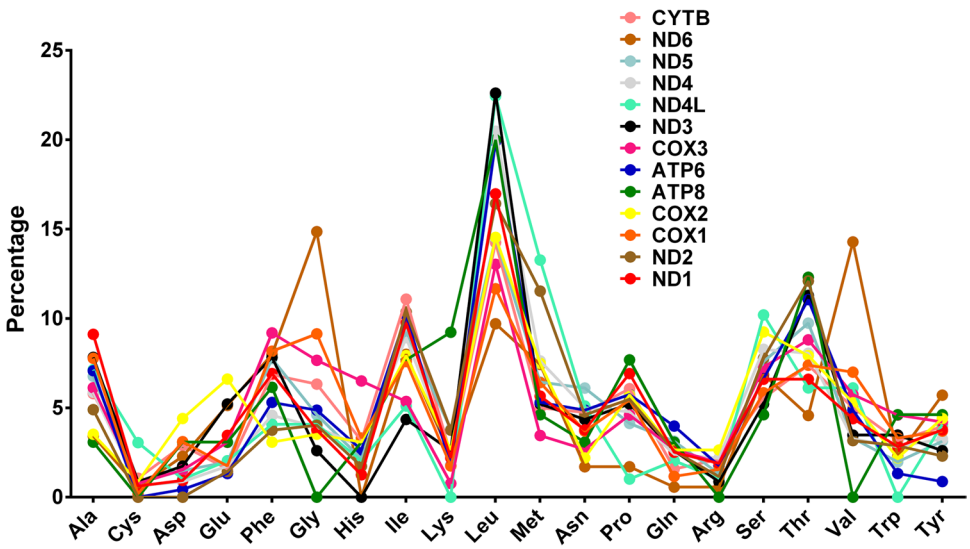

Fig. 3 Amino acid composition of all the 13 protein-coding genes of Andaman local goat mitogenome

Results

Mitogenome structure of Andaman local goat

The mitochondrial genome of Andaman local goat (ALG) was circular molecule of 16,640 bp (Fig. 1). The analysis of the mitogenome identified a total of 36 genes; 13 protein coding genes (PCGs), 22 transfer RNAs (tRNAs) and 2 ribosomal RNA subunits (rRNAs) (Table 1). Presence of a 1212 bp non-coding region (D-loop) between *tRNA-Pro* and *tRNA-Phe* was also detected. Among the genes, eight (*ND6*, *tRNA-Ala*, *tRNA-Asn*, *tRNA-Cys*, *tRNA-Tyr*, *tRNA-Ser1*, *tRNA-Glu* and *tRNA-Pro*) were encoded by the light strand (L) whereas rest of them were encoded by the heavy strand (H) (Table 1). Among the PCGs, only *ND6* was present on L strand. The gene order detected in ALG mitogenome (Fig. 1) was of a typical vertebrate mitogenome. Analysis of base composition of the mitogenome revealed a bias toward adenine and thymine; AT % ranged from 54.79 in *tRNA-Asn* to 78.26 in *tRNA-Arg* (Table 1). AT % of PCGs ranged from 56.51 in *COX3* to 67.17 in *ATP8* whereas for *12 S rRNA* and *16 S rRNA*, AT % were 58.28 and 62.26 respectively. D-loop also was AT rich with AT % of 60.56.

Length of the PCGs ranged from 198 bp (*ATP8*) to 1821 bp (*ND5*) (Table 1). AT-skew showed positive values for all the PCGs except for *COX1* (-0.0033223), *COX3* (-0.0474041) and *ND6* (-0.3254438) whereas

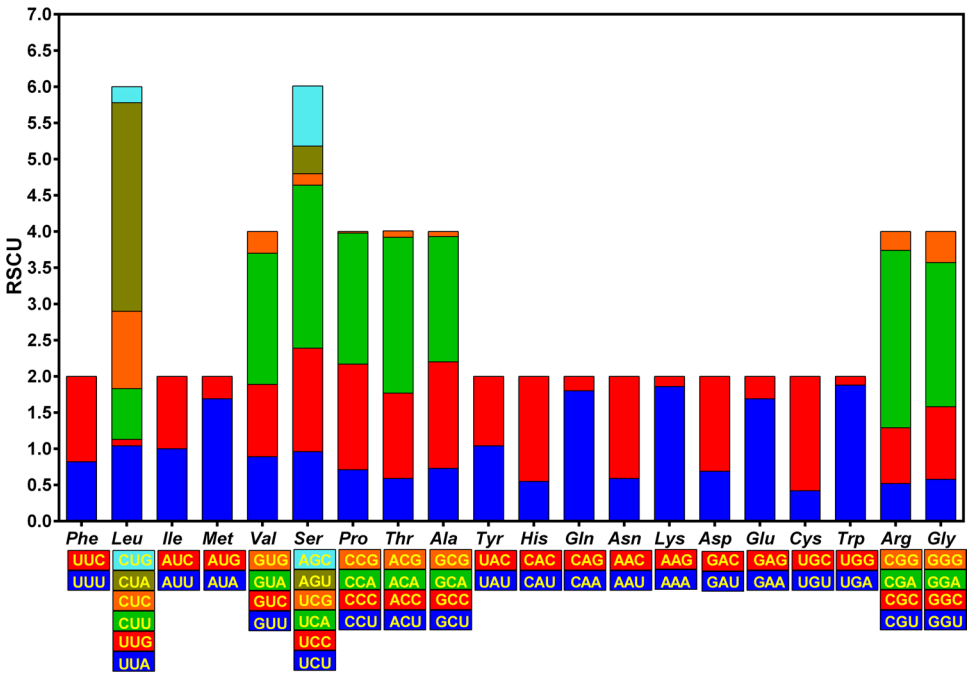

Fig. 4 The Relative Synonymous Codon Usage (RSCU) of the protein-coding genes of Andaman local goat mitogenome

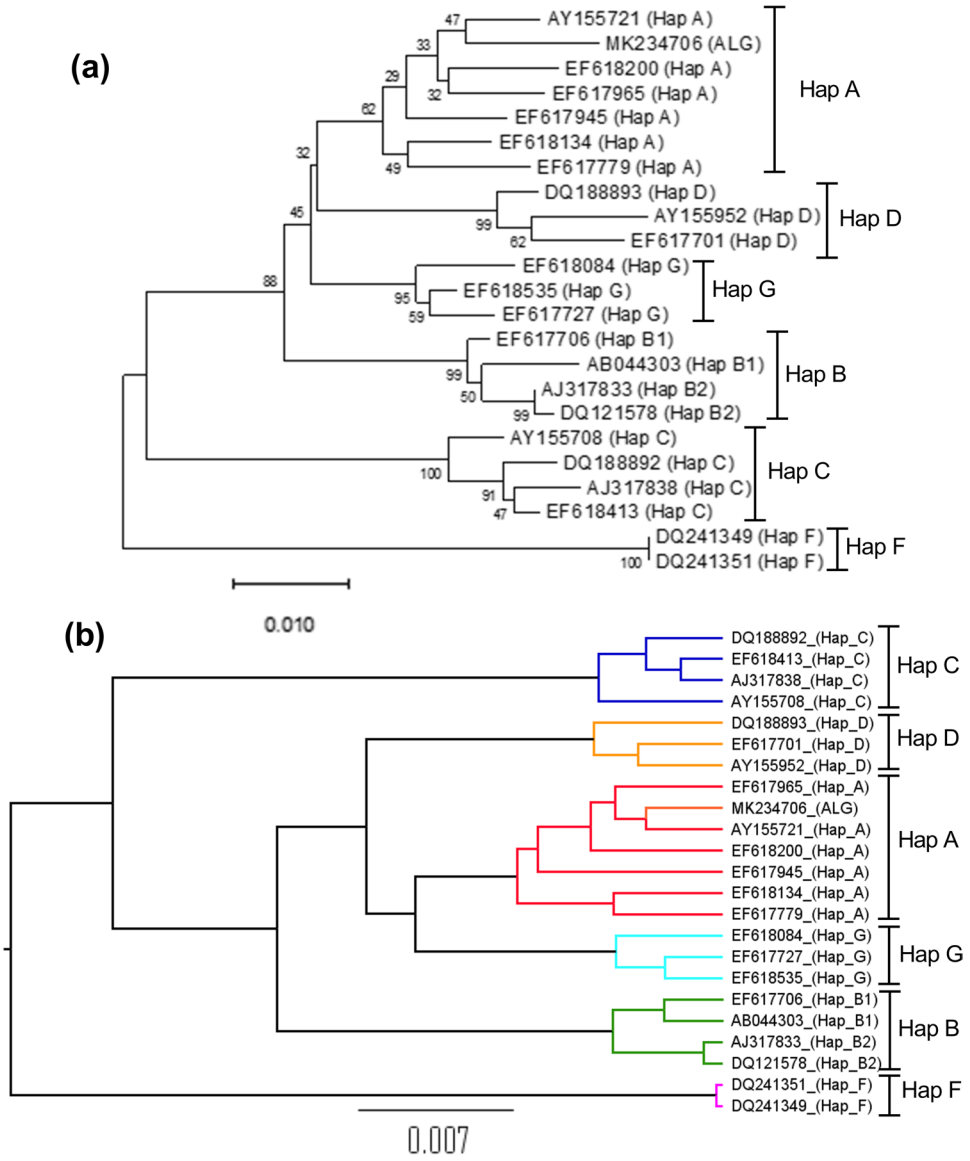

Fig. 5 Lineage assignment of Andaman goat based on mtDNA D-loop hypervariable region 1 (HVR-1). **a** Neighbor-joining (NJ) phylogenetic tree, **b** Bayesian phylogenetic tree. NJ tree was drawn in MEGAX (Kumar et al. 2018), the Bayesian phylogenetic tree was drawn in BEAST v1.10.4 (Suchard et al. 2018)

GC-skew values were negative for all the PCGs except for *ND6* (0.60) (Fig. 2). Positive values of AT-skew indicated dominance of adenine over thymine which was evidenced for all PCGs except for *COX1*, *COX3* and *ND6* (Table 1*)*. On the other hand, negative GC-skew values for all PCGs except for *ND6* indicated that all PCGs except *ND6* had higher percentage of cytosine than guanine (Table 1). Three of the PCGs (*ND2*, *ND3* and *ND5*) had ATA start codon and rest of the PCGs had ATG start codon. Incomplete stop codon was detected in *ND1*, *ND2*, *COX3*, *ND3* and *ND4*. Predicted amino acid composition of the PCGs is presented in Fig. 3. Leu was found to be the predominant amino acid for all of the PCGs except for *ND6* in which Gly was the predominant amino acid. With the exception of five amino acids (Phe, His, Asn, Asp and Cys), all amino acids had most preferred codons with A or T in the third position (Fig. 4).

D-loop was between *tRNA-Pro* and *tRNA-Phe* and was 1212 bp in length (Table 1). Positive AT-skew (0.03533686) and negative GC-skew (-0.2885396) indicated that D-loop had higher percentage of adenine and cytosine over thymine and guanine respectively. *16 S rRNA* (1566 bp) was between *tRNA-Val* and *tRNA-Leu1* whereas *12 S rRNA* (954 bp) was between *tRNA-Phe* and *tRNA-Val*. Length of tRNAs ranged from 60 bp (*tRNA-Ser2*) to 75 (*tRNA-Leu1*). The anticodons of the tRNAs are presented in Table 1 and were found similar to other vertebrates. Another interesting feature of

the mitogenome was the presence of intergenic spacer regions and overlapping regions (Table 1). A total of 16 intergenic spacer regions and 8 gene overlaps were detected. Length of the intergenic spacer regions ranged from 1 to 7 bp whereas overlapping regions varied from 1 to 40 bp. The largest gene overlap (40 bp) was placed between *ATP8* and *ATP6* (Table 1). Other overlaps were between *tRNA-Ile* and *tRNA-Gln* (3 bp), replication origin and *tRNA-Cys* (6 bp), *COX1* and *tRNA-Ser1* (3 bp), *ATP6* and *COX3* (1 bp), *ND4L* and *ND4* (7 bp), *ND5* and *ND6* (17 bp) as well as *tRNA-Thr* and *tRNA-Pro* (1 bp).

Lineage assignment and phylogenetic analysis

To delineate the lineage/haplogroup of Andaman local goat, phylogenetic analysis was done with reference sequences of all the six major lineages (A-D, F, G) of goat. Neighbor-Joining (Fig. 5a) and Bayesian (Fig. 5b) phylogenetic analysis based on mtDNA D-loop hypervariable region 1 (HVR-1) designated Andaman local goat to lineage A. A Median-Joining network tree of ALG with all lineages is presented in Fig. 6. From the network tree, it was clear that ALG was under lineage A. Haplogroup assignment of ALG was further supported by the phylogenetic analysis based on concatenated sequence information of complete D-loop, *16 S rRNA* gene and *cytochrome B* gene. Neighbor-Joining tree (Fig. 7a) and Bayesian (Fig. 7b) phylogenetic tree indicated that ALG was included under lineage A.

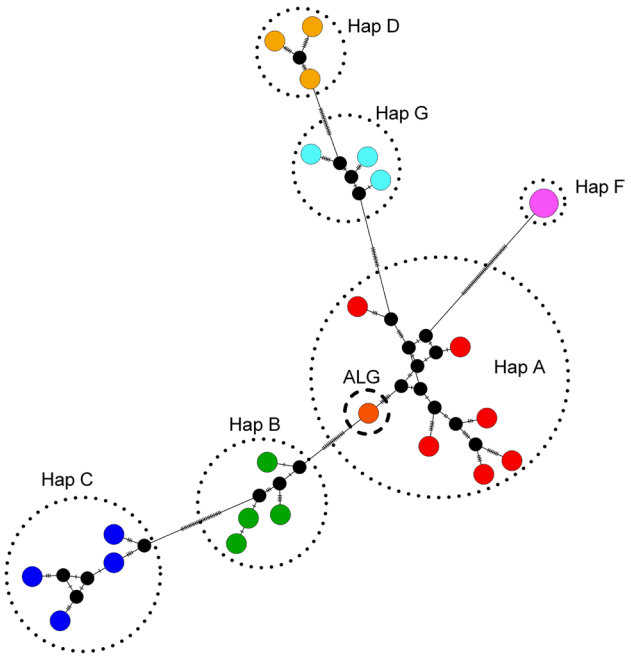

Fig. 6 Network analysis of ALG with six goat lineages based on mtDNA D-loop sequence information. Network was drawn in PopART ver. 1.7 (Leigh and Bryant 2015)

Evolutionary relationship of ALG with different goat breeds all over the world was established based on concatenated nucleotide sequence information of PCGs (Fig. 8). It was found that ALG formed a separate cluster and was phylogenetically close to some Chinese goat breeds like Hainan black goat (KM360063), Dazu black goat (KP271023), Shaannan White goat (KP195268), YouZhou Wu goat (KP677511), Hechuan white goat (KP677509), Jintang black goat (KP231536), Xiangdong black goat (KM998968), Longdong black goat (MW563732), Jianyang Daer goat (KM670319), FuShun black goat (KP662716), Chuanzhong black goat (KP273589), Nanjiang yellow goat (KM093871) and Jamnapari goat breed of Bangladesh (KY305183).

Discussion

Although India has a rich diversity of domestic goat population with 34 well characterized registered goat breeds (https://nbagr.icar.gov.in), information on their origin, genetic make-up, phylogeography and domestication history is lacking. Very little information is available on the complete mitochondrial genome structure of Indian goat breeds. Andaman and Nicobar Islands is the home of several indigenous livestock and poultry breeds like Andaman local goat, Teressa goat, Nicobari pig, Andaman local pig, Trinket cattle, Andaman buffalo and Nicobari fowl. Mitogenome structure of indigenous livestock breeds like Trinket cattle (De et al. 2019a), Andaman buffalo (De et al. 2019b), Andaman local pig (De et al. 2019c) and Nicobari pig (De et al. 2021) provided useful information on the origin, migration route and evolutionary history of the breeds. Therefore, in the present study, complete mitochondrial genome structure of Andaman local goat was characterized and its origin, migration route and evolutionary relationship with other goat breeds were inferred.

The mitochondrial genome of Andaman local goat was 16640 bp in length. The length of vertebrate mitogenomes varies from 15 to 20 kb (Boore 1999; Montaña-Lozano et al. 2022; Pereira 2000;). The mitochondrial genome size of ALG is larger than Karchaev goat of Russia (Rodionov et al. 2020) and Boer goat of South Africa (Niu et al. 2014) and similar to Yimeng black goat of China (Liu et al. 2020), Black Bengal goat of Bangladesh (Siddiki et al. 2019) and Chinese Tibetan goat (Zhang et al. 2016). Size variation in vertebrate mitogenomes is due to insertion or deletion of nucleotides

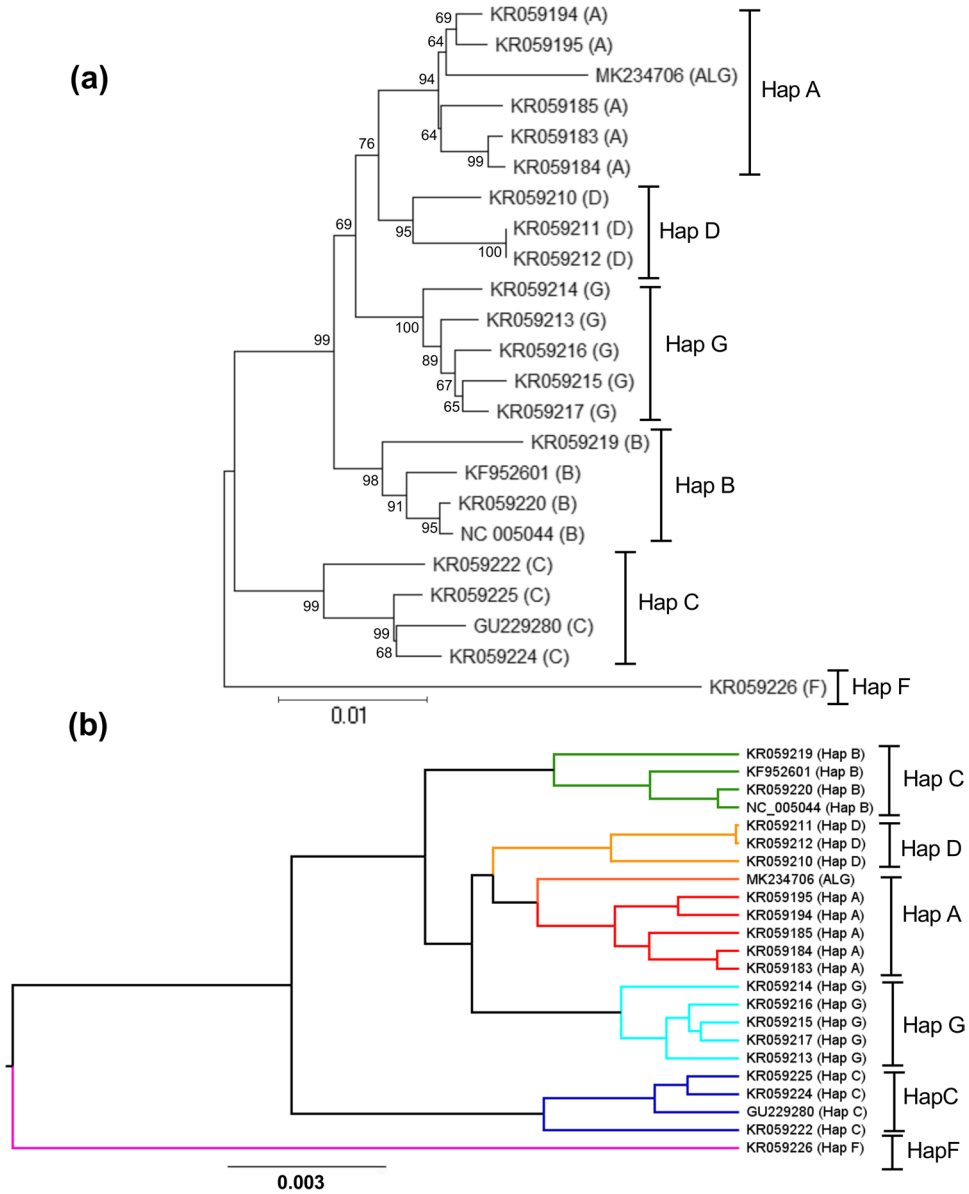

Fig. 7 Lineage assignment of Andaman goat based on concatenated sequence information of complete D-loop, 16 S rRNA and cytochrome B gene. **a** Neighbor-joining (NJ) phylogenetic tree, **b** Bayesian phylogenetic tree. NJ tree was drawn in MEGAX (Kumar et al. 2018), the Bayesian phylogenetic tree was drawn in BEAST v1.10.4 (Suchard et al. 2018)

in the hypervariable domain of control region or gene duplication or deletion in tRNAs (Formenti et al. 2021; Lee et al. 1995; Ray and Densmore 2002; Sbisà et al. 1997). The mitogenome of ALG contained 13 PCGs, 22 tRNAs, 2 rRNAs and one non-coding region. The gene order of ALG mitogenome is consistent with gene orders of other vertebrate mitochondrial genomes as vertebrate mitochondrial harbours a "conserved gene order" from fish to primates (Anderson et al. 1981; Boore 1999; Chen et al. 2016; De et al. 2019a, 2021; Jia and Wei 2016; Liu et al. 2016; Li et al. 2019a, b; Noack et al. 1996; Parma et al. 2003; Sun et al. 2015). Among the protein coding genes, only *ND6* was present on light strand (L), other genes were encoded by heavy strand (H). Among the tRNAs, seven (*tRNA-Ala*, *tRNA-Asn*, *tRNA-Cys*, *tRNA-Tyr*, *tRNA-Ser1*, *tRNA-Glu*, *tRNA-Pro*) were present on L strand and rest of the t-RNAs were present on the H stand. H strand encoded both the rRNAs. Base composition analysis of ALG mitogenome detected an A + T bias in all the 37 genes (Table 1). Moreover, positive AT-skew was detected in all PCGs except for *COX1*, *COX3* and *ND6* and negative GC-skew values were observed in all PCGs except for *ND6* (Fig. 2). The asymmetry in skewness in *ND6* is mainly due to the remarkable feature of Cordate mitochondrial genome in which the H strand is G-rich and L strand is G-poor (Sahyoun et al. 2014).

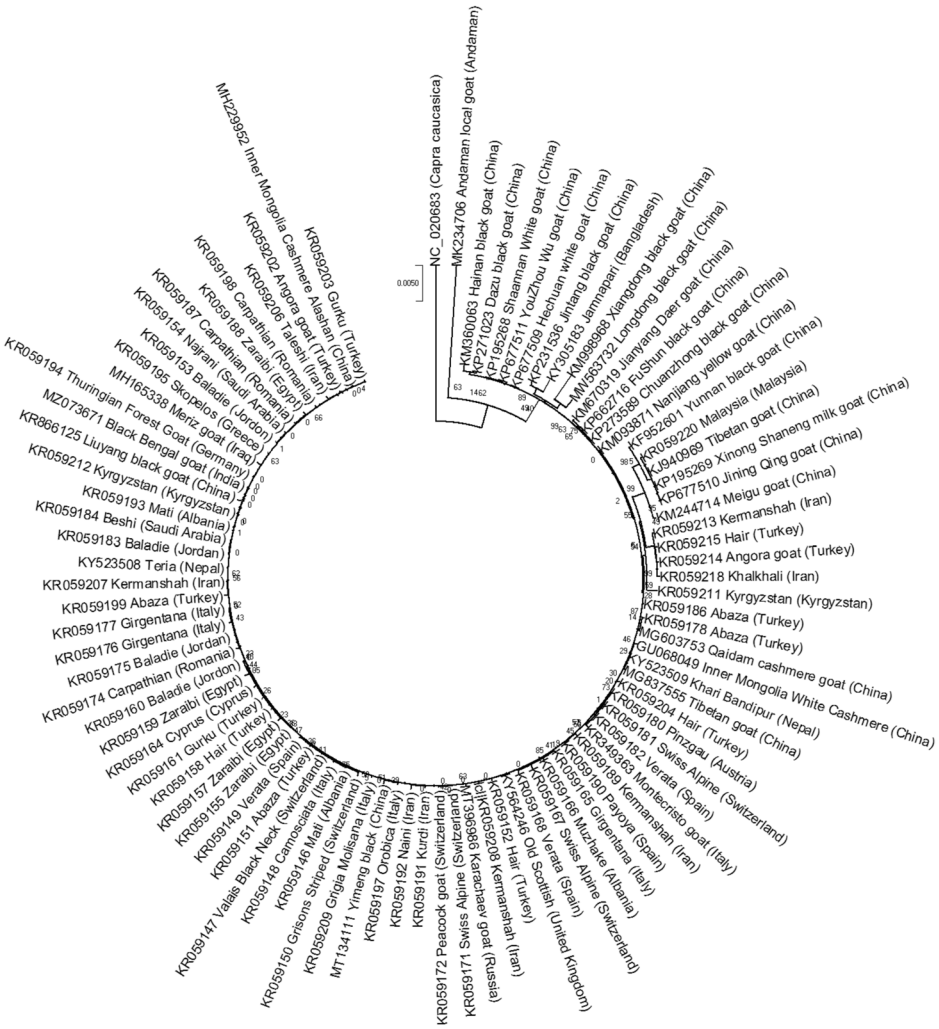

Fig. 8 Phylogenetic relationship of Andaman local goat with different goat breeds. NJ phylogenetic tree was constructed based on concatenated nucleotide sequence information of mtDNA protein coding genes (PCGs) in MEGAX (Kumar et al. 2018). *Capra caucasica* (NC_020683) was used as an outgroup

The compositional differences between the two strands of mitochondrial genome are due to the differences in the buoyant density (Gibson et al. 2005; Perna and Kocher 1995). The A + T bias, positive AT-skew and negative GC-skew detected in ALG mitogenome are consistent with vertebrate mitogenome (Faith and Pollock 2003; Gibson et al. 2005). Start codons of all the PCGs were ATN codons; ATA for *ND2*, *ND3* and *ND5* and ATG for other 10 PCGs (Table 1). Stop codons of five PCGs (*ND1, ND2*, *COX3*, *ND3* and *ND4*) were abbreviated or incomplete. Presence of incomplete stop codons is a unique feature of vertebrate mitochondrial genome and functional stop codons are generally appeared by post-transcriptional polyadenylation (Ojala et al. 1981; Slomovic et al. 2005).

Weak phylogenetic structure of goats of different regions and of different lineages has been reported by several workers (Doro et al. 2014; Fan et al. 2007; Luikart et al. 2001; Naderi et al. 2007, 2008) as extensive transportation of goats among different regions in relation to commercial trade and human migration exists from the early domestication phases (Bruford et al. 2003; Ferna´ndez et al. 2006). As identification of goat mitochondrial haplogroups might be controversial in the absence of a standard marker and standardized criteria, Naderi et al. 2007 established a standard marker for haplogroup assignment in goats. The standardization was done using large number of goat samples from all over Africa, Asia and Europe. Finally, HVR-I segment of the control region evolved as the standard marker for haplogroup assignment in goats

and it has been broadly accepted and adopted (Colli et al. 2015; Piras et al. 2012; Nguluma et al. 2021). Based on that marker, six major mitochondrial lineages of goats (A, B, C, D, F, and G) have been described (Naderi et al. 2007) and Andaman local goat was found to be under lineage A (Figs. 5 and 6). Lineage assignment of ALG was further supported by phylogenetic analysis based on concatenated nucleotide sequence information of complete D-loop, *16 S rRNA* and *cytochrome B* gene (Fig. 7). Comparison of ALG mitogenome with mitogenomes of different goat lineages (A-D, F and G, Table S1) identified no major difference in size; size varied from 16,638 to 16,643 bp and slight difference in size was due to nucleotide insertion or deletion in the hypervariable region of D-loop which is a common feature of vertebrate mitogenome (Montaña-Lozano et al. 2022; Saccone et al. 1991; Sbisà et al. 1997). Moreover, no difference in gene organization and orientation among ALG and other goat lineages was observed as gene organization in vertebrate mitochondrial genome is very much conserved (Gong et al. 2020; Pereira 2000). Goats were domesticated from wild bezoar (*Capra aegagrus*) (Alberto et al. 2018; Naderi et al. 2008; Zeder 2008) in Fertile Crescent and first migration of domestic goats to Mediterranean occurred in Neolithic age characterized by ancestral A and C lineages (Colli et al. 2015; Zeder 2008). Domestic goats acquired other haplogroups (B, D, F and G) due to different domestication events (Colli et al. 2015). Lineage A is the most predominant lineage distributed worldwide both in the Old World as well as the New World with more than 90% goats fall under this lineage (Amills et al. 2009; Naderi et al. 2007; Nomura et al. 2013). Widespread distribution of lineage A is probably due to spread of this lineage from its domestication centre to different parts of the world along with human migration and commercial trade through terrestrial and maritime routes (Colli et al. 2015; Hermes et al. 2020). Goats of lineage A might have brought to Andaman and Nicobar Islands during early maritime trade and they acted as the founding population of ALG. In addition, positioning of ALG in the phylogenetic tree of domestic goat breeds based on concatenated sequence information of all PCGs (Fig. 8) indicated that this breed is phylogenetically close to some Chinese indigenous goat breeds and Jamnapari goat breed of Bangladesh. Phylogenetic close relationship of ALG with some Chinese goat breeds might be due to geographical proximity of Andaman and Nicobar Islands with Southeast Asian countries including China and close trade relationship since prehistoric time (Hall 1985; Pereira and Amorim 2010). Mitogenome analysis of other indigenous livestock breeds like Trinket cattle (De et al. 2019a), Andaman local pig (De et al. 2019c) and Nicobari pig (De et al. 2021) also indicated that these breeds were migrated from Southeast Asian countries. Close affinity of ALG with Jamnapari goat of Bangladesh might be due to introgression of Jamnapari goat gene into the gene pool of ALG during the evolution of the breed.

In conclusion, to the best of our knowledge, the current communication is the first report on complete mitochondrial genome analysis of Andaman local goat of Andaman and Nicobar Islands. Analysis indicated that Andaman local goat is included under lineage A of domestic goat. Moreover, this indigenous goat breed showed close phylogenetic relationship with some Chinese goat breeds and Jamnapari goat breed of Bangladesh. Information on genetic signature of the breed will be of great use in future conservation strategy planning for the breed.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s11756-022-01234-0.

Acknowledgements The authors would like to acknowledge Indian Council of Agricultural Research (ICAR), New Delhi, India for providing funds to carry out the research.

Author contribution Conceptualization, A.K.D., D. B. and R.M.; methodology, A.K.D. and P.P. software, A.K.D. and J.S.; formal analysis, A.K.D. and E.B.C.; investigation, S.S., A.K.D and J.S.; data curation, A.K.D and S.S.; writing—original draft preparation, A.K.D.; writing—review and editing, D.B.; visualization, D.B.; supervision, E.B.C.; All authors have read and agreed to the published version of the manuscript.

Funding Funding has been done by Indian Council of Agricultural Research in terms of Institute funded project on "Molecular signature of eco-sustainability of indigenous livestock breeds of Andaman and Nicobar Islands and Lakshadweep" to Dr. Arun K De.

Declarations

Financial and non-financial interests There is no financial and non-financial interest.

Ethical approval This research has been approved by the Institute Animal Ethics Committee (IAEC) of ICAR-Central Island Agricultural Research Institute (ICAR-CIARI), Port Blair, Andaman and Nicobar Islands, India on 15th January, 2021 and the ethical approved project identification code is 'ICAR-CIARI/AS/Institute/IAEC/4963 dated 15 January 2021. All the methods were performed in accordance with the relevant national guidelines and regulations.

Conflict of interest On behalf of the co-author, the corresponding author states that there is no conflict of interest.

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