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### RESEARCH ARTICLE

### ANIMAL GENETICS

## Molecular Characterization of *Cytochrome b* gene in Indian Black Bengal Goat (*Capra hircus*)

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### Abstract

Black Bengal, a prolific goat breed native to West Bengal is widely distributed in Eastern India. In an attempt to resolve its phylogeny, the mitochondrial *Cytochrome b* gene of the black Bengal goat was characterized to study the base composition, RE profile, repeats, derived amino acid as well as comparative DNA sequence analysis. Mitochondrial DNA isolated from blood samples, *Cytochrome b* of black Bengal goat was amplified and sequenced. Genetic analysis of *Cytochrome b* revealed that mutation occurs in the conserved region of mtDNA and is mostly synonymous. It is predicted that *BsaI* could be used as a marker enzyme for this particular breed of goat. The highest level of genetic similarity was found between Black Bengal and *Capra aegagrus* up to the extent of 96.7% and phylogenetic analysis establishes that the black Bengal goat might be evolved from the wild goat *Capra aegagrus*. The protein sequence analysis also reveals that *Cytochrome b* protein is stable and normal. The results of the phylogenetic analysis of protein sequence and DNA sequences among different farm animals indicate that there is rare variation within the genus. The present study provides the convincing molecular phylogenetic status of the black Bengal goat together with other farm animals and this would help for an essential scientific conservation programme of the Black Bengal goat.

**Keywords:** Goat, mitochondrial DNA, *Cytochrome b*, Phylogenetic analysis and evolution

## 1 Introduction

The goat is one of the most adaptable and geographically widespread livestock species of the Indian subcontinent(1). Out of 20 recognized goat breeds of India Black Bengal, a prolific goat is native to West Bengal and mostly distributed in different states of Eastern India owing to its tremendous economic value. Archaeological evidence indicates that the goat was domesticated by humans around 10,000 years back. Some studies(2; 3) have also suggested that independent domestication in Pakistan gave rise to the Cashmere breeds. However, very less work has been conducted to know that of the Black Bengal goat. Mitochondrial DNA sequences are widely used in molecular evolutionary studies over their nuclear counterpart to investigate population structure and genetic diversity in natural populations owing to matrilineal transmission. These sequences have been proven to be useful in estimating the

time of population divergences and phylogenetic inference within and between species in vertebrates(4). In the mitochondrion of eukaryotes, *Cytochrome b* is a component of respiratory chain complex III. These complexes are involved in electron transport and the generation of ATP and thus play a vital role in the cell. The mitochondrial *Cytochrome b* gene is commonly used to determine phylogenetic relationships between organisms. It is considered to be most useful in determining relationships within families and genera. Comparative studies involving *Cytochrome b* gene have resulted in new classification schemes and have been used to assign newly described species to a genus, as well as deepen the understanding of evolutionary relationships. Studies on the variation of mitochondrial *Cytochrome b* sequence within and between species of animals often find a relative excess of low-frequency non-synonymous polymorphisms within species(5; 6; 7; 8; 9; 10; 11). Hence the present investigation has been designed to characterize mi-

tochondrial *Cytochrome b* and to study the homology across Black Bengal goats in particular and the caprine family in general.

## 2 Materials and Methods

### 2.1 Animals

Blood samples from two unrelated black Bengal goats from natural habitats of Eastern India particularly Assam and West Bengal were collected and used for DNA isolation.

### 2.2 Mitochondrial DNA Isolation and PCR Amplification

DNA was isolated from the blood samples using a standard protocol. DNA was extracted using the Qiagen DNeasy tissue kit following the manufacturer's instructions. To amplify the *Cytochrome b* gene of goat mtDNA, a pair of known primers: Forward 5'-AATGATATGAAAAACCATC-3' and Reverse 5'-TAGATGTGGTTAATAGTGG-3' was used described by Mannen et al. (2001). PCR amplification was carried out in a 50 µl reaction volume containing 100 ng of DNA, 10 pM of each primer, 200 µM of dNTPs, 1X PCR buffer containing 2.0 mM MgCl<sub>2</sub>, and 1 U of AmpliTaq. Amplification was carried out in a GeneAmp9600 thermal cycler (Perkin Elmer) employing the following conditions: 94°C for 4 min; 30 cycles at 94°C for 1 min, 50°C for 1 min, and 72°C for 2 min; and a final extension at 72°C for 10 min.

### 2.3 Sequencing of Amplicons

Amplified Samples were sequenced using Sangers' Di-deoxy sequencing method. Amplified PCR products were isolated from 1% agarose gels and purified with a Qiagen gel extraction kit. Standard double-stranded sequencing was performed for the complete *Cytochrome b* gene using 50 ng of purified PCR product and 4 pM of primer, 4 µl of Big Dye Terminator ready reaction kit (Perkin Elmer). Cycle sequencing was carried out in a GeneAmp9600 thermal cycler (Perkin Elmer) employing 30 cycles at 96°C for 10 s, 50°C for 5 s, and 60° for 4 min. Extended products were purified by alcohol precipitation followed by washing with 70% alcohol. Purified samples were dissolved in 10 µl of 50% Hi-Di formamide and analysed in an ABI3700 automated DNA Analyser (Perkin Elmer).

### 2.4 Sequences Download from NCBI

The following sequences were downloaded from the NCBI database to construct a phylogenetic tree and to understand the domestication origination of the Black Bengal goat. The accession number DQ073048 (Black Bengal goat -Present study ), DQ093614 (Black Bengal goat-Present study), AB110597 (*Capra hircus*), AF034737 (*Capra cylindricornis*), AF217256 (*Capra ibex nubiana*), AF034734 (*Capra sibirica*), AB110592 (*Capra aegagrus blythi*), AF034735 (*Capra ibex*), AF034738 (*Capra caucasica*), AB044309 (*Capra falconeri*), AF010406 (*Ovis aries*), AF492350 (*Bos indicus*), Z50079 (*Sus scrofa*), X56281 (*Camelus dromedaries*), V00654 (*Bos taurus*), AY488491 (*Bubalus bubalis*), X52392 (*Gallus gallus*), AY882393 (*Homo sapiens*) were used to study the homology across Black Bengal goats with caprine ruminant as well as with other livestock.

## 3 Analysis of Sequences

The sequence result was confirmed by NCBI/BLAST and was further analysed to know the base composition, RE profile, repetitive structure, and predicted amino acid composition.

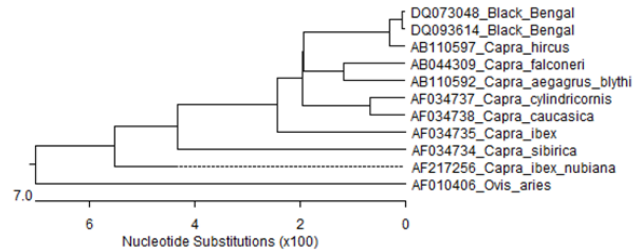


Figure 1: Phylogenetic tree constructed using Pair Distances of Untitled ClustalW using DNASTar Lasergene 17.1. Using the nucleotide substitution rate at (X100) showing that Black Bengal Goat *Cytochrome b* sequences from Assam and West Bengal are positioned in the same cluster along with modern *Capra hircus* *Cytochrome b* sequences (A)

The two black Bengal goats' *Cytochrome b* gene sequences were compared to other goat *Cytochrome b* sequences downloaded from the NCBI database using the ClustalW multiple alignment program. The aligned sequences underwent polymorphic site identification and genetic relationship determination with the black Bengal goat with other caprine families.

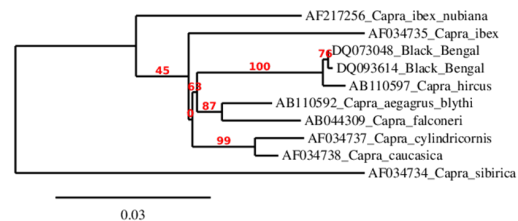


Figure 2: NJ plot with branch length showing that Black Bengal Goat *Cytochrome b* sequences from Assam and West Bengal are positioned in the same cluster along with modern *Capra hircus* *Cytochrome b* sequences. On the other hand, the highest divergence shows with *Capra sibirica* among all *Capra* genus

The present study, separately also determined the common nucleotide mutation positions present in black Bengal goats from other goat species as well as with other species including humans and birds.

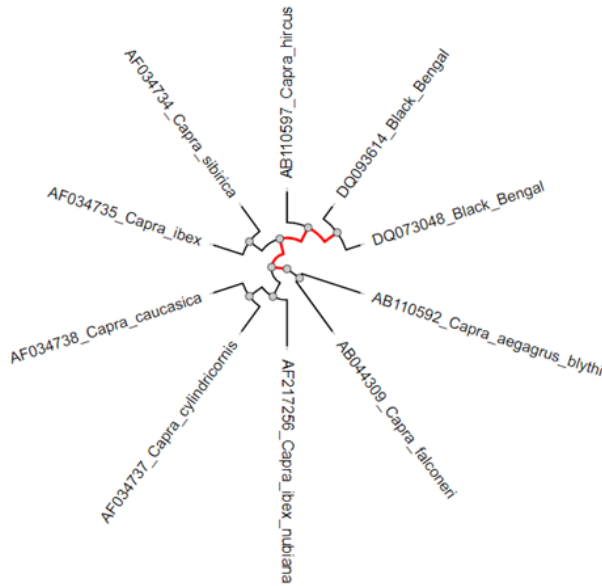


Figure 3: Radial dendrogram showing the point of origin with the diversity of *Cytochrome b* gene of Black Bengal Goat, *Capra hircus*, *Capra aegagrus blythi*, *Capra cylindricornis*, *Capra cylindricornis*, *Capra ibex*, *Capra ibex nubiana*, *Capra caucasica*, *Capra siberica* and *Capra falconari* (red highlighted)

Multiple alignments and paired distance matrix, NJ plots were calculated using the DNASTAR package of LASER-GENE software (Burland 2000) and other online software.

## 4 Results and Discussion

### 4.1 Characterization of *Cytochrome b*

Out of the total of 1140 base pairs (bp) regions of the mitochondrial *Cytochrome b* genes were amplified and sequenced from the representative samples of black Bengal goats belonging to different locations (Assam and West Bengal).

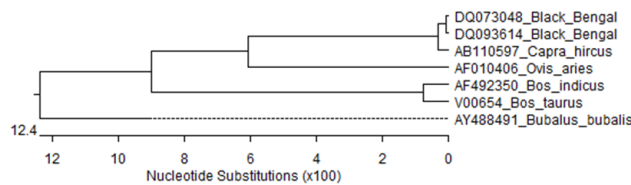


Figure 4: Phylogenetic tree constructed using Pair Distances of Untitled ClustalW using DNASTar Lasergene 17.1. Using the nucleotide substitution rate at (X100) showing that Black Bengal Goat *Cytochrome b* sequences from Assam and West Bengal are positioned in the same cluster along with modern *Capra hircus* *Cytochrome b* (A) and the closest ruminant *Ovis aries* sequences (B) followed by *Bos indicus* and (C). On the other hand, the highest divergence shows with *Bubalus bubalis* (D)

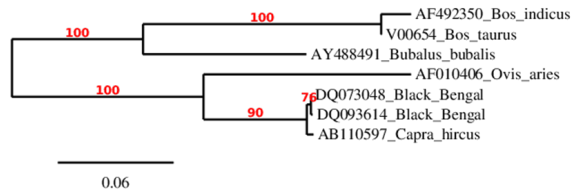


Figure 5: NJ plot with branch length showing that Black Bengal Goat *Cytochrome b* sequences from Assam and West Bengal are positioned in the same cluster along with modern *Capra hircus* *Cytochrome b* and the closest ruminant *Ovis aries* sequences followed by *Bos indicus* and *Bos taurus*. On the other hand, the highest divergence shows with *Bubalus bubalis*.

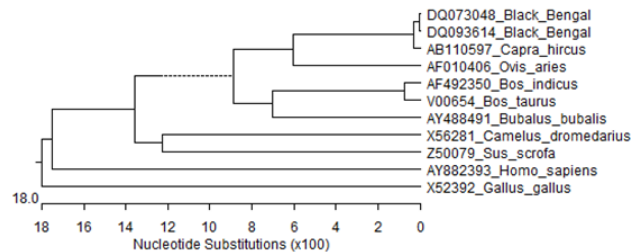


Figure 6: Radial Phylogram showing the point of origin with the diversity of *Cytochrome b* gene of Black Bengal Goat, *Capra hircus*, *Capra aegagrus blythi*, *Capra cylindricornis*, *Capra cylindricornis*, *Capra ibex*, *Capra ibex nubiana*, *Capra caucasica*, *Capra siberica* and *Capra falconari* (red highlighted)

Table 1: Nucleotide Compositions of Cytochrome *b* Gene Different Species With Black Bengal Goat

Sl No.	Species	Nucleotide	Codon Position			Total	Purine/ Pyrimidine combination	Codon Position			Total
			1	2	3			1	2	3	
1	<i>Capra hircus</i> Black Bengal Goat	T	0.187	0.431	0.176	0.265	AT	0.515	0.64	0.599	0.584
		C	0.263	0.249	0.36	0.291	GC	0.485	0.36	0.401	0.416
		A	0.328	0.209	0.423	0.32	AG	0.55	0.32	0.463	0.444
		G	0.222	0.111	0.041	0.125	CT	0.45	0.68	0.537	0.556
2	<i>Capra hircus</i> Native Goat	T	0.19	0.428	0.179	0.266	AT	0.515	0.637	0.599	0.584
		C	0.263	0.252	0.358	0.291	GC	0.485	0.363	0.401	0.416
		A	0.325	0.209	0.42	0.318	AG	0.547	0.32	0.463	0.444
		G	0.222	0.111	0.043	0.126	CT	0.453	0.68	0.537	0.556
3	<i>Capra aegagrus</i> Wild Goat	T	0.192	0.43	0.184	0.268	AT	0.511	0.638	0.605	0.585
		C	0.262	0.249	0.357	0.289	GC	0.489	0.362	0.395	0.415
		A	0.319	0.208	0.422	0.316	AG	0.546	0.322	0.459	0.442
		G	0.227	0.114	0.038	0.126	CT	0.454	0.678	0.541	0.558
4	<i>Ovis aries</i> Modern sheep	T	0.187	0.434	0.187	0.269	AT	0.512	0.642	0.593	0.583
		C	0.263	0.247	0.371	0.294	GC	0.488	0.358	0.407	0.417
		A	0.325	0.209	0.407	0.313	AG	0.55	0.32	0.442	0.437
		G	0.225	0.111	0.035	0.124	CT	0.45	0.68	0.558	0.563
5	<i>Bos taurus</i> European cattle	T	0.198	0.418	0.13	0.249	AT	0.495	0.63	0.557	0.561
		C	0.269	0.261	0.405	0.312	GC	0.505	0.37	0.443	0.439
		A	0.296	0.212	0.427	0.312	AG	0.533	0.321	0.465	0.439
		G	0.236	0.109	0.038	0.128	CT	0.467	0.679	0.535	0.561
6	<i>Bos indicus</i> Indian cattle	T	0.203	0.417	0.138	0.253	AT	0.499	0.629	0.569	0.565
		C	0.266	0.26	0.396	0.307	GC	0.501	0.371	0.431	0.435
		A	0.295	0.211	0.431	0.313	AG	0.531	0.322	0.466	0.44
		G	0.236	0.111	0.035	0.127	CT	0.469	0.678	0.534	0.56
7	<i>Bubalus bubalis</i> Buffalo	T	0.197	0.422	0.127	0.249	AT	0.503	0.63	0.546	0.559
		C	0.273	0.254	0.395	0.307	GC	0.497	0.37	0.454	0.441
		A	0.305	0.208	0.419	0.311	AG	0.53	0.324	0.478	0.444
		G	0.224	0.116	0.059	0.133	CT	0.47	0.676	0.522	0.556
8	<i>Sus scrofa</i> Pig	T	0.207	0.438	0.147	0.264	AT	0.519	0.644	0.573	0.579
		C	0.255	0.247	0.391	0.298	GC	0.481	0.356	0.427	0.421
		A	0.312	0.207	0.427	0.315	AG	0.538	0.315	0.462	0.438
		G	0.226	0.109	0.035	0.123	CT	0.462	0.685	0.538	0.562
9	<i>Camelus dromedarius</i> Camel	T	0.22	0.42	0.198	0.279	AT	0.507	0.621	0.588	0.572
		C	0.249	0.266	0.339	0.285	GC	0.493	0.379	0.412	0.428
		A	0.287	0.201	0.39	0.293	AG	0.531	0.314	0.463	0.436
		G	0.244	0.114	0.073	0.144	CT	0.469	0.686	0.537	0.564
10	<i>Homo sapiens</i> Human	T	0.211	0.412	0.125	0.249	AT	0.512	0.618	0.469	0.533
		C	0.285	0.279	0.493	0.352	GC	0.488	0.382	0.531	0.467
		A	0.301	0.206	0.344	0.284	AG	0.504	0.309	0.382	0.398
		G	0.203	0.103	0.038	0.115	CT	0.496	0.691	0.618	0.602
11	<i>Gallus gallus</i> Chicken	T	0.205	0.403	0.108	0.239	AT	0.481	0.614	0.438	0.511
		C	0.305	0.286	0.53	0.374	GC	0.519	0.386	0.562	0.489
		A	0.276	0.211	0.33	0.272	AG	0.489	0.311	0.362	0.387
		G	0.214	0.1	0.032	0.115	CT	0.511	0.689	0.638	0.613

The black Bengal goat samples from West Bengal (DQ073048) and Assam (Accession No.DQ093614) were submitted to the NCBI database and got accession numbers and were used for further downstream bioinformatics analysis.



#### 4.2 Nucleotide and derived amino acid Composition

The base composition of the 1140bp amplified fragment of the *Cytochrome b* gene was found to be A (365/32.02%), T (304/26.67%) G (149/13.07%) and C (322/28.25%) with a GC content of 41.32% (Table 1).

Figure 7: Phylogenetic tree constructed using Pair Distances of Untitled ClustalW using DNAsStar Lasergene 17.1. Using the nucleotide substitution rate at (X100) showing that Black Bengal Goat *Cytochrome b* sequences from Assam and West Bengal are positioned in the same cluster along with modern *Capra hircus* *Cytochrome b* and the closest ruminant *Ovis aries* sequences (A)

Table 2: Amino acid composition of *Cytochrome b* protein of Black Bengal Goat

Sl. No.	Name of Amino Acid	Total No in <i>Cytochrome b</i>	Percentage
1	Ala (A)	23	6.1
2	Arg (R)	8	2.1
3	Asn (N)	18	4.7
4	Asp (D)	11	2.9
5	Cys (C)	4	1.1
6	Gln (Q)	6	1.6
7	Glu (E)	6	1.6
8	Gly(G)	24	6.3
9	His(H)	12	3.2
10	Ile(I)	43	11.3
11	Leu(L)	55	14.5
12	Lys(K)	9	2.4
13	Met(M)	19	5
14	Phe(F)	24	6.3
15	Pro(P)	23	6.1
16	Ser(S)	21	5.5
17	Thr(T)	28	7.4
18	Trp(W)	12	3.2
19	Tyr(Y)	15	4
20	Val(V)	18	4.7

The complete sequence of the amino acid of black Bengal goat contains 379 amino acids with a one-stop codon at the end of the sequence which is universal for the mitochondrial *Cytochrome b* protein of modern native goats.

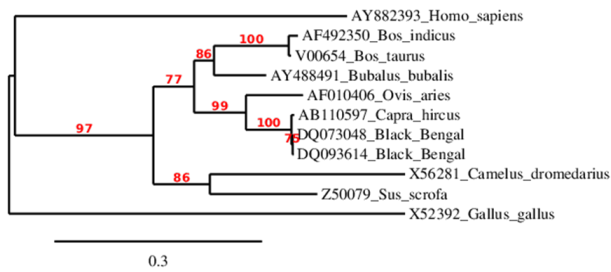


Figure 8: NJ plot with branch length showing that Black Bengal Goat *Cytochrome b* sequences from Assam and West Bengal are positioned in the same cluster along with modern *Capra hircus* *Cytochrome b* and the closest ruminant *Ovis aries* sequences. On the other hand, the highest divergence shows with *Gallus gallus*

Table 3: Number of direct, direct complementary, symmetric and invert repeats of different species with minimum length 7 and maximum length 20 with maximum mismatch 5 nucleotides

Sl. No.	Name of Spices	No of Direct Repeats	No of Direct Complementary Repeats	No of Symmetric Repeats	No of Invert Repeats
1	Black Bengal Goat ( <i>Capra hircus</i> )	79	58	50	63
2	<i>Capra hircus</i> (Native goat)	84	59	48	64
3	<i>Capra aegagrus</i> (Wild Goat)	71	61	51	62
4	<i>Ovis aries</i> (Modern sheep)	70	70	75	75
5	<i>Bos taurus</i> (European Cattle)	60	39	70	72
6	<i>Bos indicus</i> (Indian cattle)	60	48	64	76
7	<i>Bubalus bubalis</i> (Buffalo)	84	57	56	65
8	<i>Sus scrofa</i> (Pig)	80	61	82	68
9	<i>Camelus dromedarius</i> (camel)	74	56	59	71
10	<i>Homo sapiens</i> (Human)	85	59	58	71
11	<i>Gallus gallus</i> (Chicken)	87	61	68	75

The molecular weight of black Bengal goats' *Cytochrome b* protein was estimated to be 42.8 kDa. The black Bengal goat *Cytochrome b* protein contained the highest number of Lue (14.5%) followed by Ile (11.3%) and Cys was found to be the lowest (1.1%) among all amino acids (Table 2). The total number of negatively charged (Asp + Glu) and positively charged (Arg +Lys) amino acids was found 17 each. The theoretical isoelectric PH (PI) was found to be 7.19 and the atomic formula estimated C2025H3094N472O502S23 with a total of 6116 atoms.

Table 4: Restriction digestion profile of *Cytochrome b* gene of Black Bengal goat and different species with their fragment size (bp)

Enzyme Species	<i>AluI</i>	<i>BamHI</i>	<i>BsaI</i>	<i>MboII</i>	<i>EcoRI</i>	<i>XbaI</i>	<i>HpaII</i>	<i>NciI</i>
Black Bengal goat	1105bp	1039bp 101bp	746bp	604bp 436bp	630bp	812bp 328bp		
	35bp		394bp	110bp	510bp			
<i>Capra hircus</i>	1106bp	101bp		604bp 436bp	630bp	812bp 328bp		
	34bp	1039bp		110bp	510bp			
<i>Ovis aries</i>	520bp	611bp		586bp	629bp			
	419bp	529bp		554bp	511bp			
	67bp							
	34bp							
<i>Bos taurus</i>	453bp			624bp		812bp	1107b	
	437bp			526bp		328bp	33bp	
	260bp							
<i>Bos indicus</i>	526bp			526bp		812bp 328bp	773bp	713b
	327bp 187bp			186bp			333bp	427b
				238bp			34bp	
<i>Bubalus bubalis</i>	880bp 260bp	611bp		624bp 526bp	977bp	812bp 328bp	608bp	
		529bp			163bp		514bp 18bp	
<i>Sus scrofa</i>	695bp	314bp		624bp			910bp	
	343bp			526bp			142bp	
	184bp	296bp					70bp	
	28bp	530bp					28bp	
<i>Camelus dromedarius</i>	729bp			614bp			809bp	
	259bp			266bp				
	120bp			182bp			331bp	
<i>Gallus gallus</i>				240bp				
				369bp				
				252bp				
				192bp				
				54bp				
				21bp				
				12bp				
			3bp					
<i>Homo sapiens</i>	1031bp			273bp				
	109bp			420bp 447bp				

### 4.3 Repeating Structure

When the number of the mean repeats (1, kb) was calculated in a random sequence consisting of different nucleotides in the *Cytochrome b* gene, it was observed that in black Bengal goat, this was 79 (Direct Repeats), 58 (Direct complementary Repeats), 50 (Symmetric Repeats) and 63 (Invert Repeats) numbers respectively (Table 3). The repetitive structure of the mitochondrial control region of several mammals has already been identified by (12; 13; 14). But literature regarding the study of the repetitive structure of *Cytochrome b* is scanty probably because it is a conserved gene, although the present study of the different repetitive structures of *Cytochrome b* showed extensive variability in contrast to all other species.

### 4.4 Restriction Digestion Profile

Restriction digestion profiles with their interpolating experimental data are shown in Table 4 along with their fragment size across the species which shows substantial nucleotide variations among the species. A total of eight commercially variable enzymes were used to identify species-

specific restriction digestion profiles. It was observed that enzyme *BsaI* found restriction sites only in black Bengal goats, whereas this enzyme did not find restriction sites in any of the species studied. It is predicted that *BsaI* could be used as the marker enzyme for this particular breed of goat. Among the other enzyme *Alu I* could be used for species identification, which gave the polymorphic site for all the species studied. Although no such direct literature is available on the DNA sequence variation restriction digestion profile of *Cytochrome b* covering the broad spectrum of species, it is suggested that there is considerable sequence variation among different species of mtDNA *Cytochrome b* gene resulting from base changes during speciation.

### 4.5 Sequence Alignments and Phylogeny

#### 4.5.1 Sequence diversity within the family

The *Cytochrome b* sequence of black Bengal goat (DQ073048 DQ093614) were compared with the sequence of modern native and different wild species of goats available publicly to get a conclusive relation to its wild goat progenitor. The phylogenetic tree and alignment of the DNA se-

Table 5: Pair-wise Distances matrix calculated using ClustalW of mitochondrial *Cytochrome b* gene of Black Bengal Goat, *Capra hircus* *Capra aegagrus blythi*, *Capra cylindricornis*, *Capra cylindricornis*, *Capra ibex*, *Capra ibex nubiana*, *Capra caucasica*, *Capra siberica*, *Capra falconari* and *Ovis aries*. The Black Bengal Goat of present study DQ073048 and DQ093614 shows the highest similarity with AB110597- *Capra hircus* followed by AB110592-*Capra aegagrus blythi* and the highest divergence with AF034734-*Capra siberica* followed by out-group AF010406-*Ovis aries*

Name of Species		Percent Identity										
D	Accession Number	1	2	3	4	5	6	7	8	9	10	11
I	AB044309- <i>Capra falconeri</i>		97.7	96	89.4	91.5	95.4	96.1	96.7	95.2	96.3	96.2
V	AB110592- <i>Capra aegagrus blythi</i>	2.3		96.3	88.5	92.1	95.7	96.7	97.2	95.2	96.7	96.6
E	AB110597- <i>Capra hircus</i>	4.2	3.8		88.5	91.5	94.9	95.4	95.8	94.4	99.5	99.4
G	AF010406- <i>Ovis aries</i>	11.2	12.2	12.2		86.9	88.7	88.9	89.3	89.9	88.7	88.6
E	AF034734- <i>Capra siberica</i>	8.9	8.3	8.8	14		91.9	92	92	91.7	91.6	91.6
N	AF034735- <i>Capra ibex</i>	4.9	4.5	5.3	12.3	8.6		95.1	95.5	93.9	95.1	95
C	AF034737- <i>Capra cylindricornis</i>	3.9	3.3	4.7	11.6	8.1	5		98.5	95.6	95.5	95.4
E	AF034738- <i>Capra caucasica</i>	3.4	2.9	4.4	11.4	8.3	4.7	1.3		95.4	96.1	96.1
	AF217256- <i>Capra ibex nubiana</i>	5.1	5.1	5.8	10.7	8.3	6.3	4.3	4.7		94.7	94.6
	DQ073048-Black.Bengal	3.8	3.4	0.5	12	8.5	5.1	4.5	4	5.4		99.9
	DQ093614-Black.Bengal	3.9	3.5	0.6	12.1	8.6	5.2	4.6	4.1	5.5	0.1	
		1	2	3	4	5	6	7	8	9	10	11

Table 6: Pair-wise Distances matrix calculated using of ClustalW of mitochondrial *Cytochrome b* gene of Black Bengal Goat, *Capra hircus*, *Ovis aries*, *Bos indicus*, *Bubalus bubalis*, *Bos taurus*, The Black Bengal Goat of present study DQ073048 and DQ093614 of *Cytochrome b* gene of Black Bengal Goat showing the highest similarity with AB110597- *Capra hircus* followed by *Ovis aries*. On the other hand, the highest divergence shows with other ruminant species of AF492350-*Bos indicus*, V00654-*Bos taurus*, and AY488491-*Bubalus bubalis* (highlighted in grey)

Name of Species		Percent Identity						
I	Accession Number	1	2	3	4	5	6	7
V	AB110597- <i>Capra hircus</i>		89	84.8	84.7	99.5	99.4	85.1
E	AF010406- <i>Ovis aries</i>	12.2		83.2	85.2	89.2	89.1	83.2
G	AF492350- <i>Bos indicus</i>	17.4	19.5		87.4	84.9	84.8	98.5
E	AY488491- <i>Bubalus bubalis</i>	17.6	16.9	14.2		84.8	84.9	87.6
N	DQ073048-Black.Bengal	0.5	12	17.3	17.5		99.9	85.2
C	DQ093614-Black.Bengal	0.6	12.1	17.4	17.3	0.1		85.1
E	V00654- <i>Bos taurus</i>	17	19.5	1.5	13.9	16.9	17	
		1	2	3	4	5	6	7

Table 7: Pair-wise Distances matrix calculated using ClustalW of mitochondrial *Cytochrome b* gene of Black Bengal Goat, *Capra hircus*, *Ovis arie*, *Bos indicus*, *Bubalus bubalis*, *Homo sapiens*, *Bos taurus*, *Gallus gallus*, *Camelus dromedaries* and *Sus scrofa*. The Black Bengal Goat of present study DQ073048 and DQ093614 of *Cytochrome b* gene of Black Bengal Goat showing the highest similarity with AB110597- *Capra hircus* followed by AB110592-*Capra aegagrus blythi* followed by *Ovis aries* and other ruminant species (AF492350-*Bos indicus*, V00654-*Bos taurus*, AY488491-*Bubalus bubalis*). On the other hand, the highest divergence shows with X52392-*Gallus gallus* followed by AY882393-*Homo sapiens* (highlighted in grey).

Name of Species		Percent Identity										
D	Accession Number	1	2	3	4	5	6	7	8	9	10	11
I	AB110597- <i>Capra hircus</i>		89	84.8	84.7	74.1	99.5	99.4	85.1	72.4	78	81.2
V	AF010406- <i>Ovis aries</i>	12.2		83.2	85.2	73.9	89.2	89.1	83.2	71.5	77.6	81.1
E	AF492350- <i>Bos indicus</i>	17.4	19.5		87.4	73.1	84.9	84.8	98.5	73.8	79.2	80.4
E	AY488491- <i>Bubalus bubalis</i>	17.6	16.9	14.2		74.4	84.8	84.9	87.6	73.1	79.3	81.8
G	AY882393- <i>Homo sapiens</i>	32.4	32.8	34.2	31.5		74.2	74.1	73.2	73.3	71.8	74.9
E	DQ073048-Black.Bengal	0.5	12	17.3	17.5	32.4		99.9	85.2	72.4	78.2	81.3
N	DQ093614-Black.Bengal	0.6	12.1	17.4	17.3	32.5	0.1		85.1	72.3	78.2	81.3
C	V00654- <i>Bos taurus</i>	17	19.5	1.5	13.9	34.2	16.9	17		74	79.4	80.7
E	X52392- <i>Gallus gallus</i>	35.8	36.8	34.2	33.7	34.2	35.7	35.9	33.7		69.6	73.3
	X56281- <i>Camelus dromedarius</i>	26.5	27	25	24.8	36.2	26	26.2	24.7	40.7		79.6
	Z50079- <i>Sus scrofa</i>	21.8	21.9	23.1	21	31.4	21.6	21.6	22.6	34.3	24.5	
		1	2	3	4	5	6	7	8	9	10	11



Table 8: Alignment report content showing the exact mismatch of nucleotide at base pair level in Black Bengal Goat of present study DQ073048 and DQ093614 of *Cytochrome b* gene sequence of available *Cytochrome b* of *Capra* families viz. *Capra hircus* *Capra aegagrus blythi*, *Capra cylindricornis*, *Capra cylindricornis*, *Capra ibex*, *Capra ibex nubiana*, *Capra caucasica*, *Capra siberica* and *Capra falconeri*

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ATGACCAACATCCGAAAACCACCCATTAATAAAAATTGTAAACAACGCATTATTATGACCTCCCAACCCCATCAAACATCTCATCATGATGAAACTTTG Majority
10 20 30 40 50 60 70 80 90 100
1 .....T.....T..... AB044309_Capra_falconeri
1 .....T..... AB110592_Capra_aegagrus_blythi
1 .....G.....C..... AB110597_Capra_hircus
1 .....T.....C.....TA.....C.....T.....G.T.....T.T..... AF010406_Ovis_aries
1 .....T.....C.....TA.....C.....C..... AF034734_Capra_sibirica
1 .....T.....C.....T.....C.....T..... AF034735_Capra_ibex
1 .....T.....C.....T.....T..... AF034737_Capra_cylindricornis
1 .....T.....C.....T..... AF034738_Capra_caucasica
1 .....G.....C.....C..... AF217256_Capra_ibex_nubiana
1 .....G..... DQ073048_Black_Bengal
1 .....G..... DQ093614_Black_Bengal

GATCCCTCCTAGGCATTTCGCTAATTTTACAGATCCTGACAGGCCTATTCCTAGCAATACACTATACATCCGACACAATAACAGCATTCTCCTCTGTAAC Majority
110 120 130 140 150 160 170 180 190 200
101 ..... AB044309_Capra_falconeri
101 .....T..... AB110592_Capra_aegagrus_blythi
101 .....A.....C.....A.....C.....T..... AB110597_Capra_hircus
101 .....C.T.....T.....T.A.....C.T.....C..... AF010406_Ovis_aries
101 .....T.C.....A.T.A.....C..... AF034734_Capra_sibirica
101 .....C.....T.....C.....T.....G..... AF034735_Capra_ibex
101 .....G.T.....T.....C.....T.....T..... AF034737_Capra_cylindricornis
101 .....T.....A.....T..... AF034738_Capra_caucasica
101 .....A.....A.....G.....T.....C..... AF217256_Capra_ibex_nubiana
101 .....A.....C.....A.....T..... DQ073048_Black_Bengal
101 .....A.....C.....A.....T..... DQ093614_Black_Bengal

TCACATTTGTCGAGATGTAAATTATGGCTGAATTATCCGATACATACACGAAACGGAGCATCAATATCTTTATCTGCCTATTCATACATGTCGGACGA Majority
210 220 230 240 250 260 270 280 290 300
201 .....G.....G..... AB044309_Capra_falconeri
201 ..... AB110592_Capra_aegagrus_blythi
201 .....C.....C.....C.....C.....T.....T.....G.....T.....T.....G.....A..... AB110597_Capra_hircus
201 .....C.....C.....C.....C.....T.....T.....T.....G.....A..... AF010406_Ovis_aries
201 .....C.....C.....C.....T.....T.....T.....A..... AF034734_Capra_sibirica
201 .....C.....T.....T.....G..... AF034735_Capra_ibex
201 .....T..... AF034737_Capra_cylindricornis
201 .....T..... AF034738_Capra_caucasica
201 .....C.....T.....A..... AF217256_Capra_ibex_nubiana
201 .....C.....A..... DQ073048_Black_Bengal
201 .....C.....A..... DQ093614_Black_Bengal

GGTCTATATTATGGATCATATACCTTTCTAGAAACATGAAACATTGGAGTAATCTCTCTGCTCGCAACAATAGCCACAGCATTTCATAGGCTATGTCTTAC Majority
310 320 330 340 350 360 370 380 390 400
301 .....G..... AB044309_Capra_falconeri
301 ..... AB110592_Capra_aegagrus_blythi
301 .....G.....G.....T..... AB110597_Capra_hircus
301 .....C.....C.....C.....C.....AT.T.G.....T..... AF010406_Ovis_aries
301 .....C.....C.....C.....C.....C.....AT.A.....T..... AF034734_Capra_sibirica
301 .....T.....AT.....C.....C..... AF034735_Capra_ibex
301 .....T..... AF034737_Capra_cylindricornis
301 .....T..... AF034738_Capra_caucasica
301 .....C.....C.....C.....T.....A..... AF217256_Capra_ibex_nubiana
301 .....G.....G.....T..... DQ073048_Black_Bengal
301 .....G.....G.....T..... DQ093614_Black_Bengal

CATGAGGACAAATATCATTCTGAGGGCAACAGTCATCACTAATCTCTCAGCAATCCCATATATGGCACAACCTAGTCCAATGAATCTGAGGAGG Majority
410 420 430 440 450 460 470 480 490 500
401 ..... AB044309_Capra_falconeri
401 .....T..... AB110592_Capra_aegagrus_blythi
401 .....T.....T.....T.....G..... AB110597_Capra_hircus
401 .....G.....A.....T.T.C.C.C.T.....T.....G..... AF010406_Ovis_aries
401 .....G.....G.....T.C.C.C.....C.....G..... AF034734_Capra_sibirica
401 .....C.....G..... AF034735_Capra_ibex
401 .....G..... AF034737_Capra_cylindricornis
401 .....G..... AF034738_Capra_caucasica
401 .....G.....T.....C.C..... AF217256_Capra_ibex_nubiana
401 .....T.....T.....G..... DQ073048_Black_Bengal
401 .....T.....T.....G..... DQ093614_Black_Bengal

ATTCTCAGTAGACAAAGCCACTCTCACCCGATTCCTTGCCTTCCACTTTATCCTCCCAATTCATCATTGCAGCCCTCGCCATAGTCCACCTGCTCTTCTC Majority
510 520 530 540 550 560 570 580 590 600
501 .....T.....C.....A..... AB044309_Capra_falconeri
501 .....C..... AB110592_Capra_aegagrus_blythi
501 .....CA.....T..... AB110597_Capra_hircus
501 .....T.C.....T.....T.....TT.....C.....T.....A..... AF010406_Ovis_aries
501 .....G.....C.A.....C.....T.....T.....AT.....A.T..... AF034734_Capra_sibirica
501 .....C.....A..... AF034735_Capra_ibex
501 .....T.....T.....T..... AF034737_Capra_cylindricornis
501 .....T.....T..... AF034738_Capra_caucasica
501 .....T.....T.....A..... AF217256_Capra_ibex_nubiana
501 .....CA.....A..... DQ073048_Black_Bengal
501 .....CA.....A..... DQ093614_Black_Bengal

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Table 9: (Continued Table 8) Alignment report content showing the exact mismatch of nucleotide at base pair level in Black Bengal Goat of present study DQ073048 and DQ093614 of *Cytochrome b* gene sequence of available *Cytochrome b* of *Capra* families viz. *Capra hircus* *Capra aegagrus blythi*, *Capra cylindricornis*, *Capra cylindricornis*, *Capra ibex*, *Capra ibex nubiana*, *Capra caucasica*, *Capra siberica* and *Capra falconeri*

CACGAAACAGGATCCAACAACCCACAGGAATTCATCAGACACAGACAAAATCCCATTTCACCCTTACTACACCATTAAAGATATCTTAGGCGCCATGC Majority															
610	620	630	640	650	660	670	680	690	700						
601		T								AB044309_Capra_falconeri					
601						C	T			AB110592_Capra_aegagrus_blythi					
601		G								AB110597_Capra_hircus					
601			G			T	C	C		AF010406_Ovis_aries					
601			A			T				CA_AF034734_Capra_sibirica					
601		G								AF034735_Capra_ibex					
601										AF034737_Capra_cylindricornis					
601										AF034738_Capra_caucasica					
601		G							AT	AF217256_Capra_ibex_nubiana					
601										DQ073048_Black_Bengal					
601		G								DQ093614_Black_Bengal					
TACTAATTCCTGTCCCTAATATTACTAGTACTATTACACCCGACCTACTCGGAGACCCAGACAACCTATATCCCAGCAAACCCACTCAATACACCCCTCA Majority															
710	720	730	740	750	760	770	780	790	800						
701		T				T				AB044309_Capra_falconeri					
701										AB110592_Capra_aegagrus_blythi					
701										AB110597_Capra_hircus					
701		C	CA		C	GC		G	T	T	AF010406_Ovis_aries				
701											AF034734_Capra_sibirica				
701											AF034735_Capra_ibex				
701											AF034737_Capra_cylindricornis				
701											AF034738_Capra_caucasica				
701											AF217256_Capra_ibex_nubiana				
701											DQ073048_Black_Bengal				
701											DQ093614_Black_Bengal				
CATTAAACCTGAGTGGTATTTCCTATTTCATACGCAATCCTACGATCAATCCCAACAACTAGGAGGAGTCCCTAGCCCTAGTCTCTCAATCCTAATC Majority															
810	820	830	840	850	860	870	880	890	900						
801		T								AB044309_Capra_falconeri					
801										AB110592_Capra_aegagrus_blythi					
801										AB110597_Capra_hircus					
801		C	A	A	C		G	T		C	T	T	AF010406_Ovis_aries		
801													AF034734_Capra_sibirica		
801													AF034735_Capra_ibex		
801													AF034737_Capra_cylindricornis		
801													AF034738_Capra_caucasica		
801													AF217256_Capra_ibex_nubiana		
801													DQ073048_Black_Bengal		
801													DQ093614_Black_Bengal		
TTAGTACTTGTACCTTTCCTCCACACATCTAAACAACGAAGATAATTCGGCCCAATCAGCCAATGCATATTCTGAATCCTGGTAGCAGATCTATTAA Majority															
910	920	930	940	950	960	970	980	990	1000						
901			A							G			AB044309_Capra_falconeri		
901													AB110592_Capra_aegagrus_blythi		
901													AB110597_Capra_hircus		
901		C	A	A	CC		T	A	G	G		A	T	T	AF010406_Ovis_aries
901															AF034734_Capra_sibirica
901															AF034735_Capra_ibex
901															AF034737_Capra_cylindricornis
901															AF034738_Capra_caucasica
901															AF217256_Capra_ibex_nubiana
901															DQ073048_Black_Bengal
901															DQ093614_Black_Bengal
CACTCACATGAATTGGAGGACGCCAGTTCGAACATCCCTACATTATTGGACAACCTAGCATCTATTATATATTTCTCATCATTCTAGTAATAATACC Majority															
1010	1020	1030	1040	1050	1060	1070	1080	1090	1100						
1001										C					AB044309_Capra_falconeri
1001															AB110592_Capra_aegagrus_blythi
1001															AB110597_Capra_hircus
1001															AF010406_Ovis_aries
1001															AF034734_Capra_sibirica
1001															AF034735_Capra_ibex
1001															AF034737_Capra_cylindricornis
1001															AF034738_Capra_caucasica
1001															AF217256_Capra_ibex_nubiana
1001															DQ073048_Black_Bengal
1001															DQ093614_Black_Bengal
AGCAGCTAGCACCATTGAAAATAACCTCCTAAAATGAAGAXXX Majority															
1110	1120	1130	1140												
1101															AB044309_Capra_falconeri
1101															AB110592_Capra_aegagrus_blythi
1101															AB110597_Capra_hircus
1101															AF010406_Ovis_aries
1101															AF034734_Capra_sibirica
1101															AF034735_Capra_ibex
1101															AF034737_Capra_cylindricornis
1101															AF034738_Capra_caucasica
1101															AF217256_Capra_ibex_nubiana
1101															DQ073048_Black_Bengal
1101															DQ093614_Black_Bengal

Table 10: Alignment report content showing the exact mismatch of the nucleotide at the base-pair level in Black Bengal Goat of present study DQ073048 and DQ093614 of *Cytochrome b* gene sequence of available *Cytochrome b* of *Ovis arie*, *Bos indicus*, *Bubalus bubalis*, and *Bos taurus*. The common mismatch of Black Bengal Goat (DQ073048 and DQ093614) is shown with the consensus sequences of *Cytochrome b* gene sequences of other ruminants

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ATGACCAACATCCGAAAGACCCACCCACTAATAAAAATTGTAAACAACGCATTTCATTGACCTCCCAGCCCCATCAAACATCTCATCATGATGAAACTTTC Majority
10 20 30 40 50 60 70 80 90 100
1 .....TC.....T.....A..... AB110597_Capra_hircus
1 .....A.....T.....T.....T..... AF010406_Ovis_aries
1 .....T.....T.....T.....C.....T.....G.....T.....C..... AF492350_Bos_indicus
1 .....T.....AT.....C.....T.....T.....T..... AY488491_Bubalus_bubalis
1 .....T.....T.....A..... DQ073048_Black_Bengal
1 .....T.....T.....A..... DQ093614_Black_Bengal
1 .....T.....T.....T.....C.....T.....T..... V00654_Bos_taurus

GATCCCTCCTAGGAATTTGCCTAATCTTACAAATCCTGACAGGCCTATTCCTAGCAATACACTACACATCCGACACAACAACAGCATTCTCCTCTGTAAAC Majority
110 120 130 140 150 160 170 180 190 200
101 .....T.....T..... AB110597_Capra_hircus
101 .....C.....T.....C.....T.....G.....T.....A..... AF010406_Ovis_aries
101 .....T.....G.....C.....C.....C..... T..... AF492350_Bos_indicus
101 .....C.....T.....C.....C.....G.....C.....C..... C.....CG..... AY488491_Bubalus_bubalis
101 .....T.....T.....T.....T..... DQ073048_Black_Bengal
101 .....T.....T.....T.....T..... DQ093614_Black_Bengal
101 .....T.....G.....C.....C.....C..... T..... V00654_Bos_taurus

CCACATTTGCCGAGACGTAAACTATGGCTGAATCATCCGATACATACACGCAACGGAGCATCAATATTTTTATCTGCCTATTTATACATGTAGGACGA Majority
210 220 230 240 250 260 270 280 290 300
201 .....T.....T.....T.....C.....C.....A.....C..... AB110597_Capra_hircus
201 .....C.....T.....C.....T.....T.....G..... AF010406_Ovis_aries
201 .....T.....C.....G.....G.....C.....C.....T.....G.....T.....A.....G.....C..... AF492350_Bos_indicus
201 .....C.....G.....G.....A.....T.....T.....C.....T.....A.....C..... AY488491_Bubalus_bubalis
201 .....T.....T.....T.....T.....C.....C.....A.....C..... DQ073048_Black_Bengal
201 .....T.....T.....T.....T.....C.....C.....A.....C..... DQ093614_Black_Bengal
201 .....T.....C.....G.....C.....C.....T.....G.....T.....A.....G.....C..... V00654_Bos_taurus

GGCCTATATTATGGATCATATACCTTTCTAGAAACATGAAACATTGGAGTAATCCTCCTGCTCGGACAATAGCCACAGCATTTCATAGGCTATGTTTTAC Majority
310 320 330 340 350 360 370 380 390 400
301 .....T.....G..... AB110597_Capra_hircus
301 .....C.....C.....G.....AT.....T..... AF010406_Ovis_aries
301 .....T.....G.....T.....C.....T.....A.....AGT..... A.....C.....CC..... AF492350_Bos_indicus
301 .....A.....C.....C.....C.....A.....AT.....AGT..... T.....A.....C.....AC.....G..... AY488491_Bubalus_bubalis
301 .....T.....G..... DQ073048_Black_Bengal
301 .....T.....G..... DQ093614_Black_Bengal
301 .....T.....C.....G.....T.....C.....T.....T.....A.....AGT..... T.....A.....C.....CC..... V00654_Bos_taurus

CATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAACCTTCTTTTCAGCAATCCCATATATTGGCACAACCTAGTCGAATGAATCTGAGGGGG Majority
410 420 430 440 450 460 470 480 490 500
401 .....T.....T.....T..... AB110597_Capra_hircus
401 .....A.....T.....T.....C.....T.....G.....A..... AF010406_Ovis_aries
401 .....A.....CT.....A.....C.....C.....TT..... AF492350_Bos_indicus
401 .....T.....T.....C.....T.....GT.....G.....T.....T..... AY488491_Bubalus_bubalis
401 .....T.....T.....T.....T..... DQ073048_Black_Bengal
401 .....T.....T.....T.....G..... DQ093614_Black_Bengal
401 .....T.....A.....CT.....A.....C.....C.....TT.....C..... V00654_Bos_taurus

ATTCCTCAGTAGACAAGCCACCTCAGCCGATTCCTTTCGCTTCCACTTTATCCATCCCATTCATCATCACAGCCCTCGCCATAGTCCACCTACTTCTCCTC Majority
510 520 530 540 550 560 570 580 590 600
501 .....T.....G.....T..... AB110597_Capra_hircus
501 .....T.....T.....T.....TT.....G.....T..... AF010406_Ovis_aries
501 .....A.....T.....T.....T.....T.....T.....T.....AA.....T.....T.....A..... AF492350_Bos_indicus
501 .....A.....T.....A.....T.....C.....T.....G.....A.....T.....A.....T.....T..... AY488491_Bubalus_bubalis
501 .....T.....G.....A..... DQ073048_Black_Bengal
501 .....T.....G.....A..... DQ093614_Black_Bengal
501 .....A.....T.....T.....T.....T.....T.....AA.....T.....A..... V00654_Bos_taurus

CAGGAAACAGGATCCAAACAACCCACAGGAATTCATCAGACACAGATAAAATCCCATTCACCCCTTACTACACCATTAAAGACATCTTAGGGCCATGC Majority
610 620 630 640 650 660 670 680 690 700
601 .....G.....T.....T..... AB110597_Capra_hircus
601 .....C.....T.....A.....G.....T.....C.....T.....C.....T.....T.....C..... AF010406_Ovis_aries
601 .....C.....T.....A.....CT.....C.....GT.....C.....T.....G.....G.....C.....CT..... AF492350_Bos_indicus
601 .....G.....A.....CT.....C.....C.....T.....C.....C.....A..... AY488491_Bubalus_bubalis
601 .....G.....T.....T.....T..... DQ073048_Black_Bengal
601 .....G.....T.....T.....T..... DQ093614_Black_Bengal
601 .....C.....A.....T.....C.....GT.....C.....T.....G.....G.....C.....CT..... V00654_Bos_taurus

TACTAATTCCTGTTCTAATACTACTAGTACTATTTCACCCGACCTACTCGGAGACCCAGACAACCTACACCCAGCAAATCCACTCAACACACCCCTCA Majority
710 720 730 740 750 760 770 780 790 800
701 .....T.....T.....T..... AB110597_Capra_hircus
701 .....C.....CA.....C.....G.....G.....T.....T.....C.....T.....T..... AF010406_Ovis_aries
701 .....A.....C.....G.....G.....C.....T.....T.....G.....C.....T..... AF492350_Bos_indicus
701 .....T.....C.....A.....CC.....T.....G.....G.....C.....G.....C.....T.....C..... AY488491_Bubalus_bubalis
701 .....T.....T.....T.....T.....T.....T.....T.....T..... DQ073048_Black_Bengal
701 .....T.....T.....T.....T.....T.....T..... DQ093614_Black_Bengal
701 .....A.....C.....G.....C.....T.....C.....T.....C..... V00654_Bos_taurus

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Table 11: (Continued Table 10) Alignment report content showing the exact mismatch of the nucleotide at the base-pair level in Black Bengal Goat of present study DQ073048 and DQ093614 of *Cytochrome b* gene sequence of available *Cytochrome b* of *Ovis arie*, *Bos indicus*, *Bubalus bubalis*, and *Bos taurus*. The common mismatch of Black Bengal Goat (DQ073048 and DQ093614) is shown with the consensus sequences of *Cytochrome b* gene sequences of other ruminants

```

CATCAAACCTGAGTGGTACTTCTATTTCGCATACGCAATCTTACGATCAATCCCCAACAACTAGGAGGAGTCCCTAGCCCTAGTCTCTCAATCTAATC Majority
810 820 830 840 850 860 870 880 890 900
801 ..T.....T.....C..... AB110597_Capra_hircus
801 .....A..A.....G.....T..T.....C.....A.....G... AF010406_Ovis_aries
801 .....C..A..A.....T.....A.....C..T.....T AF492350_Bos_indicus
801 .....G..A.....C.....T..T.....G..T.....T..... AY488491_Bubalus_bubalis
801 ..T.....T.....C..... DQ073048_Black_Bengal
801 ..T.....T.....C..... DQ093614_Black_Bengal
801 .....C.....A.....T.....A.....C..T.....T V00654_Bos_taurus

CTAGTACTTATACCCCTCCTCCACACATCTAAACAACGAAAGCATAATATTCCGCCCAATCAGCCAATGCATATTCTGAATCCTAGTAGCAGACCTATTA Majority
910 920 930 940 950 960 970 980 990 1000
901 T.....G.....T.....G.....T..... AB110597_Capra_hircus
901 .....A.....T.....A..G.....G.....A.....T.....T.....C..... AF010406_Ovis_aries
901 ..T..CT..A..C.....A..A.....C..C.....A.....A.....C.....GC.....C..G AF492350_Bos_indicus
901 ..CA..T..C..G.....G..A..T.....C.....T..G..G.....G.....T.....C.....T.....A.....GC... AY488491_Bubalus_bubalis
901 T.....G.....T.....G.....T..... DQ073048_Black_Bengal
901 T.....G.....T.....G.....T..... DQ093614_Black_Bengal
901 ..T..CT..A..C.....A..A.....C..C.....A.....C.....C.....GC.....C..G V00654_Bos_taurus

CACTCACATGAATTGGAGGACAGCCAGTCGAACACCCTACATTATTATTGGACAACCTAGCATCTATTATATATTTCTCATCTATTCTAGTAATAATACC Majority
1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
1001 .....T..... AB110597_Capra_hircus
1001 .....C.....T.....C.....T.....C..... AF010406_Ovis_aries
1001 .....A.....A.....T.....C..CC.....CC.....C..T..TC.....C.....C..... AF492350_Bos_indicus
1001 .....G.....A.....T.....C.....C.....C.....C.....GC..... AY488491_Bubalus_bubalis
1001 .....T..... DQ073048_Black_Bengal
1001 .....T..... DQ093614_Black_Bengal
1001 .....A.....A.....T.....C..CC.....G..CC.....C..T.....C.....C.....GC..... V00654_Bos_taurus

AGCAGCTAGCACCATTGAAAACAACCTTCTAAATGAAGA Majority
1110 1120 1130 1140
1101 ..... AB110597_Capra_hircus
1101 ..T.....T.....C.....C..... AF010406_Ovis_aries
1101 ..A.....CG.....AG.....AT..A..... AF492350_Bos_indicus
1101 ..A..G..C.....TA..C.....T..T..CT..... AY488491_Bubalus_bubalis
1101 ..... DQ073048_Black_Bengal
1101 ..... DQ093614_Black_Bengal
1101 ..A..G..CG.....A..C.....AT..A..... V00654_Bos_taurus
    
```

quence are given in Figure 1 and Table 8. The highest level of genetic similarity was found between Black Bengal and *Capra aegagrus* up to the extent of 96.7% (Table 5). The wild goat (*Capra aegagrus*) appeared to be the clear progenitor of the black Bengal goat and modern native goat, which was simulated by Sultana (15) in Pakistani goats. This result can be explained by assuming a new mtDNA lineage or historical introgression from wild goats(16). The second most closely related wild goat *Capra falconari* is placed at a less genetic distance from the black Bengal goat and is strongly supported by the findings of (Figure 2 and 3). The phylogenetic tree was obtained by analyzing the nucleotide sequence of *Cytochrome b* of black Bengal goat and other related members of the Caprine family (Figure 1, 2,3 and 6 Table 5 and 8).

#### 4.6 Diversity in Ruminants

The *Cytochrome b* sequence of black Bengal goats (DQ073048 DQ093614) were compared with the sequence of relatively closer ruminants available publicly to get a picture of the evolutionary scenario. The phylogenetic tree and alignment of the DNA sequence of the *Cytochrome b* gene sequence of black Bengal goats are given in Figure 4 and Table 9. A pairwise distance matrix of sequence divergence is shown in Table 6. Interestingly it was found the closest related species is *Ovis aries* and *Bubalus bubalis* shares higher homology than *Bos taurus* and *Bos indicus*. The phylogenetic tree (Figure 5) constructed also reveals the same.

The less variation in distance matrix analysis probably occurred due to either the close relationship between the above breeds or due to consideration of *Cytochrome b* which is a conserved gene showing less variation at the intra-specific level. In the present study, an account of the molecular difference between the black Bengal goat and its modern and wild counterpart and also with distantly related other species was established (Figure 7 and 9, Tables 7 and 10). The percentage of nucleotide composition of *Cytochrome b* at different codon positions G was correlated with the overall evolution of the *Cytochrome b* gene. The fact that a change from G to A, T, or C in the first two codon positions causes an amino acid substitution and that rates of amino acid substitution are lower in basal lineages of vertebrate phylogeny (Adachi et al. 1993). The black Bengal goat nucleotide composition of *Cytochrome b* is closely related to its close relative and showed the highest A percentage among all the species. Considering the three codon position the third codon position contained 42.3% A indicating that amino acid substitution is very low in that position as changes of A cause a very low change in amino acid substitution.

Table 12: Alignment report content showing the exact mismatch of nucleotide at base pair level in Black Bengal Goat of present study DQ073048 and DQ093614 of *Cytochrome b* gene sequence of available *Cytochrome b* of *Cytochrome b* gene of *Capra hircus*, *Ovis arie*, *Bos indicus*, *Bubalus bubalis*, *Homo sapiens*, *Bos taurus*, *Gallus gallus*, *Camelus dromedaries* and *Sus scrofa*

```

ATGACCAACATCCGAAATCCCACCCACTAATAAAAATTGTAAACAACGCATTTCATTGACCTCCCAGCCCCATCAAACATCTCATCATGATGAAACT Majority
10 20 30 40 50 60 70 80 90 100
1 .....GA.....TC.....T.....A..... AB110597_Capra_hircus
1 .....T.....A.....T.....T.....T..... AF010406_Ovis_aries
1 .....T.....T.....G.....T.....C.....T..... AF492350_Bos_indicus
1 .....T.....C.....T.....T.....T..... AY488491_Bubalus_bubalis
1 .....CCA.A.C.ATTA.C.....T.AA.T.C.T.....CA.....C.....CG..... AY882393_Homo_sapiens
1 .....GA.....T.....A..... DQ073048_Black_Bengal
1 .....GA.....T.....T.....A..... DQ093614_Black_Bengal
1 .....T.....T.....G.....T.....C.....T..... V00654_Bos_taurus
1 ATGGCAC.....T.....C.....AA.T.....T.CC.A.C.....C.....TG.T.....T. X52392_Gallus_gallus
1 .....A.....A.....TC.....A.....G.....T.....C.....C.....T.....T..... X56281_Camelus_dromedarius
1 .....A.....A.....C.....C..... Z50079_Sus_scrofa

TCGGCTCCCTCCTAGGAATCTGCCTAATCTTACAAATCCTCACAGGCCTATTCCCTAGCAATACACTACACATCCGACACAACAACAGCATTCTCCTCTGT Majority
110 120 130 140 150 160 170 180 190 200
98 ..T.A.....T.....G.....T..... AB110597_Capra_hircus
98 ..T.....T.....C.T.T.T.....G.T.A.....T.....C.T..... AF010406_Ovis_aries
98 ..T.....T.....G.....C..... AF492350_Bos_indicus
98 ..T.....T.....C.....C.G.....C..... AY488491_Bubalus_bubalis
98 .....A.T.CGC.....G.C.C.....AC.....A.....C.G.....T.C.A.....G.C.T.....C.C.T.A.AA. AY882393_Homo_sapiens
98 ..T.A.....T.....G.....T.....T..... DQ073048_Black_Bengal
98 ..T.A.....T.....G.....T.....T.....T..... DQ093614_Black_Bengal
98 .....T.....G.....C..... V00654_Bos_taurus
101 .....AT.....C.G.....C.GACC.....C.....C.A.....C.G.....G.A.....T.CCT.....C.....C. X52392_Gallus_gallus
98 .....T.A.....G.T.....TA.....G.....A.....G.....T.....T.....C.....T.A..... X56281_Camelus_dromedarius
98 .....T.....T.....C.....G.....A.....G.....T.....T.....A.....A..... Z50079_Sus_scrofa

AACCCACATTTGCCGAGACGTAATATGGCTGAATCATCCGATACATACACGCAAAACGGAGCATCAATATTTCTTTATCTGCCTATTTCATACACGTCGGA Majority
210 220 230 240 250 260 270 280 290 300
198 ..T.....T.....T.....TA..... AB110597_Capra_hircus
198 .....T.....C.....T.....T.....G.....T.....T.G.T.A..... AF010406_Ovis_aries
198 ..T.....T.....G.C.C.....T.....T.....G.T.....T.....AT.G.....A..... AF492350_Bos_indicus
198 CG.....C.....G.....G.C.A.....T.T.....T.....T.....C.....T.....AT.....A..... AY488491_Bubalus_bubalis
198 CG.....CACT.....C.....C.T.....C.T.C.C.....C.....A.....G.....AY882393_Homo_sapiens
198 ..T.....T.....T.....TA..... DQ073048_Black_Bengal
198 ..T.....T.....T.....TA..... DQ093614_Black_Bengal
198 ..T.....T.....G.C.C.....T.....G.T.....T.....AT.G.....A.....V00654_Bos_taurus
201 ..C.....C.....GA.....C.A.C.....C.....GA.T.C.C.....C.....C.....T.A.C.....C.T.....A.....X52392_Gallus_gallus
198 CG.A.....C.....T.T.C.C.....T.....TT.....T.T.....T.....C.....C.T.....T.....AT.T.....G.T.X56281_Camelus_dromedarius
198 ..T.A.....T.....C.....A.....G.T.....T.C.....T.....C.....T.....C.....A.....C.....Z50079_Sus_scrofa

CGAGGCCTATATTACGGATCATATACCTTTCTAGAAACATGAAACATTGGAGTAATCCCTCCTGCTCGCAGTAATAGCCACAGCATTTCATAGGCTATGTTC Majority
310 320 330 340 350 360 370 380 390 400
298 .....T.....T.....G.....GAC..G.....T..... AB110597_Capra_hircus
298 .....C.T.....C.....C.....AT.T.GAC.....T..... AF010406_Ovis_aries
298 .....T.....T.....G.T.C.T.....T.C.....T.....A.....A.C.C.....AF492350_Bos_indicus
298 .....A.C.....A.....AT.....C.....A.....T.....T.....A.....C.....AY488491_Bubalus_bubalis
298 .....T.....T.....CT.ACTC.....C.....C.CA.T.....T.....ACT.....A.....C.....AY882393_Homo_sapiens
298 .....T.....T.....GAC.G.....T.....DQ073048_Black_Bengal
298 .....T.....T.....GAC.G.....T.....DQ093614_Black_Bengal
298 .....T.....G.T.C.T.....T.....T.....A.....A.....C.....V00654_Bos_taurus
301 .....C.....C.....CCT.ACAAG.....T.....CA.....C.....A.....C.....C.....TG.G.....X52392_Gallus_gallus
298 ..C.G.T.....C.G.....TC.....C.....G.....A.GG.TT.A.T.....A.....T.....G.....C.....C.....X56281_Camelus_dromedarius
298 .....T.....C.....C.....TA.C.....G.....A.....AT.TA.C.....T.....A.....C.....C.....Z50079_Sus_scrofa

TACCATGAGGACAAATATCATTTCTGAGGGCAACAGTCATCACTAACCTTCTTTCAGCAATCCCATATATTGGCACAAACCTAGTCGAATGAATCTGAGG Majority
410 420 430 440 450 460 470 480 490 500
398 .....T.....T.....T..... AB110597_Capra_hircus
398 .....A.....T.T.C.....C.....T.....G..... AF010406_Ovis_aries
398 .....A.....C.....CT.A.....C.....C.....TT..... AF492350_Bos_indicus
398 G.....C.....C.....C.....C.....T.....GT.G.T.....T..... AY488491_Bubalus_bubalis
398 ..C.G.....C.....C.....A.T.A.T.A.A.C.C.....C.....G.....G.....TC..... AY882393_Homo_sapiens
398 .....T.....T.....DQ073048_Black_Bengal
398 .....T.....T.....G.....DQ093614_Black_Bengal
398 .....A.....C.....CT.A.....C.....C.....TT..... V00654_Bos_taurus
401 ..C.G.C.....C.....C.T.....A.....AT.C.....T.C.C.....ACAC.C.....A.....G.....GC..... X52392_Gallus_gallus
398 ..T.....G.....A.....A.....T.....TT.G.C.....C.....C.....CA.....A.....G.....T..... X56281_Camelus_dromedarius
398 ..G.C.....A.....T.....G.....A.....T.....T.....C.....A.....G.....C.....A..... Z50079_Sus_scrofa

GGGATTCTCAGTAGACAAGCCACCCTCACCCGATTCTTCGCTTCCACTTTATCCTCCCATTCATCATCACAGCCCTCGCCATAGTCCACCTACTATTC Majority
510 520 530 540 550 560 570 580 590 600
498 .....T.....G.T..... AB110597_Capra_hircus
498 A.....T.....T.....T.....TT.....G.....T.....C..... AF010406_Ovis_aries
498 C.....A.....T.....T.....T.....T.....T.....T.....AA.T.....T..... AF492350_Bos_indicus
498 .....A.....A.....T.....C.....T.....T.....G.....A.....T.....A.....T.....T..... AY488491_Bubalus_bubalis
498 A.C.A.....GTC.....A.....TA.....T.....C.....T.G.C.....T.....TG.....A.....AGC.C.....C..... AY882393_Homo_sapiens
498 .....T.....G.....CA.....DQ073048_Black_Bengal
498 .....T.....T.....G.....CA.....DQ093614_Black_Bengal
498 .....A.....T.....T.....T.....T.....T.....AA.T..... V00654_Bos_taurus
501 .....T.....C.....CC.A.....T.....T.....A.....CC.....C.....TGCA.....G.....GTA.TA.T.CA.....CACC..... X52392_Gallus_gallus
498 T.T.....C.....T.....A.....T.....C.....A.....T.....G.....T.....A.TGGCC.A.....T..... X56281_Camelus_dromedarius
498 ...C.T.C.C.....A.....A.....G.....T.....C.....AGCC.A.T.C..... Z50079_Sus_scrofa

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Table 13: (Continued Table 12) Alignment report content showing the exact mismatch of nucleotide at base pair level in Black Bengal Goat of present study DQ073048 and DQ093614 of *Cytochrome b* gene sequence of available *Cytochrome b* of *Cytochrome b* gene of *Capra hircus*, *Ovis arie*, *Bos indicus*, *Bubalus bubalis*, *Homo sapiens*, *Bos taurus*, *Gallus gallus*, *Camelus dromedaries* and *Sus scrofa*

```

CTCCACGAAACAGGATCCAACAACCCACAGGAATTTTCATCAGACACAGATAAAATCCCATTCCACCCTTACTACACCATTAAAGACATCCTAGGCGCCC Majority
610 620 630 640 650 660 670 680 690 700
598 .....G.....C.....T.....T.....T.....A AB110597_Capra_hircus
598 .....C.....G.....T.....C.....T.....T.....TA AF010406_Ovis_aries
598 .....C.....T.....A.....C.....GT.....C.....T.....G.....T.....G..... AF492350_Bos_indicus
598 .....C.....T.....A.....C.....C.....T.....C.....T..... AY488491_Bubalus_bubalis
598 T.G.....G.....A.....CT.....CA.C.CC.TT.C.....A.C.....A.C.....GC.....TTA. AY882393_Homo_sapiens
598 .....G.....C.....T.....T.....T.....A DQ073048_Black_Bengal
598 .....G.....C.....T.....T.....T.....A DQ093614_Black_Bengal
598 .....C.....A.....C.....GT.....C.....T.....G.....T.....G..... V00654_Bos_taurus
601 A.....T.....C.....A.....CT.....C.....C.....T.....T.....C.....T.....A.....T.....T.....C.....T.....G.....TTAA X52392_Gallus_gallus
598 A.....G.....C.....C.....T.....A.....C.....T.....T.....C.....T.....G.....T.....A.....A..... X56281_Camelus_dromedarius
598 .G.....C.....T.....C.....C.....T.....C.....T.....T.....A.....T.....A.....T.....Z50079_Sus_scrofa

TGCTACTAATTTCTAGCTCTAATACTACTAGTACTATTCTCACCCGACCTACTCGGAGACCCAGACAACCTACACCCAGCAAACCCACTCAACACACCCCC Majority
710 720 730 740 750 760 770 780 790 800
698 .....T.....T.....T.....A.....T.....T.....T.....T..... AB110597_Capra_hircus
698 C.....C.....CATC.....C.....G.....A.....G.....T.....T.....T.....T..... AF010406_Ovis_aries
698 CT.....C.....T.....G.....C.....T.....T.....G.....C.....T.....T..... AF492350_Bos_indicus
698 A.....T.....C.....C.....T.....G.....C.....G.....T.....T.....T.....T..... AY488491_Bubalus_bubalis
698 T.....CT.....CC.....CT.....CT.....G.....AC.....T.....A.....C.....A.....C.....T.....T.....T.....C.....T.....A.....C.....T..... AY882393_Homo_sapiens
698 .....T.....T.....T.....A.....T.....T.....T.....T.....T.....T..... DQ073048_Black_Bengal
698 .....T.....T.....T.....A.....T.....T.....T.....T.....T.....T..... DQ093614_Black_Bengal
698 CT.....C.....T.....G.....C.....T.....C.....T.....T.....T.....T..... V00654_Bos_taurus
701 CT.....CA.....C.....CACCC.....AT.....CC.....AC.....CC.....C.....A.....C.....A.....A.....T..... AGTA.....C..... X52392_Gallus_gallus
698 A.....G.....G.....C.....C.....T.....A.....C.....T.....A.....T.....T.....T.....C.....C.....C.....T.....A..... X56281_Camelus_dromedarius
698 AT.....TA.....A.....ATC.....C.....A.....C.....T.....A.....A.....A.....A.....A.....A.....Z50079_Sus_scrofa

TCACATCAAACCTGAATGATATTTCTATTGTCATACGCAATCCTACGATCAATCCCCAACAACTAGGAGGAGTCTAGCCCTAGTCTCTCAATCCTA Majority
810 820 830 840 850 860 870 880 890 900
798 .....T.....G.....G..... AB110597_Capra_hircus
798 .....C.....C.....T.....G.....T.....T.....T.....A.....C.....A..... AF010406_Ovis_aries
798 .....C.....C.....T.....G.....C.....T.....T.....A.....C.....T.....T..... AF492350_Bos_indicus
798 C.....G.....G.....C.....C.....T.....T.....T.....T.....G.....T.....T.....T.....T..... AY488491_Bubalus_bubalis
798 C.....G.....G.....C.....C.....A.....T.....C.....CG.....T.....C.....T.....T.....A.....A.....C.....C..... AY882393_Homo_sapiens
798 .....T.....G.....G..... DQ073048_Black_Bengal
798 .....T.....G.....G..... DQ093614_Black_Bengal
798 .....C.....G.....C.....T.....A.....C.....T.....T.....T.....T..... V00654_Bos_taurus
801 A.....T.....A.....T.....C.....C.....T.....C.....C.....C.....C.....T.....T.....A.....C.....AGC.....G.....C..... X52392_Gallus_gallus
798 A.....T.....G.....G.....G.....C.....T.....T.....T.....T.....C.....A.....G.....T.....C.....T..... X56281_Camelus_dromedarius
798 C.....T.....T.....A.....T.....C.....C.....T.....T.....T.....T.....T.....T.....T.....GT.....G.....AGC.....C..... Z50079_Sus_scrofa

ATCCTAGTACTTATCCCCTTCTCCACACATCCAACAACGAAGCATAATATTCGACCCTCAGCCAATGCCTATTCTGAATCCTAGTAGCAGACCTAC Majority
910 920 930 940 950 960 970 980 990 1000
898 .....T.....G.....A.....T.....C.....A.....A.....G.....T.....T..... AB110597_Capra_hircus
898 G.....A.....A.....A.....A.....G.....G.....A.....T.....TA.....C.....T..... AF010406_Ovis_aries
898 T.....T.....CT.....A.....C.....A.....A.....C.....GC.....T.....T..... AF492350_Bos_indicus
898 .....CA.....T.....C.....G.....C.....G.....A.....T.....T.....G.....G.....G.....T.....T.....T.....A.....G..... AY488491_Bubalus_bubalis
898 .....C.....A.....A.....A.....T.....T.....A.....T.....C.....A.....CA.....T.....AT.....C.....CC.....C..... AY882393_Homo_sapiens
898 .....T.....G.....A.....T.....C.....A.....A.....A.....G.....T.....T..... DQ073048_Black_Bengal
898 .....T.....G.....A.....T.....C.....A.....A.....A.....G.....T.....T..... DQ093614_Black_Bengal
898 T.....T.....CT.....A.....C.....A.....A.....C.....GC.....T.....T.....T.....T..... V00654_Bos_taurus
901 .....CT.....C.....A.....A.....T.....CA.....CC.....TC.....AC.....C.....T.....CA.....T..... X52392_Gallus_gallus
898 .....C.....T.....GCA.....A.....A.....C.....T.....CA.....T.....T.....G.....T.....G.....A.....T.....T..... X56281_Camelus_dromedarius
898 A.....TT.....A.....G.....A.....A.....A.....T.....A.....T.....A.....CA.....Z50079_Sus_scrofa

TAACACTCACATGAATGGAGGACAACCGAGTCGAACACCCCTACATCATCATTGGACAACCTAGCATCTATCATATACTTCCTCATCATTCTAGTACTAAT Majority
1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
998 .....G.....T.....T.....T.....T.....T.....A..... AB110597_Capra_hircus
998 .....C.....G.....T.....T.....T.....T.....T.....T.....CA..... AF010406_Ovis_aries
998 G.....G.....A.....T.....C.....T.....T.....C..... AF492350_Bos_indicus
998 .....G.....G.....A.....T.....T.....C.....C.....C.....G..... AY488491_Bubalus_bubalis
998 C.....TT.....A.....C.....C.....AAGCT.....T.....TT.....C.....G.....CG.....AC.....ACA.....CA.....C.....A.....C..... AY882393_Homo_sapiens
998 .....G.....T.....T.....T.....T.....T.....T.....A..... DQ073048_Black_Bengal
998 .....G.....G.....T.....T.....T.....T.....T.....T.....A..... DQ093614_Black_Bengal
998 G.....G.....A.....T.....C.....C.....G.....C.....T.....C.....C.....G..... V00654_Bos_taurus
1001 T.....TC.....A.....C.....C.....A.....C.....A.....T.....C.....A.....CC.....TCT.....AC.....C.....A.....TA.....C.....CT..... X52392_Gallus_gallus
998 .....C.....G.....G.....A.....C.....A.....T.....A.....C.....G.....G.....TC.....CA.....A.....T.....C..... X56281_Camelus_dromedarius
998 T.....A.....A.....C.....A.....G.....T.....A.....C.....C.....C.....T.....A.....T.....G.....T.....Z50079_Sus_scrofa
    
```

The present study provides a convincing molecular phylogenetic status of black Bengal goats together with other farm animals. This study would help with an essential scientific conservation programme of the Black Bengal goat. Further investigation of other parts of mitochondrial DNA is necessary to understand the population structure of this breed. Furthermore, from the amino acid and nucleotide analysis, it can be concluded that although there is variation in nucleotide composition within a species, amino acid variation is almost nil. It strongly recommends that very

less non-synonymous mutations occur in *Cytochrome b* at the intra-specific level though it is seen at the interspecies level with low frequency.

### 5 Conclusion

Black Bengal, one of the most prolific goat breeds of India is widely distributed in Eastern India. In an attempt to resolve its phylogeny, the mitochondrial *Cytochrome b* gene of the black Bengal goat was characterized to study the base composition, RE profile, repeats, derived amino acid

Table 14: (Continued Table 12) Alignment report content showing the exact mismatch of nucleotide at base pair level in Black Bengal Goat of present study DQ073048 and DQ093614 of *Cytochrome b* gene sequence of available *Cytochrome b* of *Cytochrome b* gene of *Capra hircus*, *Ovis arie*, *Bos indicus*, *Bubalus bubalis*, *Homo sapiens*, *Bos taurus*, *Gallus gallus*, *Camelus dromedaries* and *Sus scrofa*

```

ACCAACAGCTAGCACCATTTGAAAACAACCTACTAAAATGAAGAX Majority
-----+-----+-----+-----+-----+-----+-----+-----+-----+
1110 1120 1130 1140
-----+-----+-----+-----+-----+-----+-----+-----+-----+
1098 ...G.....T..... AB110597_Capra_hircus
1098 ...GT.....T...C..... AF010406_Ovis_aries
1098 ...CG...AG...AT..... AF492350_Bos_indicus
1098 ...G...C...TA...C...T...T...CT..... AY488491_Bubalus_bubalis
1098 ...TATCTC.CTA.....AA...C.....GGCCT AY882393_Homo_sapiens
1098 ...G.....T..... DQ073048_Black_Bengal
1098 ...G.....T..... DQ093614_Black_Bengal
1098 ...G...CG...A...C...AT..... V00654_Bos_taurus
1101 C...C...ATCG.A...AC.A...AA...C...C.ACTA. X52392_Gallus_gallus
1098 G...CGT...AG.A...T.....CGTA.C..... X56281_Camelus_dromedarius
1098 ...TCA...T...C.....T..... Z50079_Sus_scrofa

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as well as comparative DNA sequence analysis. Genetic analysis of *Cytochrome b* revealed that mutation occurs in the conserved region of mtDNA and is mostly synonymous. It is predicted that BsaI could be used as a marker enzyme for this particular breed of goat. The phylogenetic analysis establishes that the black Bengal goat might be evolved from the wild goat *Capra aegagrus*. The study also reveals that *Cytochrome b* protein is stable and normal. The study provides the convincing molecular phylogenetic status of the black Bengal goat which would help in scientific conservation of the Black Bengal goat.

### Conflict of Interest

The authors declare no conflict of interest in this reported communication.

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