

Two Mitochondrial Lineages Revealed in North American Yak

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Introduction

- Domestication events are commonly illustrated by maternally inherited mitochondria because it is unaffected due to hybridization between wild and domestic animals and the lack of recombination establishes simple genetic patterns^{1,2}.
- Domestic yak of the Qinghai-Tibetan Plateau fall into one of two divergent maternal lineages established before domestication. Evidence of introgression between wild yak and Asian cattle is also present in domestic populations^{1,3}.
- Yaks herds were established in North America before lineages could be genetically determined. Cross breeding with local cattle has occurred.
- Studies of genetic lineages along with analysis of functional differences among mitochondrial genes of North American yak can contribute to management of the genetic diversity of these emerging herds and a better understanding of yak biology.

Purpose: The goal of this study was to characterize the mtDNA diversity present in North American yaks.

Methods

- Animals: 14 North American Yak, 1 Tibetan Yak, 1 Tibetan *Bos indicus*. DNA isolated and sequenced using 150bp paired-end reads.
 - GenBank Data: *B. indicus* [MF667931.1, MF667930.1, MF667929.1, KX575711.1, AY126697.1], *B. grunniens*-Chinese [NC_006380.3], *B. taurus* [NC_006853.1, DQ124403], *B. gaurus* [NC_024818.1], *B. primigenius* [NC_013996.1], *B. frontalis* [NC_036020.1], *Bison bison* [NC_012346.1], and *Ovis aries* [NC_001941.1]
- Complete mtDNA Alignment: The North American yaks and Tibetan samples were aligned to the *B. grunniens* reference (ARS_UNL_BGru_maternal_1.0)⁴, which was also included in analyses, with BWA-MEM⁵.
- Gene Annotation: mtDNA genes of a North American domestic yak (ARS_UNL_BGru_maternal_1.0) were annotated using the annotation from ARS-UCD1.2 as a reference after Clustal alignment within the Sequencher software⁶.
- Genome Variations: Single Nucleotide Polymorphisms (SNP) within the North American Yak population were identified by alignment and visual confirmation in Sequencher. Using the annotated *B. grunniens* mtDNA genome as a reference, each SNP location was recorded.
- Maximum Likelihood Tree: Aligned mtDNA genomes of the 14 individuals and similar taxa from GenBank were converted into a FASTA file. The ML tree was produced by IQtree⁷ after the data were partitioned into 22 subgroups using PartitionFinder⁸. Branch support was evaluated with 1000 bootstrap iterations.

Results

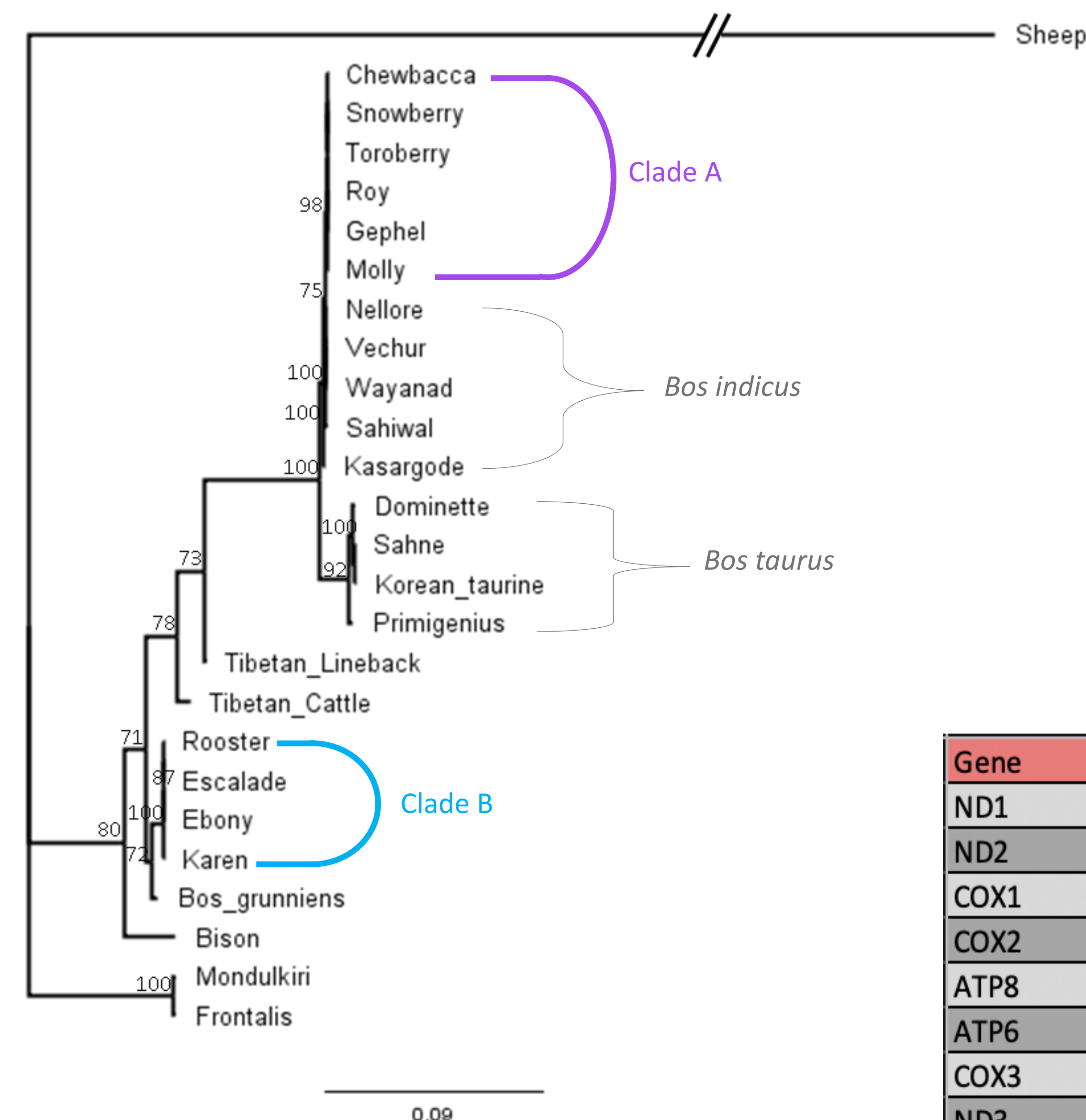


Figure 1. Maximum Likelihood Tree. Complete mitochondrial genomes of North American yak along with related Bovidae taxa show 9 North American yaks, representing 6 haplotypes, have *B. indicus* lineage and 4 North American yak with *B. grunniens* lineage. Two distinct clades are present in North American yaks. Bootstrap values >70% given.

Table 1. mtDNA SNP Variants. Using the annotated North American *B. grunniens*, location of variants in both North American clades were determined with Sequencher.



Figure 2. North American Yak. individual of one of the herds sampled for the current study.

Gene	Location (Sequencher Position)	Total SNPs	Nonsynonymous
ND1	3101-4057	59	7
ND2	4266-5307	67	9
COX1	5687-7231	86	1
COX2	7374-8057	47	2
ATP8	8129-8329	11	4
ATP6	8290-8970	45	8
COX3	8970-9750	51	7
ND3	9823-10168	21	0
ND4L	10239-10535	22	2
ND4	10529-11906	112	14
ND5	12109-13929	140	25
ND6	13913-14440	32	4
CYTB	14514-15653	15	10
Dloop	1-363, 15792-16109	1006	
tRNA/rRNA	364-3100, 4058-4265, 5308-5686, 7232-7373, 8058-8128, 9751-9822, 10169-10238, 11907-12108, 14441-14513, 15654-15791	159	

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Discussion

- Complete mitochondrial sequence place North American yak into two distinct clades supporting two mitochondrial origins (Figure 1).
- This tree suggests yak introgression was with *B. indicus* cattle, appearing to date prior to importation into North America.
- In other studies, domestic yak with Asian *B. taurus* mitochondria had either minimal cattle introgression per autosomal loci or no cattle alleles; supporting ancient introgression events⁹.
- Analysis of the whole genome of these North American yaks also shows few cattle alleles in most individuals¹⁰, also supporting older mitochondrial introgression in the North American population.
- 1879 SNPs were identified in the North American yak sequenced; 93 of these were annotated as nonsynonymous (Table 1).

Implications: Understanding the presence of multiple lineages of yak in North American benefits breeders as they plan the best management and breeding programs for their herds.

Due to significant mtDNA variation, including 93 nonsynonymous variants, the two major mtDNA haplotypes in North American yak may functionally differ. Mitochondrial genes code subunits of the electron transport chain. Characterization of the impact of these differences on cellular function is currently underway.

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CONTRIBUTORS: Breeders and owners from the IYAK and USYAKS Associations provided North American yak samples. DNA sequencing was performed at the USDA Meat Animal Research Center.