The origin and genetic diversity of native Yakutian cattle as revealed by DNA-Marker analysis

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ABSTRACT

Yakutian Cattle are the last endangered native stock of domesticated cattle in Siberia and are well adapted to sub-Arctic conditions. The main population of the breed is currently distributed among three northern villages in the Republic of Sakha in the Russian Federation where cattle production provides an important livelihood for the local people. DNA marker analyses have many applications in investigations of diversity and population structure of domesticated animal species and breeds. Three different types of genetic markers were employed to assess genetic diversity of the Yakutian Cattle breed and relationships between the Yakutian Cattle and several other Eurasian breeds of domestic cattle (Bos taurus). The data indicate that the Yakutian Cattle descended from the Near Eastern domesticated cattle, but the population also has an exceptional maternal ancestry (the T4 “dam line”), the origin of which is not well known as yet. In a global context, Yakutian Cattle are genetically unique.

Keywords: Yakutian Cattle, DNA-marker analysis, domestication, ancestry, genetic resources

INTRODUCTION

Yakutian Cattle are the last remnants of the unique Siberian Turano-Mongolian type of domesticated cattle (Bos taurus); they are well adapted to the extreme sub-Arctic Siberian conditions. Of the 1,200 purebred animals left in Sakha (Yakutia), less than 600 are dairy cows. Up to 74 percent of the Yakutian Cattle are distributed among the three northern villages of Dzhargalakh, Kustur, and Batagay-Alyta (also called Sakkaryr), collectively termed the Eveno-Bytantay district, which is located about 150 kilometers north of the Arctic Circle. During the last decade, Yakutian Cattle were returned to the southern part of the Sakha Republic from where they had previously vanished. Therefore, the cattle are currently found also in the village of Uluu-Syhy and on four farms closer to the capital of Sakha, Yakutsk City (Kantanen et al. 2009a).

Turano-Mongolian cattle can be distinguished from the European humpless taurine cattle by their characteristic cranial formation and the shape of the horns
(Ivanova 1997). Although these animals were once common in the eastern and central regions of Asia, several of the original types have disappeared due to extensive crossbreeding with modern European cattle breeds (Felius 1995; Li et al. 2005). Yakutian Cattle are a purebred, aboriginal population that produces milk and meat. These cattle currently produce approximately 1,000 kilograms of milk annually; the milk is high in fat and protein, averaging 5.03 percent and 4.69 percent respectively. The cattle have been used also as draft animals. Yakutian Cattle are currently endangered; therefore, the Sakha Republic enacted a law on the conservation and use of the cattle in 2001 (Partanen and Kantanen 2009). This breed may be unique in that there may be no other breeds of domesticated animal species whose conservation has been defined by law.

The history of Yakutian Cattle is not well known. The most common theory is that the people and their cattle came from southwest Asia or Mongolia and stayed by Lake Baikal for some time before they migrated to Sakha (Kopoteva and Partanen 2009). However, the area of the Fertile Crescent the Near East, in western Asia, was the place where humphless cattle were domesticated (Bradley et al. 1996). From there, domesticated cattle moved with migratory people, like bands of traders and armies, gradually spreading thousands of kilometers to eastern Asia and finally reaching Yakutia. According to Payne and Hodges (1997), domestic cattle appeared some 4,000 to 5,000 years ago in north-eastern Asia—Mongolia, North China, Korea, and Japan.

Genetics provides useful tools to study origins, genetic diversity, genetic characteristics of distinct breeds, and relationships among various breeds of cattle. In addition, molecular and population genetic analyses can be applied to infer the value of a breed for the maintenance of the genetic diversity of the species (e.g. Bennewitz et al. 2006; Li et al. 2007). From the long-term perspective, genetically divergent breeds, such as Yakutian Cattle, may be crucial for sustainable animal production systems in the future, especially as an important resource for economic development in marginal rural areas. Such areas are less favorable for agriculture but could be used for food production if low-input farming systems are applied. These breeds carry genes and gene combinations which are important for survival in extreme conditions. In addition, these animals are a valuable resource for the development of new breeds, as well as for scientific research work.

So far, the most popular DNA markers in population genetic analyses have been bireparentally-inherited (from both parents) autosomal 1 microsatellites or uniparentally-inherited (from a single parent) mitochondrial DNA and Y-chromosomal DNA. Microsatellites are short segments of DNA, consisting of a short unit of nucleotides which is typically repeated ten to a hundred times at a microsatellite locus (Hancock 1999). For example CA with cytosine and adenine bases is a typical unit of two nucleotides. Microsatellites are typically neutral markers, and neither natural nor artificial selection has any impact on frequencies of different microsatellite alleles. Mitochondrial DNA is a circular double-stranded DNA molecule found outside of the cell nucleus in cytoplasmic organelles termed mitochondria. It is

1 An autosome is a non-sex chromosome; X and Y are sex chromosomes and therefore non-autosomal chromosomes.
inherited maternally from the dam (Bradley et al. 1996). The Y-chromosomal markers are inherited from the father, the sire (the so-called paternal inheritance), and provide evidence of paternal origins of populations (Jobling and Tyler-Smith 1995).

At Agrifood Research Finland (MTT), these kinds of molecular genetic analyses on Eurasian cattle breeds were conducted, and the genetics of the Yakutian Cattle were investigated in a global context. In these studies, DNA markers for the Yakutian Cattle were compared with the DNA data of several European and Asiatic cattle breeds (e.g. Li et al. 2007; Kantanen et al. 2009b). The results of these studies confirm the origins of Yakutian Cattle.

**MATERIALS AND METHODS**

The Food and Agricultural Organization of the United Nations (FAO) has recommended a set of autosomal microsatellites for each domestic animal species to be used as the standard to calculate genetic diversity within the population, as well as genetic relationships among breeds. For the Yakutian Cattle all thirty microsatellites recommended by the FAO have been typed. The list of markers and the applied laboratory protocols to genotype these markers have been previously described by Li et al. (2007).

Genetic variation within one breed was quantified on the basis of microsatellite data, e.g., in terms of heterozygosity and average number of alleles per marker (Li et al. 2007). In population genetics, heterozygosity can be defined as the probability that two alleles of a particular DNA marker taken at random within a population are different. The genetic differences and relationships among the breeds were estimated, for example, by computing the genetic distance $D_A$ of Nei et al. (1983) between all breed-pairs. Genetic distance expresses the genetic difference between two populations as a single number. Li et al. (2007) offers a detailed description of the applied statistical analyses.

To shed light on the maternal history of Yakutian Cattle, the mitochondrial DNA sequences in Eurasian cattle breeds were investigated by Kantanen et al. (2009b). In this study, the mitochondrial DNA data came from the sequencing of the non-coding mitochondrial DNA segment, the “control region” or “D-loop region,” which initiates replication and transcription in the mitochondrial DNA molecule (Bradley et al. 1996; Taberlet 1996). The analyzed sequence was of 255 base-pairs long between the nucleotide positions 16021 and 16275 in relation to the entire *Bos taurus* mitochondrial DNA sequence. In total, 268 animals from 34 cattle breeds were analyzed for mitochondrial DNA variation in the study, including 24 Yakutian Cattle animals.

The paternal history and genetic diversity of the Yakutian Cattle were investigated by typing five Y-chromosomal microsatellites. A total of 405 bulls representing 54 cattle breeds were assessed: 343 bulls were from Europe; 27 from Central and East Asia; and 35 from the Near East and Anatolia. The data included typings of 17 Yakutian Cattle bulls. More basic information on the markers analyzed by Kantanen et al. (2009b) can be found in Edwards et al. (2000) and Ward et al. (2001) for the Y-chromosomal microsatellites INRA124, INRA189, BM861 and BYM−1; and in Perret et al. (1990) and Bradley et al. (1994) for the marker DYZ−1, which was amplified using a forward primer 5’ CCT GGC GAC TGT GCA ATA TT 3’ and a reverse primer 5’ CAC
ACA CAC AAC CGG TTT CT 3’.

The statistical analyses for the mitochondrial and Y-chromosomal data sets have been described in Kantanen et al. (2009b).

RESULTS AND DISCUSSION

In the study conducted by Li et al. (2007), genetic variation at 30 autosomal microsatellite loci within 21 Eurasian cattle breeds was compared. The intrapopulation variation was presented in terms of heterozygosity under Hardy-Weinberg equilibrium and average number of alleles per locus. The average heterozygosity among the 21 breeds was 0.67, while in Yakutian Cattle, Ukrainian Grey and Podolian Cattle (from Serbia), the heterozygosity estimates were 0.58, 0.64 and 0.56, respectively. Correspondingly, the average number of the alleles per DNA-marker in these breeds was 5.00, 5.07 and 3.97, respectively. In all Eurasian breeds studied, this value averaged 5.99 per breed. That is, these estimates indicate that the Yakutian Cattle, Ukrainian Grey and Podolian Cattle display the lowest levels of intrapopulation diversity.

A possible explanation for the current low level of intrapopulation diversity is that only a limited number of cattle may have been brought to the Sakha region during prehistoric times. Therefore, the foundation stock of Yakutian Cattle may have been relatively small. Moreover, like Ukrainian Grey Cattle and Podolian Cattle, Yakutian Cattle experienced a long period of genetic isolation, which may partly explain the observed lower level of genetic variation.

The autosomal microsatellite data used in this study to estimate relationships showed the large genetic distances between the Yakutian Cattle and the European and other Asiatic breeds, indicating that the breed is genetically diverged from the others (see Li et al. 2007). The long-term genetic isolation from the other breeds may best explain these distances.

Based on the nucleotide differences found in sequencing, mitochondrial DNA D-loop sequences of the taurine cattle (B. taurus) can be classified into five haplogroups (i.e., “damlines”): T, T1, T2, T3 and T4 (Troy et al. 2001; Mannen et al. 2004; but see also Achilli et al. 2008). In the Eurasian continent (see Map 1), T, T1, T2 and T3 have been found in the modern Near Eastern cattle breeds, while only T, T2 and T3 appear in European breeds (Troy et al. 2001). In East Asia, the T and T1 have not been detected in the Turano-Mongolian cattle, while the T4, which is absent in the modern Near Eastern cattle, has been so far found only in the Turano-Mongolian cattle (Mannen et al. 2004; Lai et al. 2006). This is interesting because Eurasian taurine cattle are descended from the wild ox (Bos primigenius) populations domesticated ten thousand years ago in the Near East. Some researchers have speculated that the T4 should have its origin in some other wild ox population than the Near Eastern population, most probably in an east Asian wild ox population since the T4 has been detected so far only in Turano-Mongolian breeds (Mannen et al. 2004; Lai et al. 2006). However, in the recent whole mitochondrial genomic study, it was suggested that the T4 might have originated from the same genetic sources as the T3 haplogroup or from a genetically closely-related population of aurochs (Achilli et al. 2008). Yakutian Cattle also have this T4 dam line in addition to the dam lines T3 and T2, which can be found in European samples. This suggests that the Yakutian Cattle
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Map 1. The distribution of the taurine mitochondrial DNA haplogroups T, T1, T2, T3 and T4 (‘dam lineages’) is presented in the Eurasian continent according to the data of Kantanen et al. (2009b). The larger circled region refers to the Near Eastern center for domestication of the humpless taurine cattle (Bos taurus). The animal populations in these areas typically display more genetic diversity than populations far from the centers for domestication. This is seen also in the diversity of cattle mitochondrial DNA: Near Eastern populations show more haplogroups than European breeds. However, the haplogroup T4 found in Yakutian Cattle has not been detected in the Near Eastern populations, indicating partly different maternal ancestry for the Yakutian Cattle.

share prehistoric maternal ancestries with domesticated Near Eastern cattle.

The Y-chromosomal markers on the non-recombining Y-specific part of the chromosome were transmitted from sire to son as a single block, i.e., “a haplotype.” In the study by Kantanen et al. (2009b), the allelic combinations of the five studied Y-chromosomal microsatellites were recorded as haplotypes; a total of 26 haplotypes were observed among 405 bulls tested. The Y-chromosomal microsatellite haplotype data showed that the Yakutian Cattle have a same Y-haplotype as Ala-Tau (from central Asia), Anatolian Black, East Anatolian Red (both from Turkey), Jersey (from the UK) and Podolian Cattle (from Serbia). These findings suggest a common prehistoric paternal ancestry for these breeds and offers additional evidence that the Yakutian Cattle have prehistoric ancestries in same domesticated populations as European cattle.

To conclude, the Yakutian Cattle descended from the Near Eastern domesticated cattle, but the population also has an exceptional maternal ancestry (the T4 “dam line”), the origin of which is not well known as yet. The results of the DNA marker analysis indicate that the genetic value of the Yakutian Cattle may lie particularly in the novel gene combinations that the population carries (Bennewitz et al. 2006). These combinations developed through adaptation to Siberian conditions and periods of extended isolation. A Finnish multidisciplinary research group has explored
the future conservation possibilities of the Yakutian Cattle in the original breeding sites in the eastern Siberian villages (Granberg et al. 2009). Because of their adaptation to the sub-Arctic environment, which has made cattle production in northern Siberia possible, the Yakutian Cattle have economic, socio-cultural and symbiotic values for the Yakutian people (Stammler-Gossmann 2009). However, throughout the wider republic also, Yakutian Cattle are considered to be a vital gene pool for the development of agriculture in the future (Soini & Partanen 2009).

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