Genetic diversity and population structure of domestic and wild reindeer (Rangifer tarandus L. 1958): a novel approach using BovineHD BeadChip

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Veronika Ruslanovna Kharzinova[1], Arsen Vladimirovich Dotsev[1], Tatiana Evgenievna Deniskova[1], Anastasiya Dmitrievna Solovieva[1], Valeriy Ivanovich Fedorov[2], Kasim Anverovich Layshev[3], Tatiana Michailovna Romanenko[4], Innokentiy Michailovich Okhlopkov[5], Klaus Wimmers[6], Henry Reyer[6], Gottfried Brem[7], Natalia Anatolievna Zinovieva[1]

[1]L.K. Ernst Federal Science Center for Animal Husbandry, Federal Agency of Scientific Organizations, pos. Dubrovitsy, Podolsk Region, Moscow Province, Russia, [2]Federal Government Budget Scientific Institutions Yakut Scientific Research Institute of the Agriculture Federal Agency Scientific Institutions, Yakutsk, Russia, [3]North-West Center of Interdisciplinary Researches of Food Maintenance Problems, Federal Agency of Scientific Organizations, St. Petersburg, Russia, [4]Federal Center for Integrated Arctic Research [FCIARctic] Nenets Division — Agro-Experimental Station, Federal Agency of Scientific Organizations, Naryan-Mar, Nenets AO, Russia, [5]Institute for Biological Problems of Cryolithozone Siberian Branch of RAS, Yakutsk, Russia, [6]Institute of Genome Biology, Leibniz Institute for Farm Animal Biology [FBN], Dummerstorf, Germany, [7]Institute of Animal Breeding and Genetics, University of Veterinary Medicine [VMU], Vienna, Austria

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Veronika Kharzinova

ABSTRACT

Reindeer (*Rangifer tarandus* L. 1758) are an essential element of the Russian Far North, providing a significant source of nutrition for the representatives of 18 ethnicities. The species has wild and domestic forms, which are in constant interaction. The aim of our study was to characterize the genetic structure of domestic and wild reindeer populations, using a genome-wide bovine genotyping array (BovineHD BeadChip). The wild reindeer samples were obtained from the western Taymyr Peninsula population and from the taiga and tundra populations in the Sakha Republic (Yakutia). The domestic populations included the Evenk, Even, and Chukotka-Khargin breeds of Yakutia and the Nenets breed from the Nenets Autonomous district and Murmansk region. The level of genetic diversity was higher for the wild population. Analyzing Neighbor-Net tree, multidimensional scaling, and STRUCTURE results, we observed strong genetic population structure and clear differentiation between domestic and wild populations. All regional populations of domestic reindeer were clearly separated, while wild reindeer showed similar genetic backgrounds. Nevertheless, we found contrasting patterns in the genetic structure of the tundra and taiga reindeer, in accordance with their morphological and ecological differences. Thus, our study revealed a clear genetic differentiation between domestic and wild reindeer populations. It provides novel insights into the genetic diversity and structure of reindeer populations, to support resource utilization and aid in the development of genetic improvement strategies and conservation programs for this species.

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reindeer.ped.txt

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PROTOCOL STATUS

Working

MATERIALS TEXT

A total of 135 individuals, including wild (n=61) and domestic (n=74) reindeer, were analyzed
The wild reindeer samples were represented by 27 individuals from the Taymyr population from western Taymyr (TMR) and 34 from the Yakut population from the taiga and tundra of Yakutia. In addition, the wild reindeer from Yakutia included two populations of tundra reindeer from northern Yakutia (Lena-Olenek (LNO, n=24) and Sundrun (SUN, n=6)) and one population of taiga reindeer from southern Yakutia (TGA, n=4). All samples were collected during scientific expeditions between 2014–2017
The domestic reindeer tissue samples of were taken from the Even (EVN, n=7), Evenk (EVK, n=12), and Chukotka-Khargin (CHU, n=2) breeds from three farms in Yakutia (“Yuchyygeyskoe”, Oymyakonsky district; “Reindeer Company named after I. Spiridonov”, Anabarsky district; and “Turvaurgin”, Nizhnekolymskiy district, respectively); and the Nenets breed samples were taken from the Nenets Autonomous district (NEN_N, n=33, “Indiga”, Malozemelskaya tundra) and the Murmansk region (NEN_M, n=20, “Tundra”, northern and northeastern Kola Peninsula). The biomaterial was collected during corral work on the herd throughout 2016–2017.

SAFETY WARNINGS

BEFORE STARTING

This study does not involve any endangered or protected species. All wild reindeer muscle tissue samples were collected during scientific expeditions after obtaining collection permits granted by the Department of Hunting of the Republic of Sakha and Taymyrsky Dolgano-Nenetsky District, in compliance with the Russian Federation Law No. 209-FZ of July 24, 2009. The domestic reindeer tissue samples were collected by trained personnel under strict veterinary rules. Sampling was performed in accordance with the ethical guidelines of the L.K. Ernst Federal Science Center for Animal Husbandry. The protocol was approved by the Commission on the Ethics of Animal Experiments of the L.K. Ernst Federal Science Center for Animal Husbandry (Protocol Number: 2018/1). The biomaterials from the genetic resource collection of the L.K. Ernst Federal Science Center for Animal Husbandry, supported by the Federal Agency for Scientific Organizations, were used in the study

Sample collection and preparation of genomic DNA

1 Genomic DNA was extracted from muscle and tissue samples using Nexttec columns (Nexttec Biotechnology GmbH, Germany) following the manufacturer's instructions.
The quality of the extracted DNA was examined by electrophoresis using 1 % agarose gels viewed under ultraviolet light. The concentration of DNA solutions was quantified using a Qubit 3.0 fluorimeter (Thermo Fisher Scientific (formerly Life Technologies), Wilmington, DE, USA).
The OD260/OD280 ratio of DNA solutions was determined by NanoDrop-2000 (Thermo Fisher Scientific, Wilmington, DE, USA).

SNP genotyping and quality control

2 All reindeer individuals were genotyped with Illumina BovineHD Genotyping BeadChip, which contains 777,962 SNPs. Genotypes were called and processed using Genome Studio (Illumina, Inc. San Diego. USA).
Samples with a call rate below 90 % were excluded from the data set.
Additional criteria to filter SNPs were applied:
SNPs with more than 10 % missing genotypes across all the samples;
SNPs with minor allele frequency less than 5 % (--maf 0.05);
SNPs located on sex chromosomes of the UMD 3.1 assembly;
SNPs with unknown map positions;
SNPs with the value of linkage disequilibrium (LD) between a pair of single nucleotide polymorphisms equal to r2>0.05 (we used a sliding window of 50 SNPs, sliding along in 5 SNP increments);
SNPs not corresponding to the $\chi 2$ criterion for Hardy-Weinberg equilibrium in a population ($p \leq 1 \times 10\text{-}6$).
Additionally, to assess the quality of SNP genotyping, we used GC Score (quality of reading SNP) and GT Score (level of clustering SNP) of at least 0.5 (50 %).
These quality control steps were carried out using PLINK v1.07 [37]. The final data set comprised 8357 SNPs for 135 reindeer individuals and 8145 SNPs for 61 wild reindeer from the BovineHD BeadChip (Illumina, Inc. San Diego. USA).

Genetic diversity and differentiation analysis

3 To assess genetic diversity of the studied reindeer populations, the values of observed (Ho) and unbiased expected (He) heterozygosity, inbreeding coefficient (FIS), and rarified allelic richness (Ar) were calculated in R package diveRsity.
Pairwise fixation index (FST) values were estimated through the R-package StAMMP
The neighbor-joining algorithm was applied to generate the Neighbor-Net Tree from a distance matrix of pairwise FST values and implemented in Splitstree 4.14.5.
Multidimensional scaling (MDS), based on pairwise identity-by-state distance matrix, was carried out with PLINK 1.07 (--cluster, --mds-plot 4) and visualized in R package ggplot2.

Genetic structure analysis

4 The genetic structure analysis was performed with the software package STRUCTURE 2.3.4

TreeMix

5 For inferring the patterns of population splits and gene flow between reindeer populations, we used the software TreeMix1.13
Standard errors (-se) and p-values were calculated with jackknife blocks of 10 SNPs (-k 10). Since significant effects were revealed when two migration events were allowed ($p<0.05$), we ran 100 independent replicates for each event.
The tree graph and residuals were visualized using R