Reemergence of arctic-like rabies virus in a rabies-free area in the Amur river basin

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Abstract

Background: A descriptive epidemiological study of the rabies outbreak in the Amur Region of Russia (ARR), which remained rabies-free from 1972 to 2017, was carried out. During 2018-2022, 49 animal rabies cases and one human rabies death were documented in the ARR. This study aimed to detect possible ways of incursion and features of the spatial spread of rabies virus (RABV) in ARR, which was considered rabies-free for 45 years.

Methods: After the beginning of the outbreak, 1,450 animal brain samples were tested using a direct fluorescent antibody test. Genetic analysis of RABV isolates was carried out (n = 9). GIS was used to analyze the spatial spread of rabies in ARR and adjacent territories.

Results: Rabies has been confirmed in red foxes (Vulpes vulpes) - 38.8%, raccoon dogs (Nyctereutes procyonoides) - 10.2%, wolves (Canis lupus) - 14.3%, dogs - 18.4% and farm animals - 18.3% (n = 49). The first cases were
detected south of the ARR, 30 km from the state border between Russia and China. In 2018-2022, the RABV spread within the forest-steppe landscapes of the Zeya-Bureya Plain northwesterly; the maximum distance from the first recorded event was 192.4 km (Me = 77.6). According to a phylogenetic analysis, the isolates from ARR belonged to the Arctic-like-2 RABV lineage and showed the maximum similarity to the isolates recovered in the province of Heilongjiang (China, 2011, 2018) and the Jewish Autonomous Region (Russia, 1980).

Conclusion: Rabies was most likely introduced by wild carnivores from the adjacent territories of Russia or China, located downstream of the Amur River.

Keywords: Rabies, Arctic-like, re-emerging infection, transboundary outbreak

INTRODUCTION

Rabies is a zoonotic viral infection with an almost 100% case fatality rate, caused by rabies virus (RABV) (order Mononegavirales, family Rhabdoviridae, genus Lyssavirus, species Lyssavirus rabies) and other lyssaviruses. Preventive measures can significantly reduce the incidence. According to the Global Burden of Disease Study, the number of human rabies cases globally halved between 1990-2019[1]. Many countries have joined the implementation of the Global Strategic Plan to end human deaths from dog-mediated rabies by 2030[2,3]. Significant progress has been made in China: from 2007 to 2020, the annual number of human rabies cases has dropped from 3,300 to 202[4-6]. Most of these cases were concentrated in the south of the country. Rabies in humans was recorded sporadically in the northern provinces, where wild canids serve as reservoirs of the RABV[4,7,8]. However, an uptick in human rabies cases has recently been reported in northern China[5,9]. This territory and neighboring territories of Russia and Mongolia lie in the Amur River basin [Figure 1, Supplementary Table 1 and Figure 1].

Human and animal rabies has been historically common in Russia, part of the Amur River basin. Here, rabies penetrates to the north through steppe and forest-steppe areas favorable for such rabies hosts as red foxes (Vulpes vulpes) and raccoon dogs (Nyctereutes procyonoides). This phenomenon contrasts strikingly with the vast territories of Siberia covered by conifer taiga forests, where host populations are scarce, and rabies has been recorded extremely rarely[10,11]. In the 1980s, wildlife rabies foci were described in the Russian Far East in lowland areas along the Amur River and around Khanka Lake, where raccoon dog was recognized as a reservoir of RABV[12,13]. Despite wildlife rabies, the infection mediated by domestic dogs predominated as the cause of human disease (> 80% of human rabies cases). Only rare human deaths after wolf and raccoon dog bites were reported in the Russian Far East during the previous century[12]. RABV variants of the so-called Arctic-like lineage prevail in the adjacent territories of Russia[14,15] and China[16-19]. The similarity of landscapes, genetic lineages, and natural hosts of RABV led to the conclusion about the transboundary nature of rabies outbreaks in the Amur River basin[12,16,19].

Since the 1980s, the number of human and animal rabies cases and area of rabies-enzootic territories in the Russian Far East have gradually decreased. The area between Lake Baikal and the Jewish Autonomous Region (JAR) became rabies-free. At that time, dog and cat vaccination was enhanced, but the real reasons for rabies disappearance in the rabies-enzootic territories remain unclear. However, in 2014, rabies reemerged in all regions of Russia located to the East of Baikal Lake[16,20,21]. The situation in the Amur Region of Russia (ARR) is the most striking illustration of these processes. In 1912, the specialized medical facility (Pasteur Station) was opened in Blagoveshchensk for human post-exposure rabies prophylaxis. Until 1957, 34 human deaths were recorded, mainly after dog bites. In 1972, the last several rabies cases in cattle bitten by wolves were documented[12]. Since then, the ARR has been considered rabies-free until 2017. In 2018, only rabies was registered again among wild animals, livestock, and dogs[16,19].
This study aimed to detect possible ways of incursion and features of the spatial spread of rabies in ARR, which was considered rabies-free for 45 years.

METHODS

Epidemiological analysis
Animal rabies records for 2018-2022 collected by the state epidemiological surveillance for zoonotic infections in the ARR were used for retrospective analysis. Only animals with laboratory-confirmed rabies were included in the study ($n = 49$).

Laboratory diagnosis and confirmation
After the first rabies case was reported, an active surveillance program to detect new cases was established. During 2018-2022, the ARR Regional Veterinary Laboratory examined 1,450 brain samples of wild and rabies-suspected domestic animals. Designated teams of hunters shot and trapped wild canids and other game animals in different areas of ARR. Most collected wild animals did not show clinical signs of rabies or other diseases. The direct fluorescent antibody test$^{[22]}$ with FITC-conjugated anti-rabies IgG was used as the primary method of routine diagnosis. Samples positive for RABV antigens were randomly sent for confirmation to the Federal Reference Diagnostic Centers in Vladimir and Omsk cities, where RT-PCR was additionally used$^{[22]}$.

Phylogenetic study
The list of RABV isolates analyzed phylogenetically is presented in Table 1 and Supplementary Table 2. Isolation of RNA from a 10% animal brain suspension, reverse transcription, amplification of cDNA fragments, and nucleotide sequencing were performed as described previously$^{[20]}$. Phylogenetic analysis of partial RABV nucleoprotein (N) gene sequences (1,110 nt, positions 170-1,279 relative to Pasteur Virus genome, GenBank no M 13215) was performed using the maximum likelihood algorithm implemented in
Table 1. Rabies virus isolates used for genetic analysis

<table>
<thead>
<tr>
<th>No.</th>
<th>Isolate number</th>
<th>GenBank number</th>
<th>Species</th>
<th>Location (coordinates, decimal degrees)</th>
<th>Year</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2981/2018/Amur</td>
<td>MN384722</td>
<td>Cow</td>
<td>49.68 N, 128.78 E</td>
<td>2018</td>
</tr>
<tr>
<td>2</td>
<td>Amur8853 rd</td>
<td>ON246188</td>
<td>Raccoon dog</td>
<td>49.83 N, 128.37 E</td>
<td>2018</td>
</tr>
<tr>
<td>3</td>
<td>Amur8855 f</td>
<td>ON246189</td>
<td>Red fox</td>
<td>49.97 N, 129.17 E</td>
<td>2018</td>
</tr>
<tr>
<td>4</td>
<td>Amur8854 rd</td>
<td>ON526986</td>
<td>Raccoon dog</td>
<td>49.62 N, 128.65 E</td>
<td>2018</td>
</tr>
<tr>
<td>5</td>
<td>Amur8856 f</td>
<td>ON526987</td>
<td>Red fox</td>
<td>50.16 N, 128.80 E</td>
<td>2018</td>
</tr>
<tr>
<td>6</td>
<td>Amur8857 f</td>
<td>ON526988</td>
<td>Red fox</td>
<td>49.91 N, 128.37 E</td>
<td>2018</td>
</tr>
<tr>
<td>7</td>
<td>Amur8858 hor</td>
<td>ON526989</td>
<td>Horse</td>
<td>49.62 N, 128.65 E</td>
<td>2018</td>
</tr>
<tr>
<td>8</td>
<td>Amur8944 w</td>
<td>ON526990</td>
<td>Wolf</td>
<td>49.46 N, 129.00 E</td>
<td>2019</td>
</tr>
<tr>
<td>9</td>
<td>Amur8946 w</td>
<td>ON526991</td>
<td>Wolf</td>
<td>49.60 N, 128.77 E</td>
<td>2019</td>
</tr>
</tbody>
</table>

the MEGA X program\cite{23}. For comparison, 38 N gene sequences of RABV isolates from various genetic lineages documented in Asia were retrieved from GenBank. Since the isolates of interest belong to the so-called Arctic-like-2 lineage, all the isolates of this group available in GenBank were included in the study, except for highly similar or identical ones. Bootstrap values were determined for 1,000 replicates by the maximum likelihood method.

**Cartography**

For cartographic analysis, in addition to the ARR data, we used information on laboratory-confirmed rabies cases in neighboring regions of Russia: the Trans-Baikal Region (\(n = 49\), 2014-2020)\cite{21}, the JAR (\(n = 8\), 2017-2019), the Khabarovsk Region (\(n = 25\), 2018-2019), and the Primorsky Region (\(n = 2\), 2013-2019) [Supplementary Table 3]. Mapping was performed using the QGIS 3.26.3 program based on the Natural Earth electronic landscape-geographic map (https://www.naturalearthdata.com) and OpenStreetMap database (https://www.openstreetmap.org/). Points on the map were plotted according to the geographical coordinates of where animal rabies cases were detected. The points of detection of genetic variants of the RV in the adjacent territories of China were transferred from the maps in previously published articles\cite{16-19,24,25}. The speed of the epizootic spread was estimated by the distance from the point of the first case in 2018 to all other points in annual cycles, starting from July of the current year to June of the following year (resettlement time of a new generation of wild carnivores across the territory). The median (Me), minimum, and maximum distances are presented.

**RESULTS**

The first laboratory-confirmed case of rabies in the ARR was documented in a cow on November 10, 2018, 30 km from the state border between Russia and China. The infection was presumably sourced from a fox that ran into the village and attacked dogs and farm animals. As a result of active surveillance, by the end of 2018, 16 rabies cases were detected in red foxes (\(V.\)vulpes), raccoon dogs (\(N.\)procyonoides), domestic dogs (\(C.\)lupus familiaris), and farm animals [Table 2]. In March 2019, 3 rabies cases were documented in wolves (\(C.\)lupus) that attacked humans. One of these wolves was observed by border guards within the guarded border strip in the floodplain of the Amur River. The outbreak was spreading northwesterly. During 2021, most rabies cases were detected in areas distanced by more than 200 km from the first case. Only two cases were registered in the first quarter of 2022 [Figure 1]. In total, during 2018-2022, animal rabies was detected in 13 administrative units of the ARR. In 2020, a woman died with typical symptoms of hydrophobia three months after being bitten by a domestic dog in a rabies-affected area [Figure 1]. The dog died the next day after a bite. Neither human nor dog samples were sent to a laboratory for rabies rule-out. The patient did not receive post-exposure prophylaxis.
Table 2. Laboratory-confirmed rabies cases in the ARR during 2018-2022

<table>
<thead>
<tr>
<th>Species</th>
<th>2018</th>
<th>2019</th>
<th>2020</th>
<th>2021</th>
<th>2022</th>
<th>Total</th>
<th>Proportion, % (95%CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Red fox</td>
<td>10</td>
<td>5</td>
<td>2</td>
<td>2</td>
<td>0</td>
<td>19</td>
<td>38.8 (25.2-52.4)</td>
</tr>
<tr>
<td>Wolf</td>
<td>0</td>
<td>3</td>
<td>2</td>
<td>2</td>
<td>0</td>
<td>7</td>
<td>14.3 (4.5-24.1)</td>
</tr>
<tr>
<td>Raccoon dog</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>5</td>
<td>10.2 (1.7-18.7)</td>
</tr>
<tr>
<td>Dog</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>6</td>
<td>1</td>
<td>9</td>
<td>18.4 (7.6-29.2)</td>
</tr>
<tr>
<td>Cattle</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>4</td>
<td>1</td>
<td>8</td>
<td>16.3 (6.0-26.6)</td>
</tr>
<tr>
<td>Horse</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>2.0 (0.0-6.0)</td>
</tr>
<tr>
<td>Total</td>
<td>16</td>
<td>11</td>
<td>5</td>
<td>15</td>
<td>2</td>
<td>49</td>
<td>100</td>
</tr>
</tbody>
</table>

ARR: Amur Region of Russia.

The main reservoir of the RABV during this recent outbreak was represented by wild carnivores, which accounted for 53.3% of all reported cases. Most often, especially at the beginning of the outbreak, the infection was detected in foxes [Table 2]. Dog rabies was reported mainly at the end of the analyzed period and mostly among stray dogs.

During 2018-2022, rabies spread within the forest-steppe and agricultural landscapes of the Zeya-Bureya Plain. The successive spread of rabies, mainly in the north and northwest direction from the place of first detection, can be traced on the map [Figure 1]. During the first epizootic cycle (2018-2019), the median of the distance from the primary case to other cases was 23.8 (7-107.2) km; in 2019-2020, it was 112.4 (77.6-128.9) km; in 2020-2021, it was 150.1 (57.1-192.4) km; in 2021-2022, it was 130.7 (57.1-121.4) km. The maximum distance from the first recorded event was 192.4 km for the observation period (Me = 77.6). As the epizootic wave progressed, cases in the initially affected areas decreased.

A full-size N gene nucleotide sequence (1,353 nt) of the RABV isolate from the first case in cows was determined, as well as 1,110 nt N gene fragments of six isolates from red foxes, raccoon dogs, and a horse and 556 nt N gene fragment of the two wolf isolates. The results of the phylogenetic analysis are shown in Figure 2 and Supplementary Table 2. The isolates from wolves (Amur8944w and Amur8946w) were not included in the tree because of the short lengths of their sequenced N gene fragment to prevent a decrease in tree resolution. The compared genome regions of the isolates collected during the first two months after outbreak detection were identical or differed by no more than one nucleotide. Thus, at the beginning of the outbreak, the ARR sequences shared 99.9%-100% identity. The genetic homogeneity of the isolates suggests a single initial source of the infection. It has been determined that isolates from the ARR belonged to the Arctic-like-2 genetic group of RABV and had a high degree of similarity (95.0%-99.4%) with isolates from neighboring regions of Russia and Northern China. They showed the maximum similarity to the TJ11-RD isolate from a goat (Tongjiang city, Heilongjiang province, China, 2011) - 99.4%, the HLJ01 isolate from a raccoon dog from the same province (the exact location is not known, 2018) - 98.6 %, as well as to isolate 857r from a raccoon dog (Leninskoe settlement, JAR, Russia, 1980) - 98.9%. It should be emphasized that the Leninskoye settlement in Russia and the Tongjiang city in China are located approximately 30 km from each other on opposite banks of the Amur River. Thus, this lineage of the RABV circulated in the Middle Amur Plain on both banks of the Amur River since 1980. The isolates also demonstrated 97.6%-98.3% nucleotide identity to Arctic-like-2 RABV sequences recovered in other regions of Russia, Northern China (Hebei, Jilin, Liaoning, and Inner Mongolia), and South Korea from 1977 to 2020. Even the identity of Japanese isolate Komatsugava recovered during the 1940s was as much as 97.2%. The genetic similarity of isolates from the ARR with RABV of the Arctic-like-1, Arctic, Steppe, and South-East Asia 1 (China-1) lineages does not exceed 92%.
Figure 2. The phylogenetic tree constructed by analyzing the nucleotide sequences of the 1,110 nt N gene fragment (position in the N gene: 100-1,209) of rabies virus isolates. Legend: The Gannoruwa bat Lyssavirus sequence was used as an outgroup. Square brackets indicate the genetic lineages of the rabies virus. Diamonds mark isolates from this study. The captions for the rest of the isolates indicate GenBank access number, name of the isolate, country, region of detection (if known), year of detection, and host animal species. Abbreviations for animal species: rd: raccoon dog; rf: red fox; sf: steppe fox (corsac); af: arctic fox; dog: dog; cow: cattle; w: wolf; gt: goat; hu: a person; nd: no data. Bootstrap values are presented for critical nodes.

The spatial distribution of rabies in neighboring territories is presented in Figure 3 and Supplementary Table 3.

DISCUSSION

In Russia, the nearest to the ARR rabies-enzootic territory is in the JAR, 200-300 km to the east, where the infection was historically present in lowland areas, including the Amur River valley.[10,12,13,26] During 2017-2018, animal rabies was documented in JAR[10], just before the outbreak in ARR. Later, in 2018-2020, the fox rabies spread down the Amur River valley to Khabarovsk and Komsomolsk-na-Amure cities [Figure 3]. It appears that viruses of the same lineage were present in adjacent regions of China at least since 2011 (GenBank sequence KM016898; Figure 2). According to a report from China in 2013, “…several hundred foxes and raccoon dogs have been found dead in Bayannur, the Inner Mongolia Autonomous Region (IMAR), and Tongjiangcity, Heilongjiang, and herdsmen have reported dogs, cattle, goats, horses, and camels falling ill with rabies”[16]. In 2006, 2012, 2013, and 2019, human rabies cases were reported in Heilongjiang province[4,5].

In the west, the nearest to the ARR rabies-enzootic area is in the Trans-Baikal Region (TBR) of Russia in the basin of the upper reaches of the Amur River and its tributaries. In the 1970s, animal and human rabies was prevalent in TBR. Several RABV isolates were collected and later identified as Arctic-like[14]. From 1983 to 2013, this region was considered rabies-free. Epizootic among foxes reemerged in 2014 because of an introduction of the Steppe genetic RABV lineage[10,21,27]. Thus, recent outbreaks in the Trans-Baikal Region of Russia and the ARR are disconnected and unrelated.

Since 2007, raccoon dog and fox rabies have been reported in the IMAR of China[16,17]. It has been established that RABV of the Steppe and Arctic-like-2 lineages are circulating here simultaneously; however,
the Steppe lineage prevails. Currently, foxes play a pivotal role in the spread of rabies in the IMAR and some other provinces in northern China[^5,18,25].

Because of the data collected, two scenarios of RABV incursion into the ARR were suggested. It is most likely that rabies was introduced by wild carnivores from a natural focus located in the middle reaches of the Amur River. Mountain ranges sandwich the narrow valley of the Amur River in a section about 150 km long between the Zeya-Bureya and the Middle Amur Plains. The border between Russia and China lies along the Amur River. Due to the border protection, the floodplain territory, island, and coastal biotopes are little used for economic needs in both countries. The absence of anthropogenic press creates ample opportunities for wildlife, including migrations of carnivores along frozen rivers in winter, and may contribute to the transboundary spread of RABV. Another possible incursion route might occur from the Central Manchurian Plain along the valleys of the right-bank tributaries that flow into the Amur River near the site of the first reported ARR rabies case in 2018 [Figure 3]. However, in available publications, we could not find reports with georeferencing of rabies cases in the bordering area of China.

A retrospective analysis of the outbreak of rabies in the ARR demonstrates the importance of ecological channels and natural barriers for the spread of wildlife rabies. Presumably, the relative geographical isolation of the Zeya-Bureya Plain contributed to the conservation of the rabies-free status of the ARR for a long time. The Zeya-Bureya Plain is separated from similar landscapes in Russia and China by mountain ranges covered with taiga and coniferous-broad-leaved forests (dark green shading on the maps, Figures 1 and 3). The concentration of rabies cases along river valleys and at the junctions of forest and open landscapes is remarkable on this map. The habitats of mesocarnivores in the river floodplains and foothills are preserved even in conditions of intensive use of the plains for crops. It should be emphasized that rabies

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[^5]: Figure 3. Spatial distribution of documented animal rabies cases in the Amur River basin. (1) lineage was not determined; (2) Arctic-like isolates; (3) Steppe isolates. Russian Far East: ARR - 2018-2022; TBR - 2014-2020[^21]; JAR - 2017-2019; KHR - 2018-2019; PRR: adjacent territories of China (2007-2018)[^16-19]; (4) detection of Arctic-like isolates in Russia in 1977-1989[^14], the locations were corrected according to original information about the samples collection. Black lines: state and regional borders; Arrows: probable directions of rabies virus incursion into ARR. ARR: Amur Region; JAR: Jewish Autonomous Region; KHR: Khabarovsk Region; PRR: Primorsky Region; TBR: Trans-Baikal Region.
had a similar landscape distribution in this area in the middle of the last century[12,13].

Raccoon dogs were highly susceptible to experimental inoculation with the RABV strain isolated in the Russian Far East in 1980 (presumably Arctic-like-2), and all became ill even after a dose of 5 MICLD₅₀. At the same time, some foxes did not become ill after a dose of 100 times more[28]. In 2007, raccoon dogs became ill during an outbreak of rabies caused by the Arctic-like-2 rabies virus on a fur farm, but raccoons was not observed among foxes[18]. In the last century, several human rabies cases were associated with raccoon dog bites in adjacent territories of Russia and China[4,12,26]. Singular human rabies cases after fox bites began to be registered in the Russian Far East only in 2002[26] and in China since 2016[29]. During recent years, fox rabies has been detected repeatedly in the Amur River basin[9,10,25]. Comparison with data from 1949-1978 shows significant changes in ARR’s affected species composition. In the past, dogs (48.6%) and farm animals (46.5%) dominated among the registered rabies cases, whereas cats and wild animals (wolf, raccoon dog) accounted for 2.8% and 2.1%, respectively. Foxes were not found in the list of rabid animals in ARR during that period[13].

Thus, the present rabies outbreak in the ARR confirms the increasing role of red foxes as a host of RABV in Eastern Asia. The changes in the abundance of red foxes, raccoon dogs, and wolves in the Amur River basin under the influence of human activity are suggested among the factors that contributed to the activity of rabies epizootics, host shifts, and switches, introduction and re-introduction of the infection into rabies-free territories. Intensive farming, irrigation, sown area expansion, and decreased hunting pressure led to an increasing red fox population[10,11,21]. Simultaneously, the population of raccoon dogs in ARR decreased[13]. Perhaps we are currently witnessing an establishment of the Arctic-like-2 RABV to red foxes. As suggested by Yu et al., in the past, this genetic lineage of RV evolved in Asia predominantly in dogs, domestic animals, and raccoon dogs[19].

Since the outbreak, the rabies vaccination of dogs, cats, and farm animals in the ARR has increased by five times. Since 2019, oral vaccination of wild carnivores with the Rabistav live rabies vaccine made with the PB-97 strain (Stavropol, Russia) has been performed. It would be premature to expect a quick and lasting effect from these interventions. In 2021, rabies was diagnosed in foxes in Poland, where rabies had not been detected in over 17 years. This finding occurred despite Europe’s intensive oral rabies vaccination program since 1993. New animal rabies cases were located 100 km inside the vaccination belt[31].

The median distance from the first case to new cases during the observation period in the ARR was 77.6 km. At the beginning of the fox rabies epidemic in Europe in the middle of the last century, the average speed of epizootic spread was 30-60 km per year[32,35]. However, the rate of epizootic spread in the Russian Far East can be much higher since the wolf population remains high in contrast with Europe. Using GPS tracking, the maximum movement of a healthy wolf per day in the Trans-Baikal Territory was 97 km[34]. Thus, wolves can contribute to the long-distance introduction of the RABV along the Amur River valley. The regional features of the spatial RABV spread described in the article may help improve rabies prophylaxis and control in the Amur River basin.

CONCLUSION

An outbreak of rabies in the ARR, registered in 2018 for the first time since 1972, arose because of an introduction of RABV that belongs to the Arctic-like-2 lineage, documented broadly in eastern Asia. Rabies was most likely introduced by wild carnivores from the adjacent territories of Russia or China, located downstream of the Amur River. During the freezing period, the Amur floodplain can serve as an ecological channel for the RABV spread. In 2018-2022, the epizootic expanded for about 200 km northwest within the
forest-steppe landscapes of the Zeya-Bureya Plain. An essential feature of the modern epizootic is the increased role of the red fox in RABV maintenance. International cooperation is essential for effective prophylaxis of the transboundary spread of rabies and its elimination in this region.

DECLARATIONS
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Authors’ contributions
Conceptualization and first draft of the manuscript: Botvinkin AD
Diagnosis, genetic study, and mapping: Poleschchuk EM, Chupin SA, Zarva ID, Zinyakov NG
Veterinary reports and other data collection: Meltsov IV, Sidorov GN, Yanovich VA
Writing - review and editing: Botvinkin AD, Metlin AE, Andaev E
All authors read and approved the final manuscript.
All authors contributed to the study.

Availability of data and materials
The gene sequences are available in the GenBank database.

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Conflicts of interests
All authors declared that there are no conflicts of interest.

Ethical approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

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