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Malignant catarrhal fever in cattle in the Irkutsk Region

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Abstract

Introduction: Malignant catarrhal fever (MCF) is a rare, under-explored lethal viral infection of cattle with gammaherpesvirus aetiological agents. Most often, the disease occurs on farms where cattle and sheep are kept together. However, other trigger mechanisms and environmental factors contribute. This study investigates the causation of MCF. **Material and Methods:** An outbreak of MCF occurred in June - August 2017 in Kharchev village in Irkutsk Oblast, Russia. In this paper, we provide epidemiological (sanitary status of pastures, watering places, and premises) and weather data during the outbreak, and descriptions of the clinical signs and post-mortem changes in cattle. The virus was detected and isolated from pathological material samples and identified by molecular methods. **Results:** Extreme weather conditions, mixed-herd cattle and sheep farming, and unsatisfactory feed quality contributed to the outbreak. A virus related to herpesvirus OvHV2 was isolated and typed (MCF/Irkutsk/2017). Phylogenetic analysis showed its close genetic relationship to isolates from cattle and sheep in Germany, USA, and the Netherlands. **Conclusion:** Sporadic outbreaks of MCF caused by biotic and abiotic factors together are typical for the Russian Federation, and the Irkutsk outbreak epitomised this. Temperature anomalies caused pasture depletion, resulting in feed and water deficiency for grazing animals and dehydration and acidosis. Heat stress in animals ultimately led to the occurrence of MCF in the herd.

Keywords: cattle, malignant catarrhal fever, outbreak, clinical signs, climate change, Russia.

Introduction

Malignant catarrhal fever (MCF) is an acute, sporadic viral disease of artiodactyl ruminants. Susceptible animals are cattle, deer, antelopes, giraffes, aurochs, bison, *etc*. (3, 4, 11, 25, 28), while the disease mostly affects cattle and bison. In recent years, MCF cases have nevertheless been reported in deer and elk, both in zoos and wildlife. It has also been found in giraffes, and in several countries, in domestic pigs as well. For instance, it occurs regularly on pig holdings in Norway (5, 12, 24).

MCF can occur in acute and chronic forms. The morbidity rate usually varies from 15% to 100% in cattle and from 0% to 76% in deer, and the herd mortality rate varies from 60% to 100% (16, 23, 27). Infected animals usually die within 5 to 10 days (ranging from 1 to 26 days) after the first clinical signs, which are more prominent and distinct in a long-term course of the disease. MCF is clinically characterised by fever (>41°C), loss of appetite, depression, nasal and ocular discharge, necrotic and diphtheria lesions of the oral cavity mucosa, diarrhoea, swollen lymph nodes, and corneal opacity leading to blindness (7, 20, 25). Diseased animals may also have neurological disorders, such as ataxia and nystagmus. At the cellular level, the disease manifests by lymphocyte proliferation and systemic organ and tissue damage, with the chief location being the mucous membranes of the oral cavity, respiratory system, and gastrointestinal tract.

The causative agent of the disease is a DNA virus belonging to the *Herpesviridae* family, *Gammaherpesvirinae* subfamily, *Macavirus* genus (6). Eleven variants of the virus are currently known. The most-studied variants are alcelaphine herpesvirus 1 (AlHV-1) and ovine herpesvirus 2 (OvHV-2). Each

variant of the virus is adapted to its usual host and does not cause clinical disease in it but can cause symptoms or fatalities in other susceptible species kept or pastured together with the usual host (7-9, 17, 37).

MCF is reported in many countries of Africa, Europe, Asia, and America. According to statistics, the disease was reported in Russia in 1960, 1970, 1971, 1973, 1975, 1977, 1985, 1993, 2011, 2012, 2014, 2016, and for the last time in 2017. There are no available data on circulating variants of the virus nor on its epidemiology in Russia.

It is known that MCF occurs in herds where cattle and sheep are kept together. The role of sheep as a reservoir of the virus in propagating infection in mixed herding has experimental and statistically significant confirmation (11, 26, 36). However, the circumstances when the disease occurs in cattle that are kept separately from sheep are more interesting. This points to the existence of some other trigger mechanisms and environmental factors (carriers) contributing to the disease's spread and morbidity rate (2, 19).

Environmental factors conducive to MCF infection in cattle herds are extreme weather conditions, cold, humidity, poor ventilation, and unsatisfactory feeding. Gestation can also be a stress factor facilitating the disease development (21, 29). In each case, there may be a complex of factors in a range of combinations. The causative agents of MCF *per se* have been well studied, but the role of abiotic and biotic factors associated with the introduction, mechanisms of transmission of the pathogen, and specificity of clinical signs and post-mortem changes need further study.

Weather and climatic factors influence the occurrence and course of many animal diseases. An analysis of their influence is crucial and relevant, especially in the extreme continental climate of Siberia.

Considering the impact of the disease and plurality of contributory factors, we aimed to study the features of the MCF which occurred recently in Siberia in the Russian Federation. For this purpose, we set up the following tasks:

– to analyse retrospectively the MCF situation in the Russian Federation and in the newly affected region;
– to collect and analyse epidemiological and climate data during the outbreak in Kharchev village in the Siberian Irkutsk Region;
– to describe clinical signs (including biochemical parameters) and pathological changes in the infected and dead cattle, respectively;
– to detect, isolate, identify and describe the causative agent.

Material and Methods

The study was carried out in Kharchev village of Irkutsk Oblast (54° 13' 35.9904" N and 101° 52' 41.4444" E) and at the laboratory of the Federal Research Center for Virology and Microbiology (Pokrov). To collect and evaluate data, we used the following techniques and methods: retrospective data analysis of MCF outbreaks in the Russian Federation, a semi-structured survey of animal owners, descriptive epidemiology, molecular biology, clinical diagnostics, and pathological examination.

The retrospective analysis was based on available official data on MCF outbreaks in cattle in the Russian Federation, Irkutsk region and Kharchev village for 60 years. We collected data on morbidity and mortality in the affected village.

The survey for animal owners included information on the sizes and types of herds in the affected village, characteristics of feeding, and cattle holdings. We assessed husbandry and climatic conditions during the outbreak based on the results of examination of pastures, watering places, and premises.

Meteorological data were extracted from the official website of the Federal Service for Hydrometeorology and Environmental Monitoring (31) and from the WeatherArchive.ru portal.

Symptoms and pathological changes were recorded in accordance with the standard guidelines for animal examination and autopsy with a visual assessment of pathological changes. Blood samples from the diseased animals were taken for biochemical testing for total protein, calcium, reserve alkalinity, and ketones (13).

The causative agent was detected by PCR. We extracted its DNA from samples of the spleen, mesenteric and bronchial lymph nodes, intestines, and lungs by nucleic acid adsorption method using the commercial DNA-sorb-C-M kit (Interlabservis, Moscow, Russia). Due to the suspected presence of the pathogen in samples, we used the classical PCR method (18, 35). We used culture material samples containing Aujeszky's disease virus and infectious bovine rhinotracheitis virus as positive controls for the presence of herpesvirus DNA (34). Then we analysed the products by electrophoresis with 1.5% agarose gel containing 0.001% ethidium bromide, at a current strength of 50 mA and a voltage of 150 V. Electrophoresis lasted 40 min, and we recorded data on a transilluminator in ultraviolet light at a wavelength of 254 nm.

We evaluated PCR results by detecting specific bands in tracks with test samples relative to the molecular-weight size marker fragment and the calculated length of the PCR product relative to each amplified genome fragment.

PCR products were sequenced using the Sanger method for phylogenetic analysis. The gel purification was carried out using the standard commercial Cleanup Standard kit (Eurogen, Moscow, Russia). We performed the sequencing reaction using the BigDye Terminator v3.1 cycle sequencing kit (Applied Biosystems, Waltham, MA, USA) according to the manufacturer's instructions.

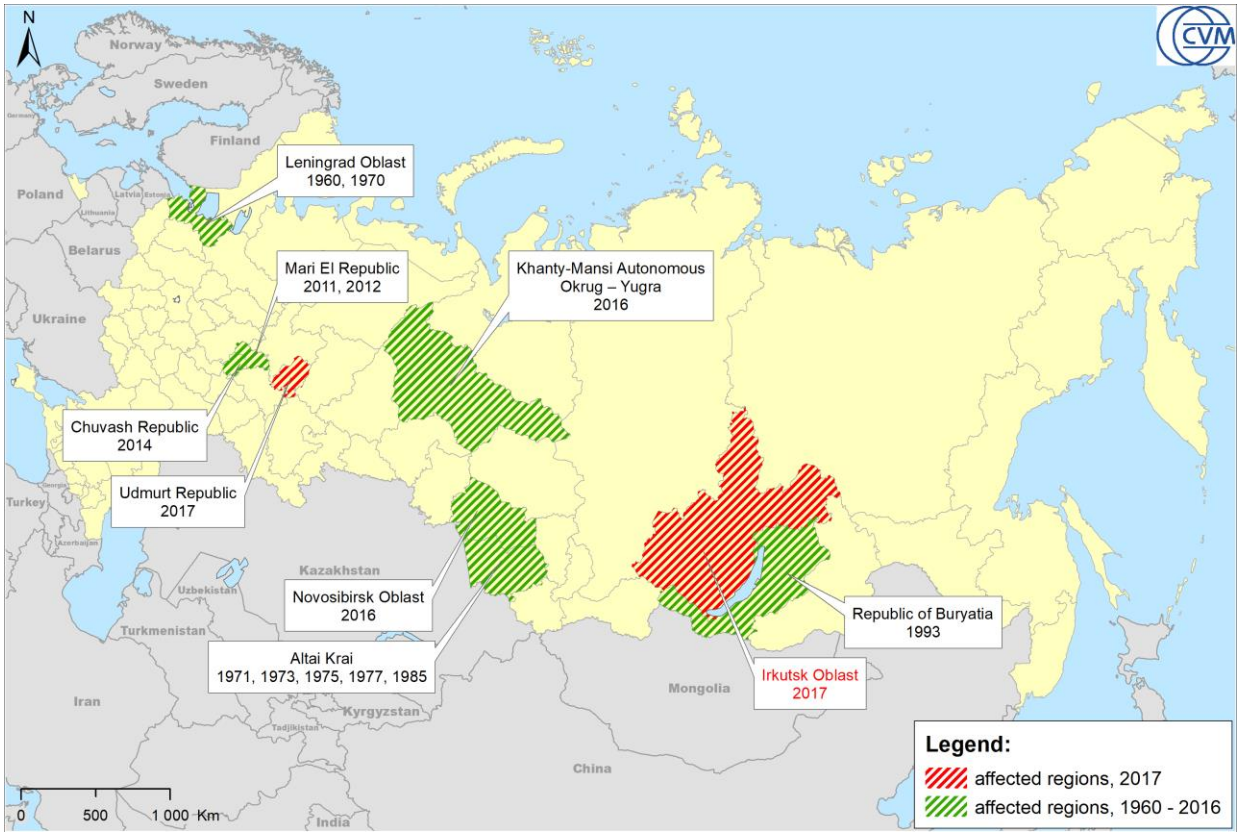

Fig. 1. Regions where MCF was recorded (1960–2017) in the USSR and Russian Federation

We assembled contigs and aligned sequences using the BioEdit v.7 computer programme (10). The construction of a phylogenetic dendrogram based on fragments of polymerase gene sequences was carried out by the MEGAv.7 programme (14). The nucleotide sequences were taken from the GenBank international database and were bovine herpesvirus 1 (BHV1) Cooper strain, accession no. KU198480.1; OvHV2, accession no. DQ198083.1; OvHV2 BJ1035 strain, NC_007646.1; OvHV2 15821 bison strain, HM216458.1; OvHV2 3525 hirsch strain, HM216456.1; OvHV2 25550 strain, HM216465.1; OvHV2 23070 pig strain, JN595788.1; OvHV2 -27846 elch strain, HM216486.1; AlHV1 C500 strain, KX905134.1; AlHV1 WC11 strain, MG000864.1; AlHV2 AY092762.1; AlHV2 topi isolate, KF274499.1; deer herpesvirus 1 (DHV1) AF181468; and DHV1 Missouri AF387516.1. For the formation of the external group, we used the DNA polymerase of the BHV1 Cooper strain since it belongs to the gammaherpes viruses but is not related to any of the isolates or strains presented in the dendrogram.

Results

Retrospective analysis. In the Russian Federation, MCF has been officially recorded in several regions: in the Altai Krai, the Leningrad Oblast, and the Republic of Buryatia. In recent years, MCF outbreaks were reported in the Mari El Republic, the Khanty-Mansi Autonomous Okrug - Yugra and Chuvash Republic (Fig. 1).

There were no official reports of MCF in the Irkutsk Oblast in the 60 years preceding the studied outbreak. It was registered for the first time in Irkutsk Oblast in cattle in 2017 in Kharchev village.

Interviews with animal owners revealed that there were two herds of ruminants in the village: one composed of cattle (n = 34), and the second one composed of cattle (n = 66) and sheep (n = 28). Over the three years previous to the outbreak, no new animals had been introduced into the herds. The two groups of animals grazed in different places. Clinical signs of the disease and the deaths of animals were observed in the second herd, which grazed on a pasture in the east of the village (Fig. 2).

Assessment of economic and climatic conditions. All animals in the affected village were kept on separate premises farms smaller than industrial-scale, as none such exist in the village. Cattle grazed, and their diet was supplemented by concentrated feeds. Watering in the pasture was provided from ponds in the field and from wells on the farms. A survey of animal owners showed that because of drought and pasture depletion, the proportion of concentrated feed in the diet was increased by a factor of 1.5–2.0. Also, the owners explained that it was impossible to continue watering because the only pond had dried.

The first clinical signs of the disease in cattle appeared on 23 June 2017. From that date to 23 August, the infection occurred simultaneously in animals on four private farms, and it gradually intensified in herds throughout the entire period of the outbreak, with no spread of infection from one farm to another being observed. These circumstances indicate that the infection derived from one constant source. At the same time, the occurrence of the disease in cattle coincided with abnormal ambient temperatures for Kharchev of 31°C–35°C. There were eight days with such a high temperature during these two months. One or two infected animals were detected after each abnormally hot day. One animal was infected on 23 June, three animals demonstrated clinical symptoms on 30 June and 1 July, six animals on 2 July, one animal on 19 July, two animals on 6 August, two animals on 7 August, and two animals on 14 August. After the mixed grazing of cattle and sheep had ended and air temperature had normalised at 17°C–22°C in August, no new cases of the disease were reported in the village (Fig. 3).

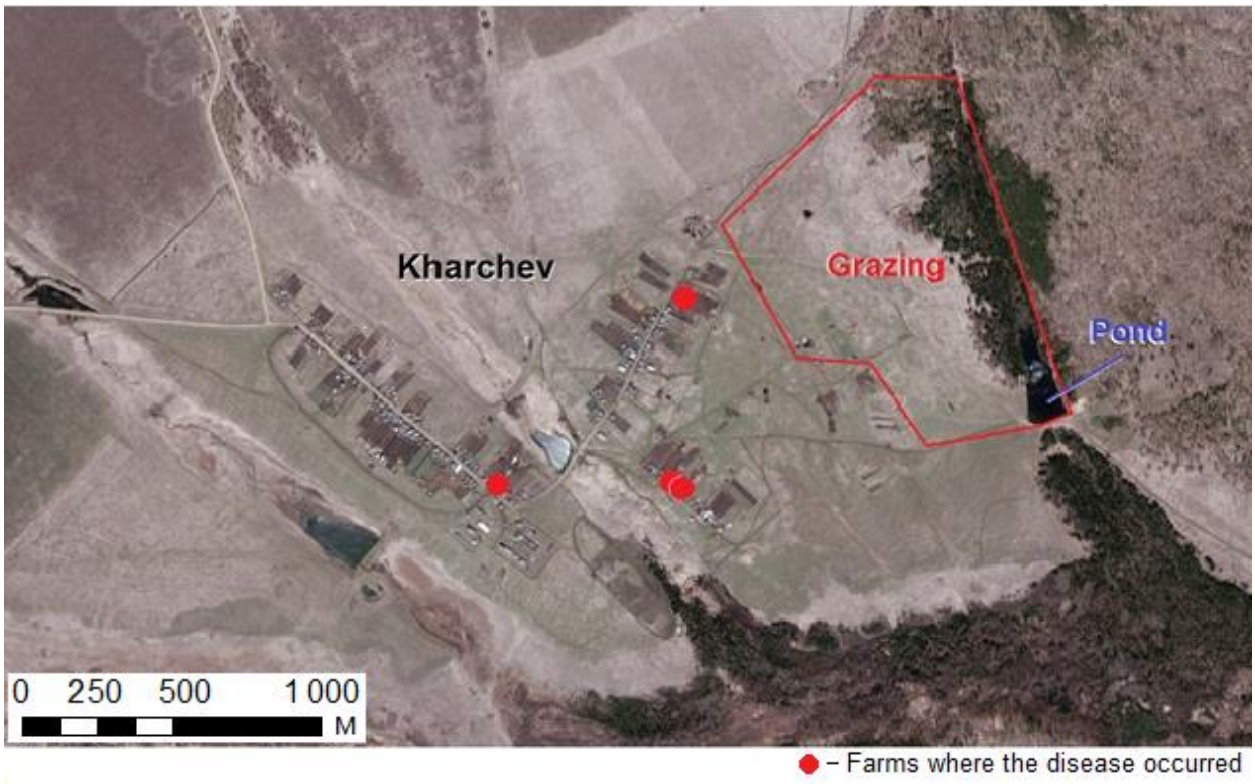

Fig. 2. MCF outbreak location in 2017

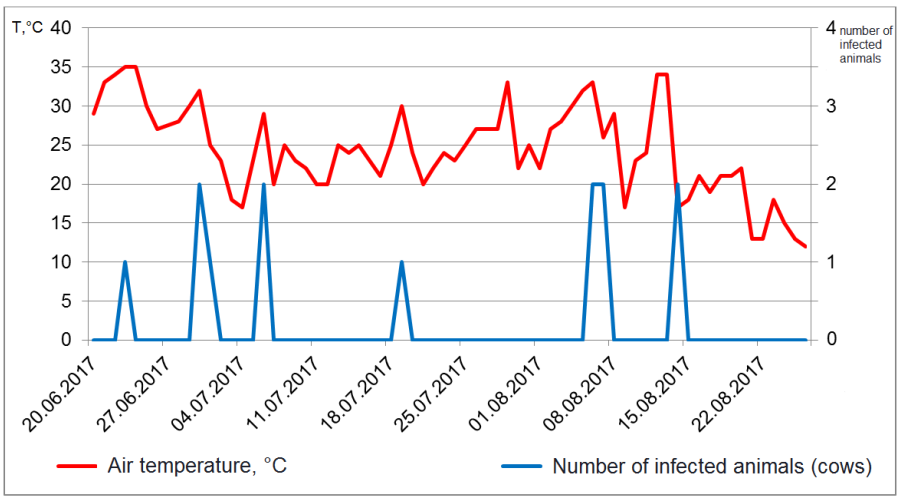

Fig. 3. Ambient temperature and number of infected animals

Clinical signs and pathological changes. On four holdings, MCF presented an identical clinical picture and pathological changes. These clinical symptoms of the disease in cattle were characterised by agalactia and hyperthermia (the body temperature in 13 infected animals was 39.5 ± 0.4°C). Severe depression was accompanied by feed refusal. We observed cloudy nasal and ocular discharge, and the corneas were cloudy. There were blood admixtures in faeces and urine. Symptoms of nervous system damage included spasms and muscle tremors that developed on the 5th day of infection, and the disease had a typical course of 5 ± 0.7 days. A total of 13 of the 66 animals contracted the infection and died. The morbidity rate was 24.5%, and the mortality rate was 100%. Autopsies of those 13 cattle found well expressed post mortem rigidity and a dull coat with ruffled hair. Blood was thick and dark red, subcutaneous tissue had haemorrhages. We observed hyperaemia, erosion, and necrotic changes with desquamation of the surface epithelium on the visible mucous membranes of nasolabial folds, the oral cavity, and the tongue (Fig. 4A).

Erosions and haemorrhages in the gastrointestinal tract were typical (Fig. 4B), and catarrhal exudate and erosion were also observed in the anatomical airways. Frontal lobular bronchopneumonia and posterior lobular interstitial oedema were present in the lungs. We noted petechial haemorrhages on the mucous membrane of the bladder. The somatic, mesenteric, and bronchial lymph nodes were enlarged, and an incision was pulpy with serous haemorrhagic lymphadenitis (Fig. 4C). The spleen was not enlarged but had petechial haemorrhages under the capsule. Meninges were diffusely hyperaemic and oedematous, and the tissue of the brain had petechial haemorrhages (Fig. 4D). The liver and kidneys had signs of dystrophic processes. The gallbladder was enlarged and also affected by petechial haemorrhages on its mucous membrane.

Biochemical studies. The study showed that 28.3% of animals had pseudo-hypercalcaemia, which was caused by dehydration and intensification of protein synthesis. Animals comprising a 47.2% proportion of the infected population had hyperproteinaemia (90.0 ±1.07 gL protein). It seems most likely that the hyperproteinaemia was caused by dehydration and the animals having been fed with a large amount of concentrated feed because of a lack of roughage on pastures. The abundance of easily digestible carbohydrates led to the development of acidosis, which was confirmed by ketosis in 13.2% of the animals and by decreased alkaline reserves in blood plasma (37.5% of the reference values in 43.4% of the animals) (Table 1).

Laboratory diagnostics. MCF herpesvirus OvHV2 (isolate MCF/Irkutsk/2017) was identified by molecular genetic methods in samples from the affected cattle.

Phylogenetic analysis. We demonstrated that the obtained sequence matches a fragment of the herpesvirus polymerase gene of sheep (OvHV2) that can act as a causative agent of MCF (Fig. 5).

The constructed dendrogram shows that the MCF/Irkutsk/2017 isolate belongs to a separate cluster along with European and American isolates, indicating significant similarity of the polymerase gene region of these strains. Genotyping over some additional sites would probably provide a more detailed picture of the phylogenetic relationships between members of this cluster.

Table 1. Clinical baseline characteristics and laboratory findings of cows with MCF

Reported cases	Date of the study of blood serum	Number of diseased cows	Air temperature (°C)	Laboratory findings		
				Total protein (g/L)	Total calcium (mmol/L)	Reserve alkalinity (mmol/L)
1	23.06.2017	1	35	95.0	4.00	18.2
2	30.06.2017	2	32	94.0 96.6	3.55 3.86	16.3 18.0
3	1.07.2017	1	32	84.3	2.84	23.4
4	6.07.2017	2	29	97.4 86.0	4.23 3.00	18.4 20.0
5	19.07.2017	1	30	82.8	2.93	22.6
6	6.08.2017	2	33	85.0 80.7	2.67 2.78	23.3 27.0
7	7.08.2017	2	29	96.5 84.0	3.67 2.50	18.7 25.0
8	14.08.2017	2	34	96.8 95.3	4.25 3.00	17.2 26.5
M±m			32 ± 1.00	90.338 ± 1.868	3.329 ± 0.179	21.123 ± 1.061
Standard* (14)				72.0–86.0	2.50–3.13	19.0–27.0

* Data are mean ±SD

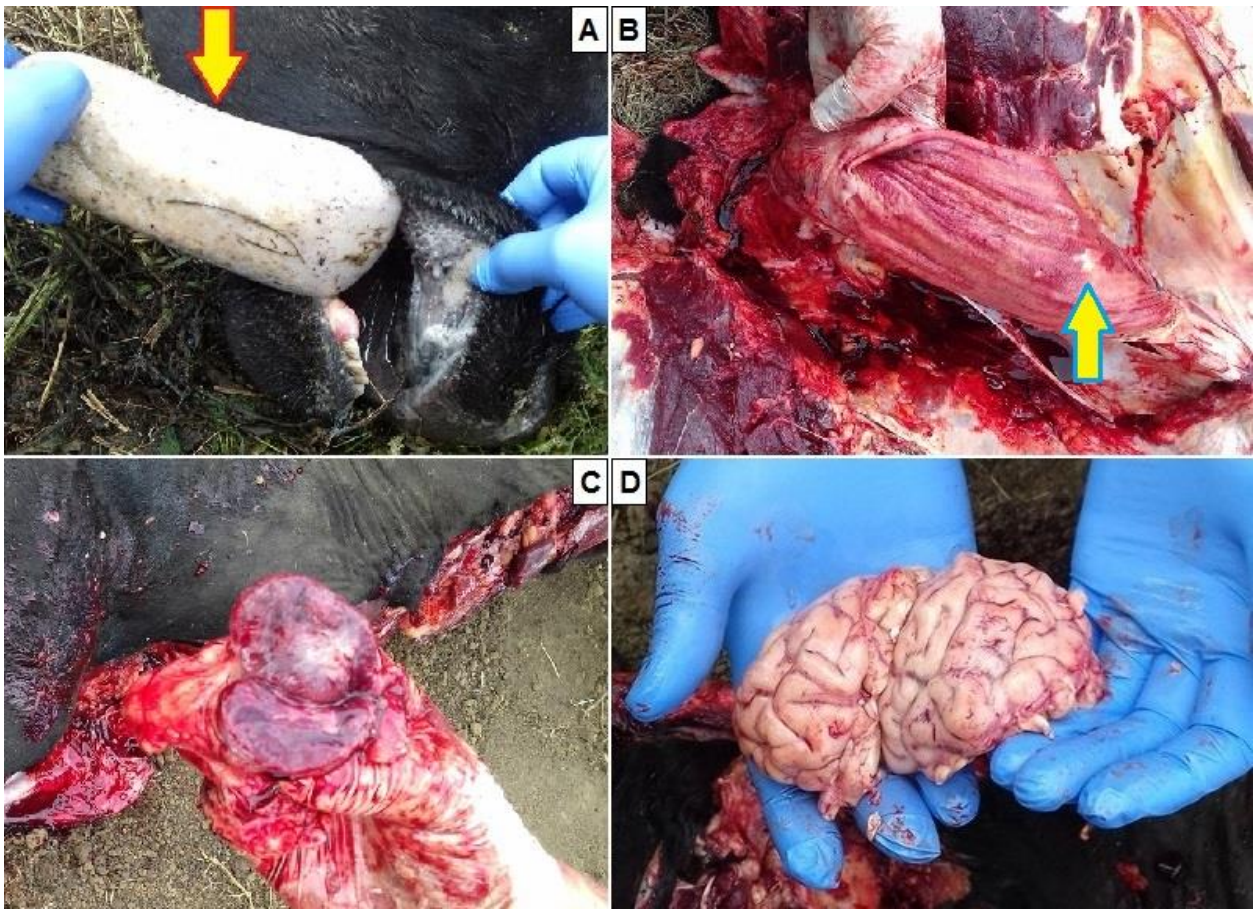

Fig. 4. Pathological changes in cattle infected with MCF: A – necrotic glossitis; B – catarrhal haemorrhagic enteritis; C – serous haemorrhagic lymphadenitis; D – petechial haemorrhages in the brain. Arrows show necrotic parts and desquamation of epithelium

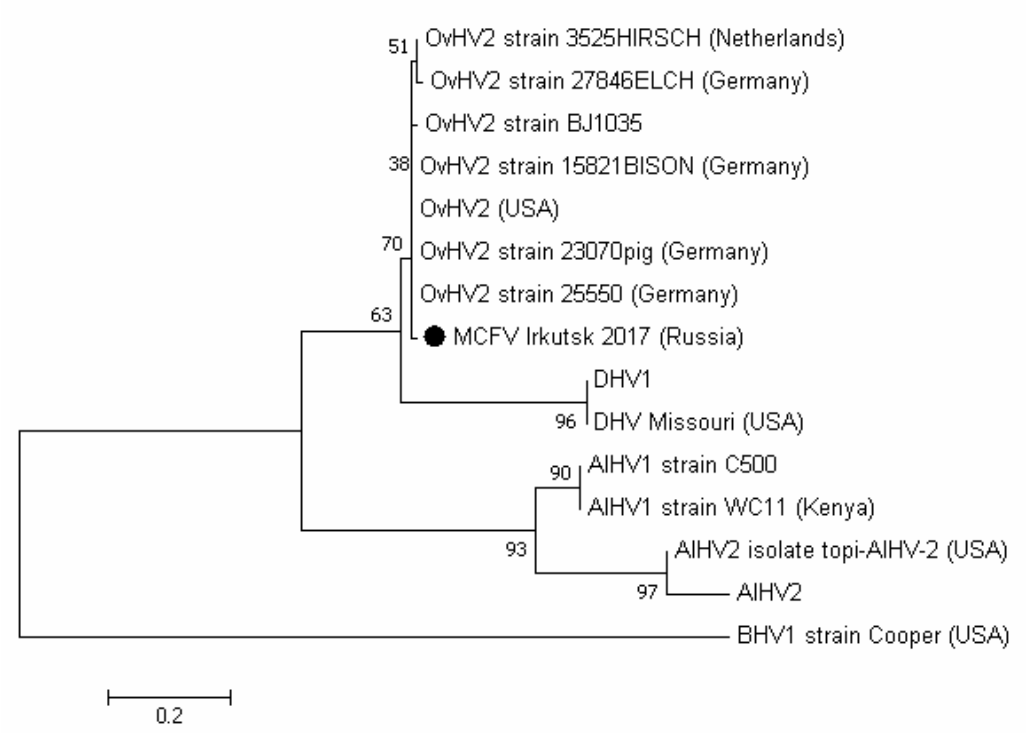

Fig. 5. Phylogenetic dendrogram on the base of polymerase gene, constructed with the help of MEGA7.0, using the neighbour-joining method

Discussion

The endemic nature of MCF is well known (1, 22, 32, 33, 37, 38). Our retrospective analysis shows that the pattern of MCF in Russia is sporadic because the disease was seen to last a short time in several locations and each outbreak was established not to be linked epidemiologically with others. These local epidemics do not spread further. However, in several regions, the disease is reported with a certain periodicity and regions of potential risk are known (the Altai Krai, the Leningrad Oblast, and the Mari El Republic). The described case of MCF was one exemplifying the discontinuity of outbreaks in the Federation and did not spread further.

Some authors suggest that a probable facilitating factor of MCF could be heat stress. The virus can be transmitted by air, and the presence of insects as mechanical vectors play a role in its local spread (30). Given climate change and global warming, the role of insects in transmission of pathogens should be taken into consideration (12).

In our case, we did not observe transmission of the pathogen over long distances because animals of the other Kharchev herd remained healthy. In recent years, climatic anomalies have been observed in the Siberian region, due to the average temperature trend. 2017 was the fourth-warmest year on record since (1936). At the same time, in the Baikal and Irkutsk regions, the temperature anomaly was 3.69°C in the spring of 2017 and 1.11°C in the summer, which was beyond the 95% range of anomalies for the whole Russia. The amount of precipitation was 80% of the norm (31). In the affected village of Kharchev, cases of infection were noted on days of the highest air temperatures, which were 31°C–35°C (average 33°C). A total of eight such days were observed during two months: 23.06., 30.06., 01.07., 06.07., 19.07., 06.08., 07.08., and 14.08.2017. At the same time, the average air temperature for this area according to five-year (2014–2019) observations is 16.45°C in June, 18.82°C in July, and 16.5°C in August. Recorded temperature anomalies resulted in drought and intensive vegetation and pasture depletion. The pond at the border of the pasture became shallow. As a result of this, the grazing animals suffered from a significant feed and water deficiency, which caused dehydration in cows and heat stress. This heat stress resulted in MCF.

The clinical picture and pathological changes in the described cases were similar to MCF descriptions in veterinary literature (3, 7, 8, 11, 21, 28, 32). However, the duration of the disease in Kharchev was 5 ± 0.7 days, whereas it is usually 1–26 days (21).

As mentioned earlier, MCF is not one of the widespread diseases in Russia. Therefore, to study whether Russian OvHV-2 is genetically different from other viruses, we performed a phylogenetic analysis using a fragment of the gene encoding polymerase. The results of our study showed a close genetic relationship between Russian OvHV-2 and isolates obtained from cattle and sheep from Germany, the USA, and the Netherlands.

Conclusively, retrospective analysis of MCF outbreaks in the Russian Federation showed the absence of disease endemicity in the country and lack of connection with the described case. Considering that no new reservoir animals or susceptible cattle appeared in the village of Kharchev, and the disease was not reported in previous years, we can conclude that the described case for this area was isolated.

The outbreak was caused by a climatic anomaly of increased air temperature to 31°C–35°C. All infected animals showed clinical signs of the disease on hot days or the next day. MCF in cattle was manifested by clinical signs: an increase in body temperature to 39.5 ±4°C, clouding of the cornea, cloudy nasal and ocular discharge, haematuria, the presence of blood admixture in excrement, convulsions, and muscle tremors. Pathological signs were characterised by erosive-haemorrhagic processes on the mucous membranes of the digestive system, bladder, nasolabial folds, and oral cavity, as well as lobular bronchopneumonia and haemorrhages in the brain and lymph nodes.

The results of biochemical studies confirmed the dehydration of animals and indicated disorders of protein metabolism associated with pasture depletion and increased consumption of concentrated feed (crushed grain). The latter was confirmed by animal owner surveys.

According to the results of laboratory diagnostics of pathological material, the viral agent OvHV-2 was definitively identified. Phylogenetic analysis of the virus showed its close genetic relationship with isolates obtained from cattle and sheep in Germany, the USA, and the Netherlands.

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References

1. Alcaraz A., Warren A., Jackson C., Gold J., McCoy M., Cheong S.H., Li H.: Naturally occurring sheep-associated malignant catarrhal fever in North American pigs. J Vet Diagn Invest 2009, 21, 250–253.
2. Barnard B.J.H., van der Lugt J., Mushi E.Z.: Malignant catarrhal fever. In: *Infectious diseases of livestock with special reference to Southern Africa*, edited by J.A. Coetzer, G.R. Thomson, R.C.

Tustin, Oxford University Press, Cape Town, Oxford, 1994, pp. 40–44 and 61–63.
3. Bildfell R.J., Li H., Alcantar B.E., Cunha C.W., Bradway D.S., Thomas K.S.: Alcelaphine gamma herpesvirus 1-induced malignant catarrhal fever in a Watusi (*Bostaurusafricanus*) steer in a North American game park. J Vet Diagn Invest 2017, 29, 579–582.
4. Goldman M.: Tracking wildebeest, locating knowledge: Masaai and conservation biology understandings of wildebeest behaviour in northern Tanzania, Environment Planning D. Society and Space 2007, 25, 307 – 331.
5. Epp T., Uehlinger F.D., Wojnarowicz C., Malhi P.S., Savi S., Woodbury M.R.: Observations of mortality in farmed bison in the Canadian prairies: 2003–2016. Prev Vet Med 2018, 157, 1–7.
6. Fauquet C.M., Fargette D.: International Committee on Taxonomy of Viruses and the 3,142 unassigned species. Virol J 2005, 2, 64,doi: 10.1186/1743-422X-2-64.
7. Fernandez-Aguilár X., Esperón F., Cabezón O., Velarde R., Mentaberre G., Delicado V., Jesus Muñoz M., Serrano E., Lavín S., López-Olvera J.R.: Identification of a gamma herpesvirus belonging to the malignant catarrhal fever group of viruses in Pyrenean chamois (*Rupicapra p. pyrenaica*). Arch Virol 2016, 161, 3249–3253.
8. Foyle K.L., Fuller H.E., Higgins R.J., Russell G.C., Willoughby K., Rosie W.G., Stidworthy M.F., Foster A.P.: Malignant catarrhal fever in Sika deer (*Cervusnippon*) in the UK. Vet Rec 2009, 165, 445–447.
9. Frontoso R., Autorino G.L., Friedrich K.G., Li H., Eleni C., Cocomelli C., Di Cerbo P., Manna G., Scicluna M.T.: An acute multispecies episode of sheep-associated malignant catarrhal fever in captive wild animals in an Italian zoo. Transbound Emerg Dis 2016, 63, 621–627.
10. Hall T.A.: BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucl Acids SympSer 1999, 41, 95–98.
11. Headley S.A., Pimentel L.A., Oliveira V.H., Toma H.S., Alfieri A.F., Carvalho A.M., dos Santos M.D., Alfieri A.A.: Transplacental transmission of ovine herpesvirus 2 in cattle with sheep-associated malignant catarrhal fever. J Comp Pathol 2015, 153, 206–211.
12. Hussain I., Kashoo Z.A., Wani A.H., Hasin D.: Malignant catarrhal fever: recent update. Indian J Anim Sci 2017, 87, 260–269.
13. Jones K.E., Patel N.G., Levy M.A., Storeygard A., Balk D., Gittleman J.L., Daszak P.: Global trends in emerging infectious diseases. Nature 2008, 451, 990–993.
14. Kondrakhin I.P.:Metody veterinarnoy klinicheskoy laboratornoy diagnosticki. Edited by I.P. Kondrakhin, Kolos, Moscow, 2004, pp. 520. (in Russian).
15. Kumar S., Stecher G., Tamura K.: MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. Molecular Biology and Evolution 2015, 33, 1870–1874.
16. Lankester F., Lugelo A., Kazwala R., Keyyu J., Cleaveland S., Yoder J.: The economic impact of malignant catarrhal fever on pastoralist livelihoods. PLoS One 2015, 10, e0116059.
17. Li H., Cunha C.W., Taus N.S., Knowles D.P.: Malignant catarrhal fever: inching toward understanding. Annu Rev Anim Biosci 2014, 2, 209–233.
18. Li H., Dyer N., Keller J., Crawford T.B.: Newly recognized herpesvirus causing malignant catarrhal fever in white-tailed deer (*Odocoileusvirginianus*). J ClinMicrobiol 2000, 38, 1313–1318.
19. Li H., Karney G., O'Toole D., Crawford T.B.: Long distance spread of malignant catarrhal fever virus from feedlot lambs to ranch bison. Can Vet J 2008, 49, 183–185.
20. The Center for Food Security and Public Health: Malignant catarrhal fever, malignant catarrh, malignant head catarrh, gangrenous coryza, catarrhal fever, snotsiekte. Institute for International Cooperation in Animal Biologics, Iowa State University 2016, p. 9.
21. Moore D.A., Kohrs P., Baszler T., Faux C., Sathre P., Wenz J.R., Eldridge L., Li H.: Outbreak of malignant catarrhal fever among cattle associated with a state livestock exhibition. J Am Vet Med Assoc 2010, 237, 87–92.
22. Neimanis A.S., Hill J.E., Jardine C.M., Bollinger T.K.: Sheep-associated malignant catarrhal fever in free-ranging moose (*Alcesalces*) in Saskatchewan, Canada. J Wildl Dis 2009, 45, 213–217.
23. Nightingale K., Levy C.S., Hopkins J., Grey F., Esper S., Dalziel R.G.: Expression of ovine herpesvirus-2 encoded microRNAs in an immortalised bovine – cell line. PLoS One, 2014, 9, e97765.
24. Oliveira M.C., Pereira G.O., Daoualibi Y, Dutra V.: An outbreak of malignant catarrhal fever in Sambar deer (*Rusa unicolor*). Pesq Vet Bras 2018, 38, 1675–1680.
25. O'Toole D., Li H.: The pathology of malignant catarrhal fever, with an emphasis on ovine herpesvirus-2. Vet Pathol 2014, 51, 437–452.
26. Palmer M.V., Thacker T.G., Madison R.J., Koster L.G., Swenson S.L., Li H.: Active and latent ovine herpesvirus-2 (OvHV-2) infection in a herd of captive white-tailed deer (*Odocoileusvirginianus*). J Comp Path 2013, 149, 162–166.
27. Patel J.R., Heldens J.G.M., Bakonyi T., Rusvai M.: Important mammalian veterinary viral immune diseases and their control. Vaccine 2012, 30, 1767–1781.
28. Plowright W., Ferris R.D., Scott G.R.: Blue wildebeest and the etiological agent of bovine malignant catarrhal fever. Nature 1960, 188, 1167–1169. doi:10.1038/1881167a0.
29. Pfitzer S., Last R., Espie I., van Vuuren M.: Malignant catarrhal fever: an emerging disease in the African buffalo (*Synceruscaffer*). Transbound Emerg Dis 2015, 62, 288–294.
30. Radostits O.M., Gay C.C., Hinchcliff K.W., Constable P.D.: Veterinary medicine: a textbook of the diseases of cattle, sheep, goat, pigs, and horses. W.B. Saunders, Philadelphia, 2007, p. 1245.
31. Report on climate features in the Russian Federation in 2017, Moscow, 2018, pp. 69.
32. Schultheiss P.C., van Campen H., Spraker T.R., Bishop C., Wolfe L., Podell B.: Malignant catarrhal fever associated with ovine herpesvirus-2 in free-ranging mule deer in Colorado. J Wildl Dis 2007, 43, 533–537.
33. Swai E.S., Kapaga A.M., Sudi F., Loomu P.M., Joshua G.: Malignant catarrhal fever in pastoral Maasai herds caused by wildebeest associated alcelaphine herpesvirus-1: an outbreak report. Vet Res Forum 2013, 4, 133–136.
34. Titov I.A., Malogolovkin A.S., Kolbasov D.V.: Identification of the causative agent of malignant catarrhal fever by molecular genetic methods. Veterinariya 2019, 5, 24–27.
35. Van Devanter D.R., Warrener P., Bennett L., Schultz, E.R., Coulter S., Garber R.L., Rose T.M.: Detection and analysis of diverse herpes-viral species by consensus primer PCR. J Clin Microbiol 1996, 34, 1666–1671.
36. Vikoren T., Klevar S., Li H.: A geographic cluster of malignant catarrhal fever in moose (*Alcesalces*) in Norway. J Wildl Dis 2015, 51, 471–474.
37. World Organization for Animal Health. Malignant catarrhal fever, chapter 2.4.15. In: *OIE Terrestrial Manual 2013*, edited by the OIE Biological Standards Commission, World Organisation for Animal Health (OIE), Paris, 2012. https://www.oie.int/doc/ged/D12008.PDF.
38. Zamila Z., Azila Z., Shuhaini A., Esdy A., Yusniza M.: Malignant catarrhal fever (MCF) in Bali cattle (*Bosjavanicus*) in a commercial farm in Malaysia. Malaysian J Vet Res 2011, 2, 35–39.