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Surveillance of West Nile Fever in the Republic of Kazakhstan, 2023–2025

In 2023–2025, comprehensive monitoring of West Nile fever (WNF) was conducted across 14 regions of the Republic of Kazakhstan to assess virus circulation in natural foci. The study included the main potential reservoirs and vectors of the pathogen, namely wild migratory birds, mosquitoes, ixodid ticks, and bats. A total of 362 biological samples from wild birds, 84 samples from bats, 679 ticks, and 1,554 mosquitoes were examined. Laboratory diagnostics were performed using polymerase chain reaction (PCR) with primers specific to West Nile virus. According to the results, West Nile virus RNA was detected exclusively in wild birds—in 5 of 362 samples, corresponding to a prevalence of 1.38 % (95 % CI: 0.45–3.19 %). No West Nile virus RNA was detected in samples obtained from mosquitoes, ticks, or bats. Positive samples were detected in wild birds from the Pavlodar and Karaganda regions. The obtained data confirm the leading role of migratory birds in the introduction of West Nile virus into the territory of Kazakhstan and indicate the need for continued systematic epizootiological and molecular monitoring to assess the risk of the formation and maintenance of natural infection foci.

Keywords: monitoring, PCR, West Nile fever, flaviviruses, wild birds, mosquitoes, ticks, bats, epizootiological monitoring.

Introduction

West Nile fever (WNF) is a zoonotic arboviral disease with a global distribution. The virus was first isolated in Uganda in 1937, and since the late 1990s it has caused epidemic outbreaks in North America, Europe, and Asia [1–6], making it one of the most significant arboviral infections worldwide, alongside Zika, Chikungunya, and Dengue viruses.

Virus circulation is maintained through an enzootic “mosquito–bird” cycle, in which wild birds, particularly migratory species, serve as the main reservoir and play a key role in long-distance virus dissemination [7, 8].

Most West Nile virus infections are asymptomatic; however, a proportion of patients develop uncomplicated febrile illness, and in rare cases severe neuroinvasive forms occur [9–11]. Mortality in neuroinvasive disease may exceed 10 % among elderly individuals, and survivors often experience long-term neurological sequelae. Recent studies have confirmed the first clinical cases of neuroinvasive WNF in the Almaty region in 2019, indicating a real public health threat and confirming active virus circulation in southern regions of Kazakhstan [12].

Over the past two decades, the nosoarea of WNF has been continuously expanding, including territories of the Russian Federation and regions bordering Kazakhstan. Positive results for West Nile virus have been reported in the West Kazakhstan region, while in Almaty an increase in the incidence of serous meningitis during the summer period has been observed, the etiology of which remains unidentified [13].

Kazakhstan, located at the intersection of the Central Asian and Siberian–South Asian bird migration flyways, is at risk of West Nile virus introduction. Climatic conditions, including warm summer periods and the presence of numerous water bodies, favor mass breeding of Culex mosquitoes, the primary vectors of the virus. Early studies conducted in 2013-2014 detected virus circulation in seven bird species in the vicinity of major water bodies in the Almaty region—Sorbulak, Aksu, and Alakol [14]. Subsequent investigations in 2022-2023 in the Almaty and Zhambyl regions confirmed the presence of the virus in the hooded crow

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(*Corvus corone*), Eurasian jackdaw (*Corvus monedula*), and Eurasian sparrowhawk (*Accipiter nisus*), indicating long-term circulation of WNF in southern Kazakhstan [15].

In contrast to European countries and the United States, where systematic epidemiological surveillance of WNF is conducted, studies in Kazakhstan have been sporadic and have not encompassed all key components of the epizootic chain, including birds, mosquitoes, ticks, and bats. The lack of comprehensive long-term studies hampers accurate assessment of the current epizootiological situation and limits the ability to predict risks to human and animal health.

Therefore, large-scale epizootiological monitoring of West Nile virus in Kazakhstan during 2023–2025 among potential reservoirs and vectors is critically important for identifying areas and intensity of virus circulation, developing an effective epidemiological surveillance system, and integrating Kazakhstan into international arbovirus control programs.

Experimental

Sample Collection

Sampling was conducted during the active seasons of vectors, primarily from May to September, with peak sampling occurring in June–August, corresponding to the highest activity of mosquitoes. Samples were obtained from clinically healthy animals in natural biotopes (wetlands, river floodplains, forest belts) located near human settlements and agricultural areas.

Samples from free-living migratory and synanthropic birds were collected using ornithological mist nets, as well as from birds obtained during legally authorized hunting activities.

Bats were captured in old and abandoned buildings, attics, caves, and tunnels. An ultrasonic detector Batbox Baton (NHBS, United Kingdom) was used to locate bat colonies. Individuals were captured using entomological nets and mist nets in caves or manually in buildings. Swabs from mucosal surfaces and guano samples were collected from bats. After sampling, all animals were released at the capture sites.

Mosquitoes were collected using entomological nets, CDC light traps, and aspirators during daytime and nighttime in areas of mass breeding and resting. Ticks were collected by flagging (dragging) vegetation and shrubs, as well as by removal from the bodies of captured mammals. For each sample, the date of collection, species, number of individuals, and geographic coordinates were recorded. Transportation to the laboratory was carried out on the day of collection; when immediate delivery was not possible, adult ticks were temporarily stored in tubes with moistened filter paper at +4 °C for no more than 10 days. In the laboratory, live ticks were surface-sterilized by double washing in 70 % ethanol for 30 s.

To improve PCR efficiency mosquitoes and ticks were pooled according to species, sampling location, and collection date, with pool sizes ranging from 9 to 15 individuals for mosquitoes and from 1 to 5 individuals for ticks, depending on their size and degree of blood engorgement (Table 2). All samples were immediately placed in transport medium and stored at −80 °C until laboratory analysis.

RNA Extraction and cDNA Synthesis

RNA was extracted from homogenized tissue samples and arthropod pools using the QIAamp Viral RNA Mini Kit (Qiagen, Germany) in accordance with the manufacturer's instructions. Reverse transcription for first-strand cDNA synthesis was performed using SuperScript™ III Reverse Transcriptase (Invitrogen, USA) and random hexamer primers.

PCR Detection of West Nile Virus

Detection of viral RNA was performed using a two-round PCR assay with primers recommended by the OIE (Table 1) [16].

Table 1

Primers used for detection of West Nile virus by RT-PCR

No.	Primer name	Sequence (5′→3′)	Product size
1	1401F	ACC-AAC-TAC-TGT-GGA-GTC	445 bp
	1845R	TTC-CAT-CTT-CAC-TCT-ACA-CT	
2	1485F	GCC-TTC-ATA-CAC-ACT-AAA-G	248 bp
	1732R	CCA-ATG-CTA-TCA-CAG-ACT	

PCR amplification was performed in a Mastercycler thermal cycler (Eppendorf, Germany) using the OneStep RT-PCR Kit (Qiagen, Germany). The total reaction volume was 20 µL per sample.

The amplification program for the first round included: 45 °C for 45 min (reverse transcription); 95 °C for 11 min; followed by 35 cycles of 95 °C for 30 s, 55 °C for 45 s, and 72 °C for 60 s, with a final extension at 72 °C for 5 min. For the second round, the program consisted of 95 °C for 11 min followed by 35 cycles of 95 °C for 30 s, 55 °C for 45 s, and 72 °C for 62 s.

Amplification products were visualized by electrophoresis in a 1.5 % agarose gel stained with ethidium bromide.

Additionally, commercial real-time RT-PCR kits were used:

AmpliSens® WNV-FL (Central Research Institute of Epidemiology, Rospotrebnadzor, Russia). Analysis was performed on a Rotor-Gene Q amplifier (Qiagen, Germany) according to the manufacturer's instructions, with fluorescence detection in the FAM and JOE channels.

West Nile Virus (WNV) TaqMan RT-PCR Kit (Norgen Biotek, Canada). Real-time RT-PCR was conducted strictly following the manufacturer's protocol using a Rotor-Gene Q instrument.

Sequencing and Phylogenetic Analysis

Sequencing was performed using the dideoxy chain-termination (Sanger) method with fluorescently labeled dideoxynucleotides on an automated 16-capillary Genetic Analyzer 3130xl (Applied Biosystems, USA). POP-7 polymer was used for capillary electrophoresis. Sequencing reactions were generated using the cycle sequencing method.

Phylogenetic analysis was conducted using MEGA version 6.06 [17] with the following parameters: statistical method—Neighbor-Joining; test of phylogeny—bootstrap method; number of bootstrap replications—500; model/method—Kimura 2-parameter model; substitutions included—transitions and transversions; gaps/missing data treatment—complete deletion; codons included—1st + 2nd + 3rd + noncoding positions.

Statistical and Geospatial Analysis

Statistical analysis was performed using GraphPad Prism software. Descriptive statistics were applied to calculate overall and regional prevalence rates. Chi-square tests were used to assess significant differences in prevalence between regions. A p-value < 0.05 was considered statistically significant. Results were presented as percentages with 95 % confidence intervals to reflect uncertainty around the estimates.

Geographic coordinates of sampling sites were mapped using QGIS version 3.34.

Results and Discussion

During 2023–2025, biological samples were collected in 14 regions of the Republic of Kazakhstan (Zhambyl, Almaty, Zhetisu, Turkestan, Kyzylorda, West Kazakhstan, Atyrau, Aktobe, Mangystau, Akmola, North Kazakhstan, Karaganda, Abay, and East Kazakhstan regions). In total, samples were obtained from 362 wild migratory birds, 84 bats, 679 ticks, and 1,554 mosquitoes. Survey locations, sampling sites, and numbers of collected samples are presented in Table 2 and Figures 1-2. During field investigations, no diseased or dead animals were detected. Samples from birds and bats were collected exclusively from clinically healthy individuals.

Table 2

Number of samples collected in the regions of Kazakhstan

No.	Region	Birds	Ticks	Ticks (pools)	Mosquitoes	Mosquitoes (pools)	Bats
1	2	3	4	5	6	7	8
2023							
1	Kostanay	10	10	3	-	-	-
2	Akmola	6	-	-	-	-	-
3	Zhambyl	60	25	8	-	-	1
4	Atyrau	-	5	5	-	-	17

Continuation of Table 2

No.	Region	Birds	Ticks	Ticks (pools)	Mosquitoes	Mosquitoes (pools)	Bats
1	**2**	**3**	**4**	**5**	**6**	**7**	**8**
	2023						
5	Aktobe	-	5	3	-	-	12
6	Abay	-	10	3	-	-	-
7	West Kazakhstan	-	10	3	-	-	22
8	Almaty	-	17	7	-	-	-
9	Zhetisu	-	15	6	-	-	-
	Total	76	97	38	-	-	52
	2024						
1	Aktobe	13	-	-	208	20	-
2	Pavlodar	3	-	-	12	1	-
3	Zhambyl	27	18	13	12	1	-
4	Karaganda	32	-	-	-	-	-
5	Kyzylorda	29	45	21	41	4	-
6	Turkestan	3	90	40	30	3	32
7	Zhetisu	12	49	20	-	-	-
8	Almaty	20	38	13	-	-	-
9	Abay	-	45	26	-	-	-
10	West Kazakhstan	-	35	11	51	5	-
11	Atyrau	-	-	-	-	-	-
12	Mangystau	-	-	-	-	-	-
	Total	139	320	144	354	34	32
	2025						
1	Almaty	131	43	16	101	10	-
2	Zhambyl	2	7	7	100	10	-
3	Karaganda	14	-	-	-	-	-
4	West Kazakhstan	-	74	64	100	10	-
5	North Kazakhstan	-	50	22	84	8	-
6	Zhetisu	-	45	41	103	10	-
7	Atyrau	-	13	13	100	10	-
8	Mangystau	-	30	21	-	-	-
9	Aktobe	-	-	-	100	10	-

Continuation of Table 2

No.	Region	Birds	Ticks	Ticks (pools)	Mosquitoes	Mosquitoes (pools)	Bats
1	2	3	4	5	6	7	8
2025							
10	Kostanay	-	-	-	99	10	-
11	Turkestan	-	-	-	100	10	-
12	Kyzylorda	-	-	-	100	10	-
13	Akmola	-	-	-	116	12	-
14	East Kazakhstan	-	-	-	97	10	-
	Total	147	262	184	1200	120	-
	Total	362	679	366	1554	154	84

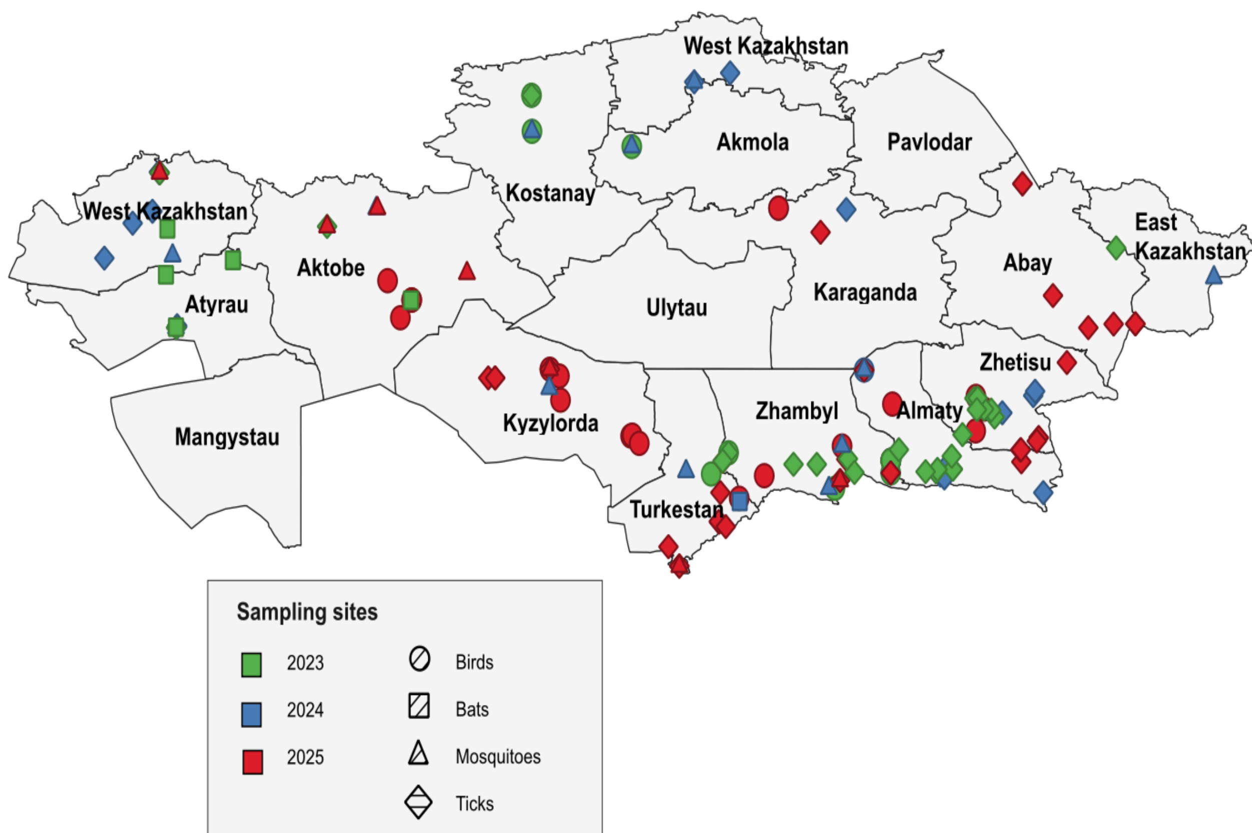

Figure 1. Survey and sampling sites for birds in 2023–2025

All collected samples were tested for the presence of West Nile virus (WNV) RNA. As a result of the study, WNV was detected only in samples from five birds (Table 3). The overall prevalence of WNV among wild birds was 1.38 %, including 2.16 % in 2024 and 2.04 % in 2025. WNV RNA was detected in samples from wild birds—common shelduck, duck, and black-headed gull—collected in the Pavlodar region in 2024 (prevalence 100 %), as well as in two samples—Eurasian jackdaw and magpie—collected in the Karaganda region in 2025 (prevalence 35.7 %). The geographic distribution of WNV among birds is shown in Figure 3.

Table 3

Results of PCR testing of wild bird samples for West Nile virus

No.	Region	Tested	Positive	% Positive	95 % CI (%)	p-value*
2023						
1	Kostanay	10	0	0.0	0.0–4.7	—
2	Akmola	6	0	0.0	0.0–4.7	—
3	Zhambyl	60	0	0.0	0.0–4.7	—
	Total	76	0	0.0	0.0–4.7	—
2024						
1	Aktobe	13	0	0.0	0.0–2.7	—
2	Pavlodar	3	3	100.0	29.2–100	0.000001
3	Zhambyl	27	0	0.0	0.0–2.7	—
4	Karaganda	32	0	0.0	0.0–2.7	—
5	Kyzylorda	29	0	0.0	0.0–2.7	—
6	Turkestan	3	0	0.0	0.0–2.7	—
7	Zhetisu	12	0	0.0	0.0–2.7	—
8	Almaty	20	0	0.0	0.0–2.7	—
	Total	139	3	2.16	0.45–6.2	0.27
2025						
1	Almaty	131	0	0.0	0.0–2.8	—
2	Zhambyl	2	0	0.0	0.0–2.8	—
3	Karaganda	14	2	35.7	1.78–42.8	0.013
	Total	147	2	1.36	0.17–4.8	0.27
	Total	362	5	1.38	0.45–3.2	—
* p<0,05						

Figure 2. Geographic distribution of West Nile virus among wild birds in Kazakhstan

Analysis of published data indicates that more than 300 bird species are involved as hosts and carriers of West Nile virus (WNV) [18]. In the present study, the sampled avifauna included representatives of different ecological groups, including waterfowl (*Anas platyrhynchos, Tadorna tadorna*), synanthropic and passerine birds (*Corvidae* and other passerines, including *Coloeus monedula and Pica pica*), and semi-aquatic species (*Chroicocephalus ridibundus*). Raptor species were also represented to a limited extent (*e.g., Accipiter nisus*).

WNV-positive samples were detected in the common shelduck (*Tadorna tadorna*), mallard (*Anas platyrhynchos*), and black-headed gull (*Chroicocephalus ridibundus*) from the Pavlodar region, as well as in the Eurasian jackdaw (*Coloeus monedula*) and magpie (*Pica pica*) from the Karaganda region (Table 4).

Table 4

Characteristics of WNV-positive bird samples by species, location, and sampling date

Species	Region	District	Sampling site	Date	Ecological group	Result
Tadorna tadorna	Pavlodar	Bayanaul	Lake Shalkarkol	17.08.2024	Waterfowl	Positive
Anas platyrhynchos	Pavlodar	Bayanaul	Lake Shalkarkol	17.08.2024	Waterfowl	Positive
Chroicocephalus ridibundus	Pavlodar	Bayanaul	Lake Shalkarkol	17.08.2024	Semi-aquatic	Positive
Coloeus monedula	Karaganda	Nura	Lake Balkhash	31.03.2025	Passerine	Positive
Pica pica	Karaganda	Nura	Lake Balkhash	31.03.2025	Passerine	Positive

Previously, in the Almaty region, WNV RNA had been detected in seven avian species serving as virus carriers of West Nile fever. In 2015, WNV RNA was identified in samples from the common chiffchaff (*Phylloscopus collybita*), Turkestan shrike (*Lanius phoenicuroides*), mallard (*Anas platyrhynchos*), great cormorant (*Phalacrocorax carbo*), common whitethroat (*Sylvia communis*), common sandpiper (*Actitis hypoleucos*), and Caspian gull (*Larus cachinnans*) [14].

Subsequently, during 2021–2023, in addition to the seven previously identified avian carriers, four more bird species were identified as WNV carriers [15, 19]. In 2021, WNV was detected in samples from the barn swallow (*Hirundo rustica*) and common chiffchaff (*Phylloscopus collybitus*) in the Zhambyl region, while in 2022-2023 it was identified in samples from the hooded crow (*Corvus corone*), Eurasian jackdaw (*Corvusmonedula*), and Eurasian sparrowhawk (*Accipiter nisus*). Based on these findings, it can be assumed that many bird species previously given little attention actively participate in WNV circulation and likely play a significant role in the maintenance and persistence of natural WNV foci. Occupying diverse ecological niches, these bird species may serve as natural reservoirs of WNV.

Detection of WNV in birds in the Pavlodar region (2024) and Karaganda region (2025) is consistent with the hypothesis that migratory birds play a leading role in virus introduction [20, 21]. While earlier WNV activity had been documented mainly in western Kazakhstan [22], the present data provide the first evidence of virus detection in birds from central and northeastern regions of the country. This may indicate both an expansion of the virus activity range and the existence of previously unrecognized local foci along migratory flyways.

Our recent studies also confirm the expansion of the WNV distribution range in Kazakhstan [23]. In the present study, the role of horses in WNV circulation in Kazakhstan was demonstrated for the first time. Antibodies to WNV were detected in horse sera from the Aktobe, Turkestan, Almaty, Zhetisu, West Kazakhstan, and Atyrau regions. The overall seroprevalence among horses was 8.7 %, indicating active virus circulation in these regions and highlighting the need for targeted monitoring in equine populations. Horses, like humans, are dead-end hosts [24] and do not play a significant role in further virus transmission; however, their high susceptibility and pronounced clinical manifestations make them highly valuable sentinel animals [25, 26]. Detection of WNV-specific antibodies or clinical cases among horses that have not traveled outside the region provides direct evidence of local virus transmission and serves as a warning signal of increased risk to public health.

At the same time, WNV RNA was not detected in any of the analyzed samples from mosquitoes (n = 1,554), ticks (n = 679), or bats (n = 84).

The absence of virus detection in mosquitoes in regions where WNV was identified in birds may be explained by several factors, including sporadic virus introduction, insufficient density of competent vector populations (*Culex spp.*) for sustained transmission, sampling outside peak transmission seasons, or extremely low circulation intensity below the detection limit of the applied methods [27]. When interpreting these results, several limitations of the study should be considered: sampling may not have fully covered key periods of bird migration and peaks of mosquito activity; reliance solely on PCR screening without parallel serological monitoring may have led to underestimation of overall infection prevalence; and variation in sample numbers across regions and years complicates assessment of long-term trends.

Within the framework of the present study, one sequence fragment of the WNV E gene with a length of 546 bp was obtained. Phylogenetic analysis showed that this sequence was most closely related to isolates previously detected in the West Kazakhstan region of Kazakhstan and the Volgograd region of the Russian Federation. The analysis assigned the virus to genotype 1.

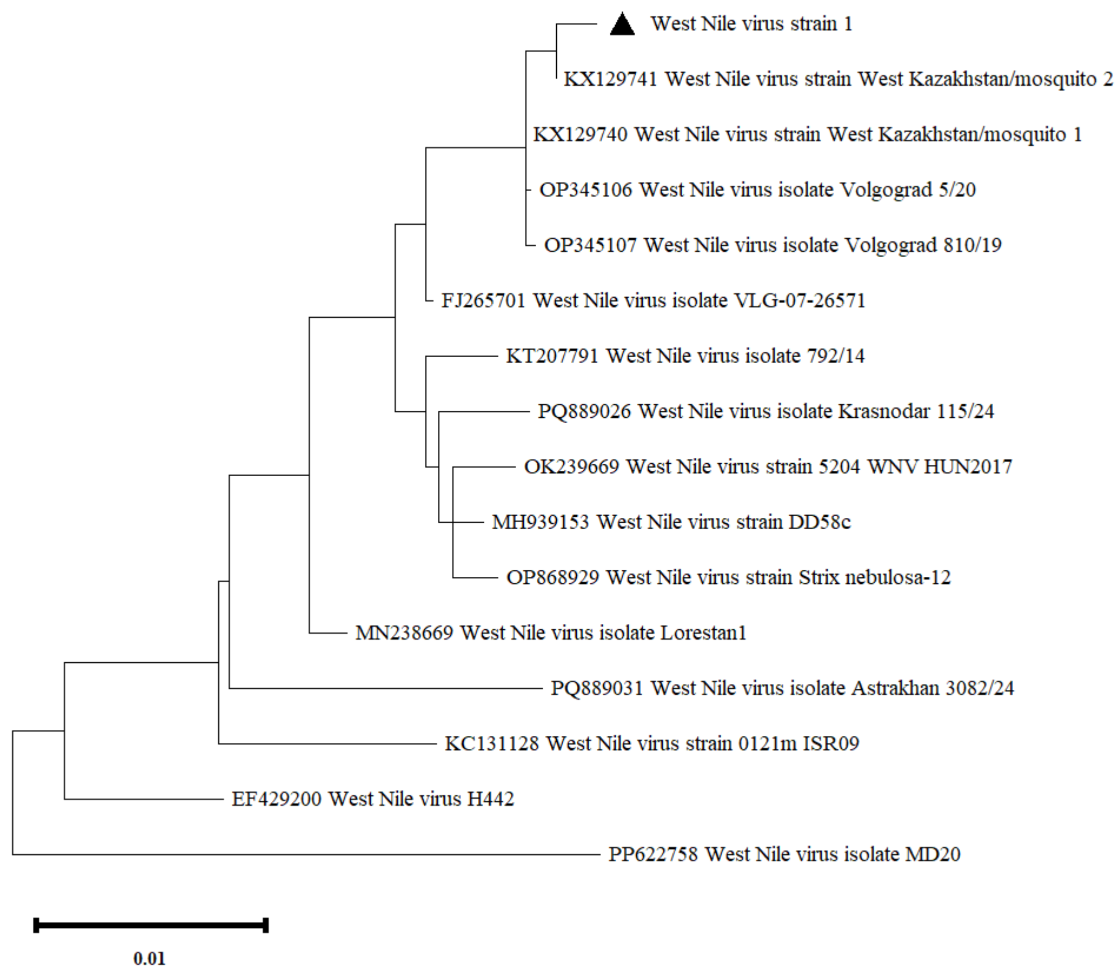

Figure 3. Phylogenetic analysis of the Kazakhstan West Nile virus isolate

Phylogenetic analysis demonstrated that the obtained E gene sequence, classified as genotype 1a, showed the highest similarity to isolates from the West Kazakhstan region of Kazakhstan and the Volgograd region of the Russian Federation [28, 29]. This finding supports the hypothesis of a unified transboundary circulation area of West Nile virus [30] and once again highlights the key role of migratory birds in virus dissemination.

These findings highlight the need to improve West Nile virus surveillance in Kazakhstan. Monitoring efforts should be focused on priority targets, including wild migratory birds at key stopover sites and Culex mosquitoes. It is critically important to incorporate regular serological screening (ELISA) of horses into the

national surveillance system, particularly in regions identified in this study as potential points of virus introduction (Pavlodar and Karaganda). To accurately track virus dissemination routes and evolutionary dynamics, further studies aimed at sequencing complete genomes of Kazakhstan West Nile virus isolates are required.

Conclusion

Based on the results of epizootiological monitoring conducted in 2023–2025 across 14 regions of Kazakhstan, the following conclusions can be drawn. A total of 362 samples from wild migratory birds, 84 from bats, 679 from ticks, and 1,554 from mosquitoes were collected from clinically healthy animals and analyzed. The overall prevalence of West Nile virus (WNV) RNA among wild birds was 1.38 %, with positive results detected only in 2024 and 2025 (2.16 % and 1.36 %, respectively) and geographically confined to the Pavlodar and Karaganda regions. These findings confirm the role of migratory birds in the introduction of WNV into the central and northeastern regions of the country. No viral RNA was detected in any samples from mosquitoes, ticks, or bats, which may indicate a sporadic introduction of the virus or a low level of local circulation.

Phylogenetic analysis of the obtained nucleotide sequence of the E gene fragment (546 bp) classified the isolate as genotype 1a and revealed its closest similarity to strains circulating in the West Kazakhstan region of Kazakhstan and the Volgograd region of the Russian Federation, supporting the existence of a unified transboundary circulation area of WNV. The obtained results substantiate the need for further optimization of the surveillance system, with emphasis on monitoring wild birds and mosquito vectors, as well as the inclusion of serological screening of horses as a sensitive indicator of local virus transmission in the identified high-risk areas.

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Author Contributions

The manuscript was written through contributions of all authors. All authors have given approval to the final version of the manuscript. CRediT: **Alibekova D.A.** — conceptualization, data curation, methodology, investigation, visualization, manuscript drafting; **Omarova Z.D.** — data curation, methodology, investigation, manuscript drafting; **Rystayeva R.A.** — data curation, methodology; **Argimbayeva T.U.** — methodology, investigation, visualization; **Tulendibayev A.B.** — methodology, investigation; **Aubakir N.A.** — methodology, investigation; **Yermekbay T.T.** — methodology, investigation; **Barakbayev K.B.** — conceptualization, data curation, study management, project administration, funding; **Smith G.J.** — conceptualization, data curation, formal analysis, writing draft, editing; **Orynbayev M.B.** — conceptualization, data curation, formal analysis, supervision, writing draft, editing.

Conflict of Interest

The authors declare no conflict of interest.

References

1 Nash D. The outbreak of West Nile virus infection in the New York City area in 1999 / D. Nash, F. Mostashari, A. Fine, et al. // New England Journal of Medicine. — 2001. — Vol. 344, No. 24. — P. 1807–1814.

2 Chancey C. The global ecology and epidemiology of West Nile virus / C. Chancey, A. Grinev, E. Volkova, M. Rios // BioMed Research International. — 2015. — Vol. 2015. — Art. ID 376230. DOI: 10.1155/2015/376230.

3 Balanca G. Low West Nile virus circulation in wild birds in an area of recurring outbreaks in Southern France / G.Balanca, N. Gaidet, G. Savini, et al. // Vector-Borne and Zoonotic Diseases. — 2009. — Vol. 9, No. 6. — P. 737–741. DOI: 10.1089/vbz.2008.0147.

4 Bernkopf H. Isolation of West Nile virus in Israel / H. Bernkopf, S. Levine, R. Nerson // Journal of Infectious Diseases. — 1953. — Vol. 93, No. 3. — P. 207–218.

5 Jupp P.G. The ecology of West Nile virus in South Africa and the occurrence of outbreaks in humans / P.G. Jupp // Annals of the New York Academy of Sciences. — 2001. — Vol. 951. — P. 143–152.

6 Murgue B. West Nile virus in the Mediterranean basin: 1950–2000 / B. Murgue, S. Murri, H. Triki, V. Deubel, H.G. Zeller // Annals of the New York Academy of Sciences. — 2001. — Vol. 951. — P. 117–126.

7 Hayes E.B. Epidemiology and transmission dynamics of West Nile virus disease / E.B. Hayes, N. Komar, R.S. Nasci, S.P. Montgomery, D.R. O'Leary, G.L. Campbell // Emerging Infectious Diseases. — 2005. — Vol. 11, No. 8. — P. 1167–1173.

8 Swetnam D. Terrestrial bird migration and West Nile virus circulation, United States / D. Swetnam, S.G. Widen, T.G. Wood, et al. // Emerging Infectious Diseases. — 2018. — Vol. 24, No. 12. — P. 2184–2194.

9 Campbell G.L. West Nile virus / G.L. Campbell, A.A. Marfin, R.S. Lanciotti, D.J. Gubler // The Lancet Infectious Diseases. — 2002. — Vol. 2, No. 9. — P. 519–529.

10 Petersen L.R. West Nile virus: review of the literature / L.R. Petersen, A.C. Brault, R.S. Nasci // JAMA. — 2013. — Vol. 310, No. 3. — P. 308–315.

11 World Health Organization. West Nile virus: Fact sheet. — Geneva: WHO, 2017. — [Electronic resource]. — Access mode: https://www.who.int/news-room/fact-sheets/detail/west-nile-virus.

12 Ostapchuk Y.O. Two case reports of neuroinvasive West Nile Virus infection in the Almaty region, Kazakhstan / Y.O. Ostapchuk, A.V. Zhigailov, Y.V. Perfilyeva, A.G. Shumilina, L.T. Yeraliyeva, A.S. Nizkorodova, T.V. Kuznetsova, F.A. Iskakova, Z.A. Berdygulova, A.S. Neupokoeva, S.M. Mamadaliyev, A.M. Dmitrovskiy // IDCases. — 2020. — Art. e00872. DOI: 10.1016/j.idcr.2020.e00872.

13 Егембердиева Р.А. Лихорадка Западного Нила: клинико-эпидемиологические проявления / Р.А. Егембердиева, Ж.Ж. Шапиева, А.М. Дмитровский, Н.С. Майканов, Л.З. Мусралина, А.А. Ергалиева // Вестник КазНМУ. — 2019. — № 2. — С. 17–20.

14 Керимбаев А.А. Мониторинг лихорадки Западного Нила среди диких птиц на территории РК / А.А. Керимбаев, Г.К. Мусаева, З.Д. Омарова, Р.А. Рыстаева, С.К. Копеев, Н.М. Раметов, М.Б. Орынбаев // Вестник Государственного университета имени Шакарима города Семей. — 2015. — № 4 (72). — С. 150–162.

15 Әлібекова Д.Ә. Лихорадка Западного Нила среди диких птиц в южных регионах Казахстана / Д.Ә. Әлібекова, Г.Дж. Смит, Т.У. Аргимбаева, З.Д. Омарова, Р.А. Рыстаева, Т.Т. Ермекбай, А.Б. Тулендибаев, Н.А. Әубәкір, М.Б. Орынбаев // Биотехнология и биологическая безопасность: достижения и перспективы развития. Материалы Международной научно-практической конференции, посвященной 65-летию Научно-исследовательского института проблем биологической безопасности МЗ РК (6–8 сентября). — Алматы, 2023. — С. 170-171.

16 World Organisation for Animal Health. Manual of Diagnostic Tests and Vaccines for Terrestrial Animals. Chapter 2.1.24. West Nile fever. — 13th ed. — Paris: WOAH, 2024.

17 Tamura K. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0 / K. Tamura, G. Stecher, D. Peterson, A. Filipski, S. Kumar // Molecular Biology and Evolution. — 2013. — Vol. 30. — № 12. — P. 2725–2729. DOI: 10.1093/molbev/mst197.

18 Palmieri C. Pathology and immunohistochemical findings of West Nile virus infection in Psittaciformes / C. Palmieri, M. Franca, F. Uzal, M. Anderson, B. Barr, L. Woods, J. Moore, P. Woolcock, H.L. Shivaprasad // Veterinary Pathology. — 2011. — Vol. 48. — P. 975–984.

19 Sultankulova K.T. Detection of West Nile fever among wild birds in Kazakhstan / K.T. Sultankulova, A.M. Melisbek, N.S. Kozhabergenov, Y.D. Burashev, N.N. Mukhami, K.D. Zakarya, M.B. Orynbaev // Eurasian Journal of Ecology. — 2021. — Vol. 68, No. 3. — P. 64–71. DOI: 10.26577/EJE.2021.v68.i3.07.

20 Hook S.A. West Nile virus: biology, transmission, and human infection / S.A. Hook, C.A. Nelson, P.S. Mead // Clinical Microbiology Reviews. — 2021. — Vol. 35, No. 1. — e00103-21. DOI: 10.1128/CMR.00103-21.

21 Anderson J.F. Isolation of West Nile virus from mosquitoes, crows, and a Cooper's hawk in Connecticut / J.F. Anderson, T.G. Andreadis, C.R. Vossbrinck, S. Tirrell, E.M. Wakem, R.A. French, A.E. Garmendia // Science. — 1999. — Vol. 286. — P. 2331–2333. DOI: 10.1126/science.286.5448.2331.

22 Гражданов А.К. О выявлении новых природных очагов актуальных инфекционных болезней на западе Казахстана / А.К. Гражданов, Т.З. Аязбаев, А.В. Топорков, Ф.Г. Бидашко, А.В. Захаров, Л.Б. Белоножкина, М.В. Пак, А.В. Андрющенко // Проблемы особо опасных инфекций. — 2014. — № 3. — С. 20–24.

23 Alibekova D.A. Serological investigations on West Nile virusinhorsesin Kazakhstan / D.A. Alibekova, K.B. Barakbayev, Z.D. Omarova, R.A. Rystaeva, K.T. Sultankulova, Y.D. Burashev, T.U. Argimbayeva, A.B. Tulendibayev, N.A. Aubakir, T.T. Yermekbay, K.B. Abeuov, A.A. Kerimbayev, M.B. Orynbayev // Microorganisms. — 2025. — Vol. 13. — Art. 2541. DOI: 10.3390/microorganisms13112541.

24 World Organisation for Animal Health. West Nile Fever // Manual of Diagnostic Tests and Vaccines for Terrestrial Animals. — Paris: WOAH, 2023.

25 Metz M.B.C. Systematic review and meta-analysis of seroprevalence studies of West Nile virus in equids in Europe between 2001 and 2018 / M.B.C. Metz, O.T. Olufemi, J.M. Daly, M. Barba // Transboundary and Emerging Diseases. — 2021. — Vol. 68, No. 4. — P. 1814–1823. DOI: 10.1111/tbed.13866.

26 Centers for Disease Control and Prevention. West Nile Virus: Veterinary Impact. — Atlanta: CDC, 2022. — [Electronic resource]. — Access mode: https://www.cdc.gov/westnile/veterinarians/index.html (Date of request: ...2025).

27 Platonov A.E. Epidemiology of West Nile infection in Volgograd, Russia, in relation to climate change and mosquito bionomics / A.E. Platonov, M.V. Fedorova, L.S. Karan, T.A. Shopenskaya, O.V. Platonova, V.L. Zhuravlev // Parasitology Research. — 2008. — Vol. 103, Suppl. 1. — P. S45–S53. DOI: 10.1007/s00436-008-1050-0.

28 Platonov A.E. Outbreak of West Nile virus infection, Volgograd Region, Russia, 1999 / A.E. Platonov, G.A. Shipulin, O.Y. Shipulina, E.N. Tyutyunnik, T.I. Frolochkina, R.S. Lanciotti, S. Yazyshina, O.V. Platonova, I.L. Obukhov, A.N. Zhukov, Y.Y. Vengerov, V.I. Pokrovskii // Emerging Infectious Diseases. — 2001. — Vol. 7, No. 1. — P. 128–132. DOI: 10.3201/eid0701.010118.

29 Nurmakhanov T. Phylogenetic characteristics of West Nile virus isolated from Culex modestus mosquitoes in West Kazakhstan / T. Nurmakhanov, Y. Sansyzbaev, B. Atshabar, V. Berlin, D. Kobzhasarov, O. Yeskhojayev, A. Vilkova, T. Ayazbayev, A. Andryushchenko, F. Bidashko, J. Hay, A. Shvetsov // Frontiers in Public Health. — 2021. — Vol. 8. — Art. 575187. DOI: 10.3389/fpubh.2020.575187.

30 Гражданов А.К. Сравнительный анализ проявлений опасных инфекций в Саратовской и Западно-Казахстанской областях в целях современной оценки эпидемиологических рисков / А.К. Гражданов, О.И. Кожанова, А.В. Топорков, Т.З. Аязбаев, Н.И. Матвеева, И.Г. Карнаухов, Н.В. Попов, А.С. Раздорский, Г.Н. Архипова // Проблемы особо опасных инфекций. — 2013. — № 4. — С. 38–44.

Д.Ә. Әлібекова, З.Д. Омарова, Р.А. Рыстаева, Т.У. Аргимбаева,
А.Б. Тулендибаев, Н.А. Әубәкір, Т.Т. Ермекбай., К.Б. Баракбаев,
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2023–2025 жылдары Қазақстан Республикасындағы Батыс Ніл қызбасына мониторинг

2023–2025 жылдары Қазақстан Республикасының 14 облысының аумағында Батыс Ніл қызбасы вирусының табиғи ошақтардағы айналымын бағалау мақсатында кешенді эпизоотологиялық және молекулалық мониторинг жүргізілді. Зерттеу жұмыстары әртүрлі табиғи-климаттық аймақтарды қамтып, қоздырғыштың негізгі ықтимал резервуарлары мен тасымалдаушыларын анықтауға бағытталды. Зерттеу объектілері ретінде жабайы қоныс аударатын және синантропты құстар, масалар, иксодты кенелер және жарқанаттар қарастырылды. Биологиялық материалдар табиғи биотоптарда, су айдындарына жақын аумақтарда және елдімекендер маңында клиникалық сау жануарлардан алынды. Барлығы жабайы құстардан алынған 362 үлгі, жарқанаттардан 84 үлгі, 679 кене және 1554 маса зерттелді. Зертханалық диагностика Батыс Ніл қызбасы вирусына спецификалық праймерлерді қолдана отырып, полимеразды тізбекті реакция (ПТР) әдісімен жүргізілді. Зерттеу нәтижесінде БНҚ вирусының РНҚ-сы тек жабайы құстардан алынған үлгілерде ғана анықталды, яғни 362 үлгінің 5-еуінде, бұл жалпы таралу деңгейінің 1,38 %-ын құрады (95 % СА: 0,45–3,19 %). Масалардан, кенелерден және жарқанаттардан алынған үлгілерде вирус РНҚ-сы анықталған жоқ. Оң нәтижелер Павлодар және Қарағанды облыстарында тіркелді, бұл қоныс аударатын құстардың Батыс Ніл вирусын Қазақстан аумағына енгізудегі жетекші рөлін растайды. Алынған деректер инфекцияның табиғи ошақтарының қалыптасуы мен сақталу қаупін уақтылы бағалау үшін жүйелі эпизоотологиялық және молекулалық мониторингті жалғастырудың маңыздылығын көрсетеді.

Кілт сөздер: мониторинг, ПТР, Батыс Ніл қызбасы, флавивирустар, жабайы құстар, масалар, кенелер, жарқанаттар, эпизоотологиялық мониторинг.

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Мониторинг лихорадки западного Нила в Республике Казахстан в 2023–2025 гг.

В 2023–2025 гг. на территории 14 областей Республики Казахстан проведён комплексный эпизоотологический и молекулярный мониторинг лихорадки Западного Нила (ЛЗН) с целью оценки циркуляции вируса в природных очагах и выявления потенциальных рисков формирования устойчивых эпидемиологических зон. Исследование охватывало основные предполагаемые резервуары и переносчики возбудителя, включая диких перелётных птиц, комаров, иксодовых клещей и летучих мышей, отобранных в природных биотопах и вблизи населённых пунктов. Всего было исследовано 362 образца биологического материала от диких птиц, 84 образца от летучих мышей, 679 клещей и 1554 комара. Лабораторную диагностику проводили методом полимеразной цепной реакции с использованием праймеров, специфичных к вирусу лихорадки Западного Нила. По результатам исследований РНК вируса ЛЗН была выявлена исключительно у диких птиц — в 5 из 362 образцов, что соответствует общей распространённости 1,38 % (95 % ДИ: 0,45–3,19 %). В образцах, полученных от комаров, клещей и летучих мышей, РНК вируса ЛЗН обнаружена не была. Положительные пробы зарегистрированы в

Павлодарской и Карагандинской областях, что подтверждает ведущую роль мигрирующих птиц в заносе вируса на территорию Казахстана. Полученные данные указывают на необходимость продолжения систематического эпизоотологического и молекулярного мониторинга для своевременной оценки рисков формирования и поддержания природных очагов инфекции.

Ключевые слова: мониторинг, ПЦР, лихорадка Западного Нила, флавивирусы, дикие птицы, комары, клещи, летучие мыши, эпизоотологический мониторинг.

References

1 Nash, D., Mostashari, F., Fine, A., et al. (2001). The outbreak of West Nile virus infection in the New York City area in 1999. *New England Journal of Medicine, 344*(24), 1807–1814.

2 Chancey, C., Grinev, A., Volkova, E., & Rios, M. (2015). The global ecology and epidemiology of West Nile virus. *BioMed Research International, 2015*, Art. ID 376230. https://doi.org/10.1155/2015/376230

3 Balanca, G., Gaidet, N., Savini, G., et al. (2009). Low West Nile virus circulation in wild birds in an area of recurring outbreaks in Southern France. *Vector-Borne and Zoonotic Diseases, 9*(6), 737–741. https://doi.org/10.1089/vbz.2008.0147

4 Bernkopf, H., Levine, S., & Nerson, R. (1953). Isolation of West Nile virus in Israel. *Journal of Infectious Diseases, 93*(3), 207–218.

5 Jupp, P.G. (2001). The ecology of West Nile virus in South Africa and the occurrence of outbreaks in humans. *Annals of the New York Academy of Sciences, 951*, 143–152.

6 Murgue, B., Murri, S., Triki, H., Deubel, V., & Zeller, H.G. (2001). West Nile virus in the Mediterranean basin: 1950–2000. *Annals of the New York Academy of Sciences, 951,* 117–126.

7 Hayes, E.B., Komar, N., Nasci, R.S., Montgomery, S.P., O'Leary, D.R., & Campbell, G.L. (2005). Epidemiology and transmission dynamics of West Nile virus disease. *Emerging Infectious Diseases, 11*(8), 1167–1173.

8 Swetnam, D., Widen, S.G., Wood, T.G., et al. (2018). Terrestrial bird migration and West Nile virus circulation, United States. *Emerging Infectious Diseases, 24*(12), 2184–2194.

9 Campbell, G.L., Marfin, A.A., Lanciotti, R.S., & Gubler, D.J. (2002). West Nile virus. *The Lancet Infectious Diseases, 2*(9), 519–529.

10 Petersen, L.R., Brault, A.C., & Nasci, R.S. (2013). West Nile virus: Review of the literature. *JAMA, 310*(3), 308–315.

11 World Health Organization. (2017). West Nile virus: Fact sheet. *www.who.int.* Retrieved from https://www.who.int/news-room/fact-sheets/detail/west-nile-virus

12 Ostapchuk, Y.O., Zhigailov, A.V., Perfilyeva, Y.V., Shumilina, A.G., Yeraliyeva, L.T., Nizkorodova, A.S., Kuznetsova, T.V., Iskakova, F.A., Berdygulova, Z.A., Neupokoeva, A.S., & Mamadaliyev, S.M. (2020). Two case reports of neuroinvasive West Nile virus infection in the Almaty region, Kazakhstan. *IDCases,* Art. e00872. https://doi.org/10.1016/j.idcr.2020.e00872

13 Egemberdieva, R.A., Shapieva, Zh.Zh., Dmitrovskii, A.M., Maikanov, N.S., Musralina, L.Z., & Ergalieva, A.A. (2019). Likhoradka Zapadnogo Nila: kliniko-epidemiologicheskie proiavleniia [West Nile fever: Clinical and epidemiological manifestations]. *Vestnik Kazakhskogo Natsionalnogo Meditsinskogo Universiteta — Bulletin of the National Medical University,* 2, 17–20 [in Russian].

14 Kerimbayev, A.A., Musaeva, G.K., Omarova, Z.D., Rystaeva, R.A., Kopeev, S.K., Rametov, N.M., & Orynbaev, M.B. (2015). Monitoring likhoradki Zapadnogo Nila sredi dikikh ptits na territorii RK [Monitoring of West Nile fever among wild birds in Kazakhstan]. *Vestnik Gosudarstvennogo universiteta imeni Shakarima goroda Semei — Bulletin of the Shakarim State University of Semey,* 4(72), 150–162 [in Russian].

15 Alibekova, D.A., Smith, G.J., Argimbayeva, T.U., Omarova, Z.D., Rystaeva, R.A., Yermekbay, T.T., Tulendibayev, A.B., Aubakir, N.A., & Orynbaev, M.B. (2023). Likhoradka Zapadnogo Nila sredi dikikh ptits v yuzhnykh regionakh Kazakhstana [West Nile fever among wild birds in southern Kazakhstan]. *Biotekhnologiia i biologicheskaia bezopasnost: dostizheniia i perspektivy razvitiia. Materialy Mezhdunarodnoi nauchno-prakticheskoi konferentsii, posviashchennoi 65-letiiu Nauchno-issledovatelskogo instituta problem biologicheskoi bezopasnosti Ministerstvo Zdravookhraneniia Respubliki Kazakhstan — Biotechnology and Biological Safety: Achievements and Development Prospects Proceedings of the International Scientific and Practical Conference dedicated to the 65th anniversary of the Research Institute for Biological Safety Problems of the Ministry of Health of the Republic of Kazakhstan* (pp. 170-171) [in Russian].

16 World Organisation for Animal Health (WOAH). (2024). Manual of diagnostic tests and vaccines for terrestrial animals (13th ed., Chapter 2.1.24: West Nile fever). Paris: WOAH.

17 Tamura, K., Stecher, G., Peterson, D., Filipski, A., & Kumar, S. (2013). MEGA6: Molecular evolutionary genetics analysis version 6.0. *Molecular Biology and Evolution, 30*(12), 2725–2729. https://doi.org/10.1093/molbev/mst197

18 Palmieri, C., Franca, M., Uzal, F., Anderson, M., Barr, B., Woods, L., Moore, J., Woolcock, P., & Shivaprasad, H. L. (2011). Pathology and immunohistochemical findings of West Nile virus infection in Psittaciformes. *Veterinary Pathology, 48*, 975–984.

19 Sultankulova, K.T., Melisbek, A.M., Kozhabergenov, N.S., Burashev, Y.D., Mukhami, N.N., Zakarya, K.D., & Orynbaev, M.B. (2021). Detection of West Nile fever among wild birds in Kazakhstan. *Eurasian Journal of Ecology, 68*(3), 64–71. https://doi.org/10.26577/EJE.2021.v68.i3.07

20 Hook, S.A., Nelson, C.A., & Mead, P.S. (2021). West Nile virus: Biology, transmission, and human infection. *Clinical Microbiology Reviews, 35*(1), e00103-21. https://doi.org/10.1128/CMR.00103-21

21 Anderson, J.F., Andreadis, T.G., Vossbrinck, C.R., Tirrell, S., Wakem, E.M., French, R.A., & Garmendia, A.E. (1999). Isolation of West Nile virus from mosquitoes, crows, and a Cooper's hawk in Connecticut. *Science, 286,* 2331–2333. https://doi.org/10.1126/science.286.5448.233

22 Grazhdanov, A.K., Ayazbayev, T.Z., Toporkov, A.V., Bidashko, F.G., Zakharov, A.V., Belonozhkina, L.B., Pak, M.V., & Andryushchenko, A.V. (2014). O vyiavlenii novykh prirodnykh ochagov aktualnykh infektsionnykh boleznei na zapade Kazakhstana [Identification of new natural foci of infectious diseases in western Kazakhstan]. *Problemy osobo opasnykh infektsii — Problems of especially dangerous infections,* 3, 20–24 [in Russian].

23 Alibekova, D.A., Barakbayev, K.B., Omarova, Z.D., Rystaeva, R.A., Sultankulova, K.T., Burashev, Y.D., Argimbayeva, T.U., Tulendibayev, A.B., Aubakir, N.A., Yermekbay, T.T., Abeuov, K.B., Kerimbayev, A.A., & Orynbaev, M.B. (2025). Serological investigations on West Nile virus in horses in Kazakhstan. *Microorganisms, 13,* Art. 2541. https://doi.org/10.3390/microorganisms13112541

24 World Organisation for Animal Health (WOAH) (2023). West Nile fever. In Manual of diagnostic tests and vaccines for terrestrial animals. Paris: WOAH.

25 Metz, M.B.C., Olufemi, O.T., Daly, J.M., & Barba, M. (2021). Systematic review and meta-analysis of seroprevalence studies of West Nile virus in equids in Europe between 2001 and 2018. *Transboundary and Emerging Diseases, 68*(4), 1814–1823. https://doi.org/10.1111/tbed.13866

26 Centers for Disease Control and Prevention. (2022). West Nile virus: Veterinary impact. *www.cdc.gov*. Retrieved from https://www.cdc.gov/westnile/veterinarians/index.html

27 Platonov, A.E., Fedorova, M.V., Karan, L.S., Shopenskaya, T.A., Platonova, O.V., & Zhuravlev, V. I. (2008). Epidemiology of West Nile infection in Volgograd, Russia, in relation to climate change and mosquito bionomics. *Parasitology Research, 103*(Suppl. 1), S45–S53. https://doi.org/10.1007/s00436-008-1050-0

28 Platonov, A.E., Shipulin, G.A., Shipulina, O.Y., Tyutyunnik, E.N., Frolochkina, T.I., Lanciotti, R.S., Yazyshina, S., Platonova, O.V., Obukhov, I.L., Zhukov, A.N., Vengerov, Y.Y., & Pokrovskii, V.I. (2001). Outbreak of West Nile virus infection, Volgograd Region, Russia, 1999. *Emerging Infectious Diseases, 7*(1), 128–132. https://doi.org/10.3201/eid0701.010118

29 Nurmakhanov, T., Sansyzbaev, Y., Atshabar, B., Berlin, V., Kobzhasarov, D., Yeskhojayev, O., Vilkova, A., Ayazbayev, T., Andryushchenko, A., Bidashko, F., Hay, J., & Shvetsov, A. (2021). Phylogenetic characteristics of West Nile virus isolated from *Culex modestus mosquitoes* in West Kazakhstan. *Frontiers in Public Health, 8,* Art. 575187. https://doi.org/10.3389/fpubh.2020.575187

30 Grazhdanov, A.K., Kozhanova, O.I., Toporkov, A.V., Ayazbayev, T.Z., Matveeva, N.I., Karnaukhov, I.G., Popov, N.V., Razdorskii, A.S., & Arkhipova, G.N. (2013). Sravnitelnyi analiz proiavlenii opasnykh infektsii v Saratovskoi i Zapadno-Kazakhstanskoi oblastiakh v tseliakh sovremennoi otsenki epidemiologicheskikh riskov [Comparative analysis of dangerous infections in Saratov and West Kazakhstan regions]. *Problemy osobo opasnykh infektsii — Problems of especially dangerous infections,* 4, 38–44 [in Russian].

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