



Abstract

The aim of this study is to identify possible reservoirs of the camelpox virus in Western Kazakhstan. Despite considerable efforts by researchers, the natural reservoir of the virus remains unknown and represents a significant challenge. It is hypothesized that camelpox virus may persist in a latent form within camels themselves or between outbreaks in rodent or arthropod reservoirs. The findings of this study will contribute to identifying the etiology of the virus in collected samples and can be used for mapping, monitoring, and controlling the spread of the disease in Western Kazakhstan. Determining potential virus reservoirs will help prevent large-scale outbreaks and assist in effective eradication strategies.

Relevance: Camelpox virus belongs to the Orthopoxvirus genus, which includes the viruses of smallpox, cowpox, and monkeypox. The genomic sequence identity among these viruses ranges from 94% to 98.6%, raising concerns among researchers about the potential for the virus to become pathogenic to humans through genome modifications. After a 24-year absence, a camelpox outbreak has re-emerged in Western Kazakhstan. The disease manifests in a severe form in young camels, with a mortality rate of up to 30%. In adult animals (over 4 years old), despite pronounced generalized symptoms, mortality does not exceed 4–7%.

Introduction

The Republic of Kazakhstan is traditionally one of the world's leading producers of camel milk. The camel population in the country is increasing every year, making optimal management of these animals critically important. Sudden outbreaks of infectious diseases pose serious challenges to maintaining and expanding the camel population, improving productivity, and enhancing product quality – all of which significantly impact the national economy. One of these infectious diseases is camelpox.



Figure 2: Biological Sample Collection

1. Method of trapping small mammals (rodents) using live traps (mesh or box-type).
2. Types of camels (dromedaries and Bactrian camels) inhabiting the Mangystau Region.
3. Types of ticks – *Hyalomma dromedarii* (a - unfed; b - engorged).

Results

Camelpox virus identification in the samples was conducted using real-time PCR. All collected blood samples from camels and rodents, as well as ticks and insects, were tested for the presence of camelpox virus DNA. As a result, 21 out of 300 camel blood samples tested positive for camelpox virus.



Camel serum and blood samples were tested for camelpox antibodies using ELISA and virus neutralization (VN) tests. ELISA results showed that 86 out of 150 adult camel serum samples were positive for camelpox antibodies, while no antibodies were detected in the young animals. Among 80 tick samples tested, 2 samples were positive for camelpox virus DNA. No antibodies or viral DNA were detected in serum samples from rodents or blood-sucking insects.

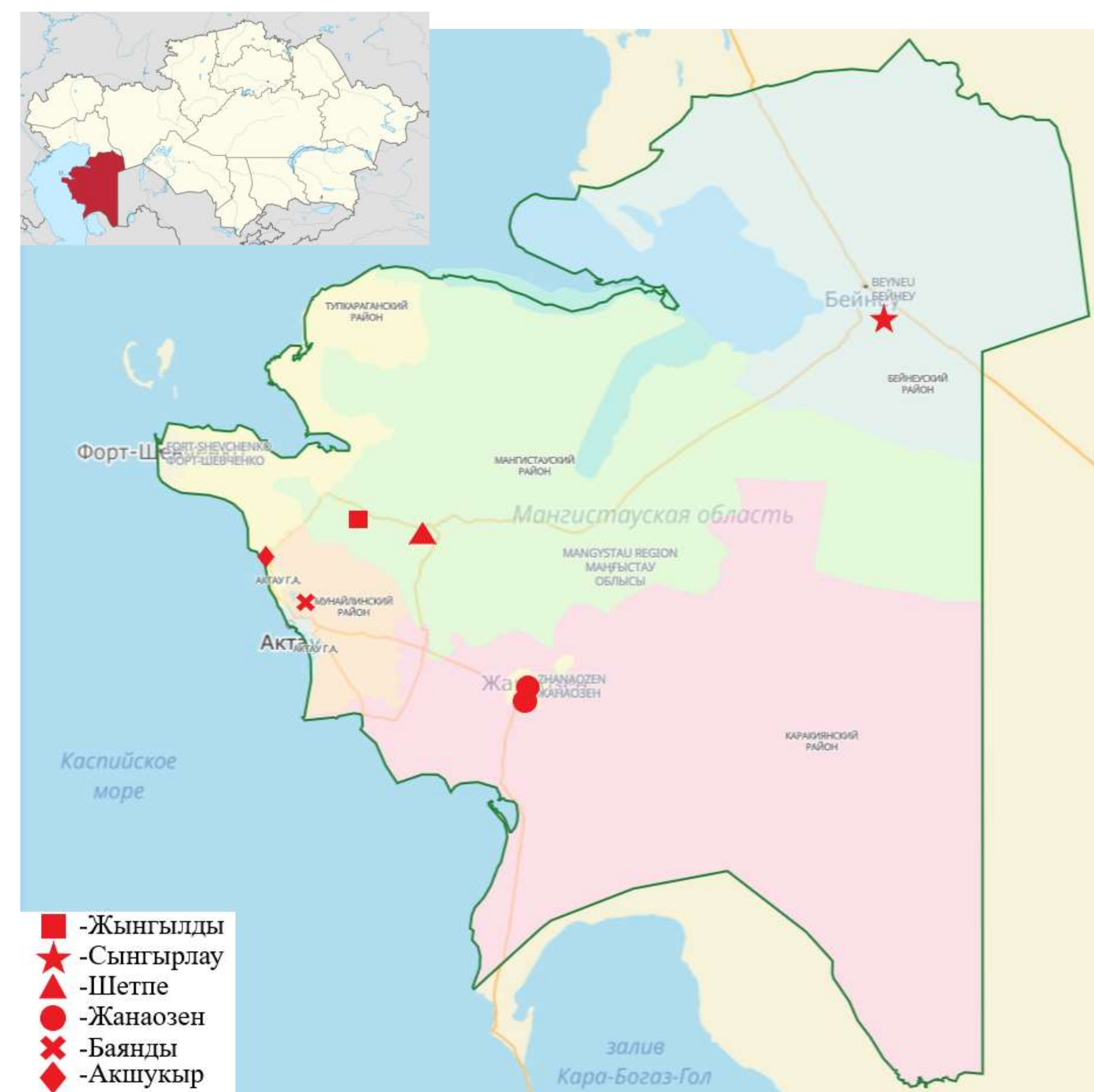
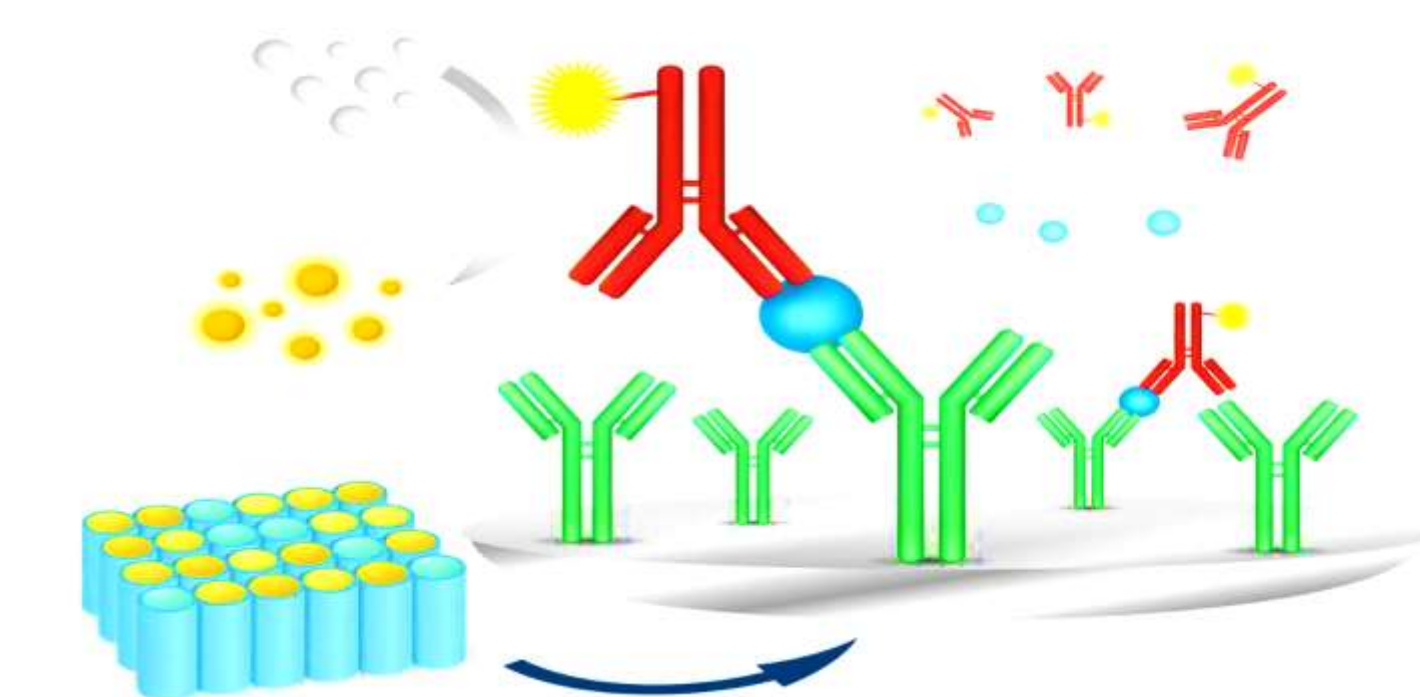


Figure 1: Sampling Locations Districts of the Mangystau Region where biological samples were collected from camels, rodents, *Hyalomma dromedarii* ticks, and blood-sucking insects.

Progress of work

An expedition was conducted across livestock farms in the Mangystau Region (Beineu, Karakiyan, Mangystau, Munaily, and Tupkaragan districts) to collect biological samples from camels and rodents and to gather ticks and blood-sucking insects. A total of 300 blood and serum samples were collected from camels (150 from young animals, n=30/district; 150 from adults, n=30/district), 50 rodent serum samples (n=10/district), 100 insect samples (n=20/district), and 80 tick samples (n=20/district). No camel ticks were found in the Beineu district due to recent tick control measures.



Next steps: Differences in the nucleotide sequences of the camelpox virus DNA will be analyzed across ticks, rodents, insects, and camels. The results will help determine the viral etiology in these samples and support disease mapping, monitoring, and control efforts in Western Kazakhstan.

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