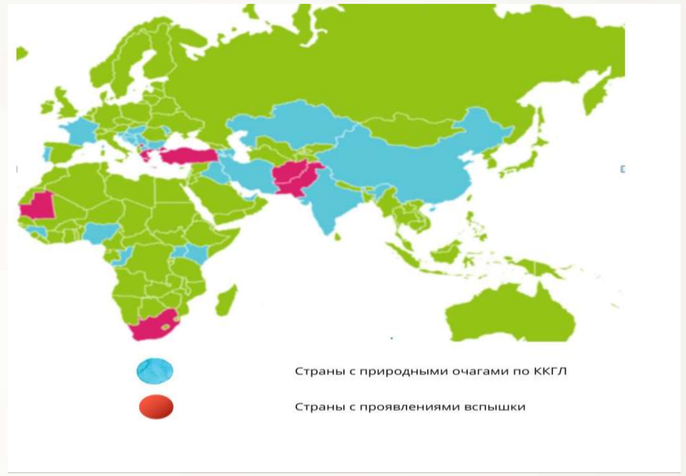
IRN AP23488595 "Crimean-Congo Hemorrhagic Fever: Monitoring and Study of Molecular-Genetic and Biological Characteristics of the Pathogen" (2024–2026)

Project manager: Doctor of Biological Sciences, Professor Zh.K. Koshemotov.

Annotation

For the first time, a study on the epizootiological situation of Crimean-Congo Hemorrhagic Fever (CCHF) is being conducted in central Kazakhstan, as previously its circulation was confirmed only in the southern, northern, and western regions. Monitoring will be carried out in the Karaganda and Ulytau regions, including sampling of blood from cattle and small ruminants (SR), as well as ticks, for molecular-genetic and immunological analyses. The biological properties of viral strains will be studied, a phylogenetic tree will be constructed, strain passports will be compiled, and anti-epizootic recommendations will be developed. The project is aimed at strengthening the surveillance system for CCHF and training specialists in epizootiology and virology.



Purpose and objectives

Objective:
The objective of the study is to conduct monitoring of Crimean-Congo Hemorrhagic Fever in the central region of the Republic of Kazakhstan and to study the molecular-genetic and biological characteristics of the virus.

Tasks:

- To achieve the project's goals, the following tasks will be completed:
- Organize and conduct monitoring studies on the incidence of CCHF in Kazakhstan.
- Apply molecular and immunological methods to identify and detect the CCHF virus in collected samples.
- Study the biological properties of the isolated CCHF virus strains.
- Analyze the molecular-genetic characteristics of the isolated virus strains.
- Develop recommendations for anti-epizootic measures against CCHF for veterinary service personnel in the Republic.

Methods and materials

Monitoring studies will be carried out in the Karaganda and Ulytau regions, which border endemic areas. Blood samples from cattle and small ruminants (50 from each region), along with tick samples (3 pools, 5–6 individuals per pool), will be collected and transported to a BSL-3 laboratory. Viral RNA will be extracted using the QIAamp Viral DNA Mini Kit (Qiagen), followed by real-time PCR and ELISA to detect the pathogen and antibodies. Virus cultivation will be performed in Vero-E6 cells and newborn white mice. Genetic typing will include sequencing of the S, M, and L genome segments, followed by phylogenetic analysis. The findings will be analyzed using GraphPad Prism 6.0 and used to formulate veterinary recommendations.

Results and discussion

In 2024, an epizootiological survey of CCHF was conducted in the Ulytau and Karaganda regions to assess the risk of infection spread. Considering the expanding natural focus areas in Kazakhstan, the study examined factors contributing to the virus's range expansion. During the expedition, 700 blood and serum samples from cattle and small ruminants and 21 tick samples were collected. Real-time PCR and ELISA revealed CCHF viral RNA in one tick sample from Karazhal (Ulytau region) and antibodies in two SR serum samples. The isolated strain, "Kazakhstan/Karazhal/11/2024," was successfully cultivated in Vero and PK-15 cells as well as in white mice, confirming its antigenic properties. Molecular-genetic analysis showed that the strain belongs to the Asia-1 lineage. Sequencing of the S segment revealed 100% identity with isolate KX096770.1, previously detected in South Kazakhstan in 2016. The data obtained allow for forecasting the spread of CCHF and developing preventive measures.

Contacts

email: zh.koshemetov@biosafety.kz