

<b>Наименование проекта, ИРН</b>	<b>AP23490023</b> Lumpy skin disease: main vectors, distribution area, public awareness and genetic characteristics of a recombinant vaccine-like strain circulating in Kazakhstan
<b>Сроки реализации</b>	01.01.2024-31.12.2026
<b>Руководитель проекта</b>	Issimov Arman, PhD
<b>Реферат</b>	The project is aimed at studying the epizootic situation of nodular dermatitis (ND) among unvaccinated cattle (cattle) in Northern and Western Kazakhstan. For the first time, complete nucleotide gene sequences of recombinant vaccine-like virus strains circulating in Kazakhstan will be determined. The results of the project will form the basis for assessing the effect of recombination on virulence and transmission capacity of the virus, as well as for the development of an inactivated vaccine. The project supports animal health protection, ND prevention and improvement of veterinary safety. The data obtained will contribute to improving diagnosis, monitoring and reporting, as well as raising awareness about ND in Central Asian countries.
<b>Цели</b>	The aim of the project is to identify the nodular dermatitis virus (GND), determine the main vectors of its transmission (vectors), analyze the geographical distribution, as well as the genetic characteristics of the virus circulating in the territory of the republic of Kazakhstan.
<b>Ожидаемые результаты</b>	<ul style="list-style-type: none"> <li>• Sampling of biological material from animals, as well as catching flies and ticks for testing for the presence of GNI.</li> <li>• Carrying out the determination of antibodies and DNA of GNI in the studied animal samples. It is expected that some of the analyzed samples will be positive for antibodies and DNA of the ND virus, which will reveal recombinant events associated with vaccine-like field isolates circulating in Kazakhstan.</li> <li>• Establishment of species belonging of flies <i>Stomoxys</i> spp. and ticks <i>Ixodes</i> spp. as the main vectors of GNI living on the territory of Kazakhstan.</li> <li>• Sequencing to compare genomic components with a phylogenetic tree in order to determine the origin of the virus.</li> <li>• Conducting a survey of farmers and veterinary specialists by random sampling in areas without a history of vaccination located in the north and west of the country.</li> </ul>
<b>Исследовательская группа</b>	<p><i>Head:</i> Arman Isimov, PhD  ORCID 0000-0002-0486-0054; Scopus Author ID 57215650499  web of Science-6.0, Scopus - 8.0.  Kutumbetov Lespek, doctor of veterinary science, professor.  Hirsch index (h-index) web of Science-8.0, Scopus - 9.0. • Scopus Author ID 56204110000;  ORCID 0000-0001-8481-0673  Zhugunisov Kuandyk, PhD, has more than 15 publications Scopus Author ID 56784395500; ORCID 0000-0003-4238-5116  Nisanova Raikhan, K. B. N, More than 10 publications Scopus Author ID 56149053800  Sarzhigitova Asylai, Master of Science, Hirsch index (h-index) Scopus-1, Scopus Author ID 58141523200; ORCID 0000-0002-0394-4053  Kemalova Nazerke, Master of Science ORCID 0000-0002-1507-</p>

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