

# IRN AP19677632 “Metagenomics of the microbiome of ixodid ticks in Kazakhstan” 2023-2025.

Project leader: Sultankulova K.T., Ph.D., professor



## Purpose of the work

Study of microbiological diversity of pathogens of ixodid ticks of Kazakhstan by the method of next generation sequencing (NGS) in identification of pathogens of tick-borne infections and analysis of metagenomic data

## Tasks

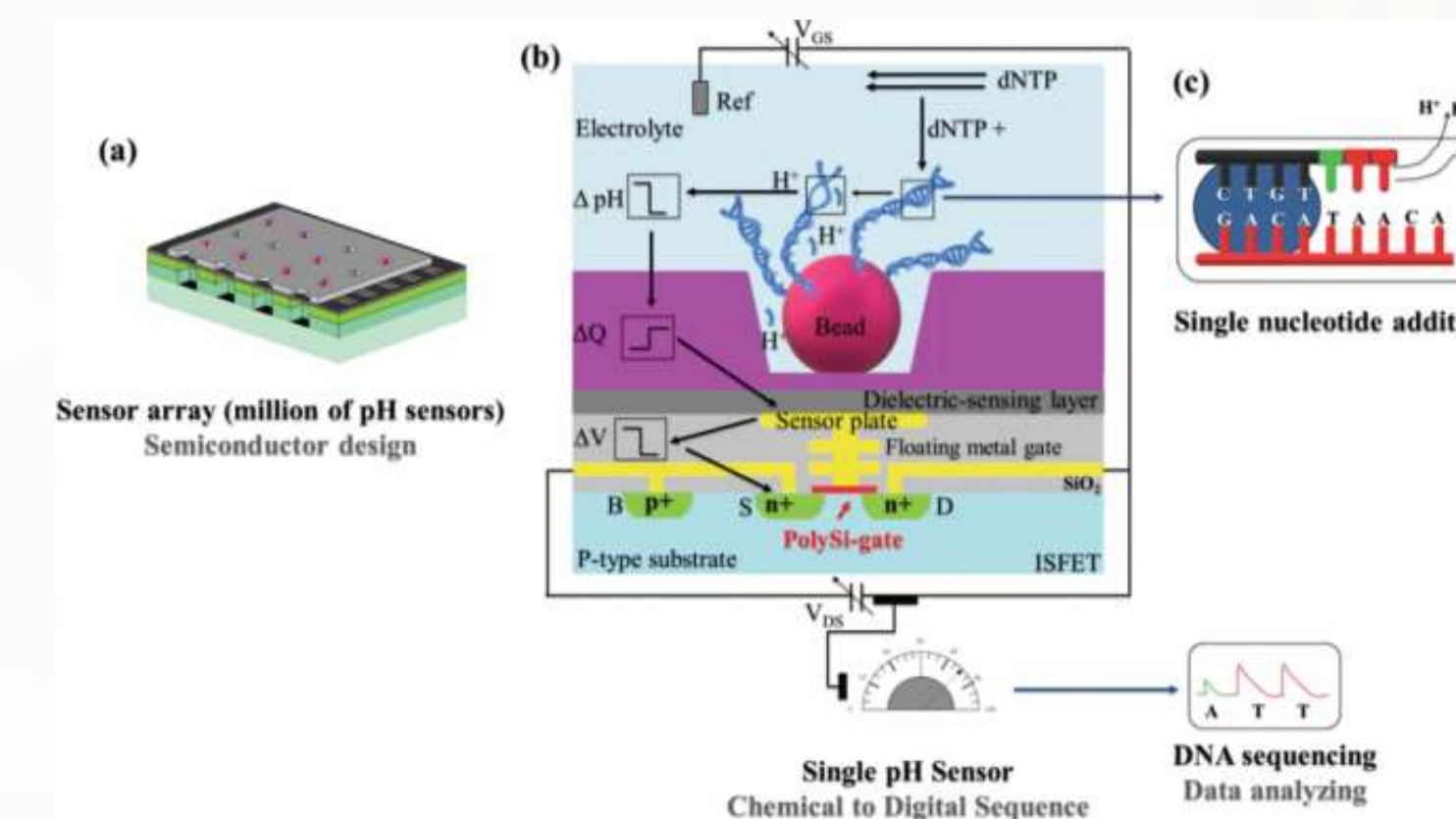
1. Analysis of Tick Microbiome and Assessment of the Current Status of Natural Foci of Tick-Borne Pathogens in the Republic of Kazakhstan.
2. Organization and Implementation of an Expedition to Collect Tick Biological Material from Various Regions of Kazakhstan.
3. Molecular-Genetic Identification of Ixodid Ticks. The species affiliation of ticks will be determined through molecular-genetic analysis.
4. Tick Microbiome Analysis via NGS Sequencing. NGS sequencing of the tick microbiome will be conducted. An algorithm will be developed to analyze data generated using the Ion GeneStudio™ S5 platform. Bioinformatic processing of genetic information will be performed. The genus- and species-level composition of the microbiome will be identified. Taxonomic annotation of the tick microbiome will be carried out. Regional differences in the tick microbiome across Kazakhstan will be assessed using metagenomic data. A digital map will be created using GIS software. A gene catalog of the microbiome of ixodid ticks in Kazakhstan will be compiled. A repository for storing metagenomic sequencing data, microbial genes, and genomes will be established. The role of metagenomic analysis of the tick microbiome in preventing biological threats from natural foci of dangerous infections will be evaluated.



<https://msk.sesuslugi.ru/info/kleshchi/139-iksodovye-kleschi.html>



<https://www.medical-xprt.com/products/ion-genestudio-model-s5-ngs-system>



[https://www.google.com/search?q=NGS+Ion&sca\\_esv](https://www.google.com/search?q=NGS+Ion&sca_esv)

## Expected results

The microbiological diversity of pathogens in ixodid ticks will be determined using NGS sequencing for the identification of tick-borne pathogens, including anthrozoonotic, asymptomatic, and rare microorganisms. A gene and genome catalog of the tick microbiome will be compiled. Additionally, a repository will be established for storing metagenomic sequencing data, microbial genes, and genomes. Comprehensive data on the microbiological diversity of ixodid tick pathogens in Kazakhstan will be presented, which may serve as a foundation for effective and targeted control of infectious diseases.