WEB-BASED REPOSITORY FOR SPATIAL MONITORING VIRAL TICK-BORNE PATHOGENS[1]

Molorodov Yu.I., Chernenko V.V., Fedotov A.M.

Abstract A study of the genetic diversity of tick-borne encephalitis (TBE) in the samples of individual ticks *I. persulcatus* and *I. pavlovskiy*, is one of the urgent problems of modern molecular biology and bioinformatics to come after 2000, "the post-genomic era". Basically, this is due to the complete sequencing of genomes as part of large-scale international programs. This study suggests combining existing computer resources and databases on molecular biology.

An important task of research in this direction was to evaluate the molecular and genetic diversity of bacteria *Borrelia spp.* Circulating on the territory of Siberia. For further cultivation of the full genome sequencing was carried out two types of Borrelia, selected genetic variants often detected in Western Siberia. Another of the objectives is to determine the molecular genetic diversity of potentially pathogenic microorganisms to humans (tick-borne encephalitis virus, anaplasma, ehrlichia, babesia).

On the basis of factual material for the collection of mites in field expeditions on the territory of the Altai, Kazakhstan and Siberia, and the results of whole genome sequencing, developed the architecture and created a pilot version of an interactive information system (IS), intended for the organization of the collection, storage and processing of field work, resettlement and Migration ticks and they carry pathogens. With it built an interactive map displaying locations of field gathering and habitat areas, including sections of publications show the number of ticks and mites population by sex. The possibility of watching the occurrence of infections and genes. Created block analysis of existing da

Key words: Interactivity, information systems, data integration, mites, sequencing, Lyme disease, encephalitis.

AMS Mathematics Subject Classification: 68U35, 92D20, 92D25, 97R50

1 Introduction

Russia — one of the world's largest areas of infectious diseases transmitted by ticks. Ticks are found in a wide variety of geographical landscapes, which are related to the existence of natural foci of infectious diseases. tick species have been found quite a lot. The indicator is the date of their initial descriptions: *I. persulcatus [Schulze 1930]*, *Ixodes pavlovskyi [Pomerantzev 1946]*, *Ixodes kashmiricus [Pomerantzev 1948]*, *Ixodes riipponensis [Kitaoka et Saito 1967]*, *Ixodes kazakstani [Olenev et Sorokoumov 1934]*, and *I. ricinus [L. 1758]*. Also *taiga Ixodes* persulcatus showed even more dangerous *Ixodes pavlovskyi*.

These insects are carriers of various infections: tick-borne encephalitis, Lyme disease, ehrlichiosis and others. The most common is the tick-borne (epidemic) encephalitis. Serious complications of acute infections may end paralysis and death. The problem is that "the list of infectious agents carried by ticks, is constantly growing, but the set of suitable diagnostics, vaccines and drugs is replenished much slower." Natural foci of tick-borne encephalitis are registered in all forest and taiga regions. Particularly high incidence in the Urals, the Urals and Siberia [1, 2].

In Siberia, a carrier of the pathogen heavy (with mortality rates up to 25% during the outbreaks) disease — *encephalitis* — traditionally considered *Ixodes persulcatus*, taiga tick he is [2]. In recent years, it began to spread rapidly *pavlovskyi Ixodes* — the most dangerous infections carrier. According to the survey the surrounding area of the Novosibirsk Scientific Center — infection of *Ixodes pavlovsky*i virus encephalitis, pathogenic for laboratory mice (and humans) is almost three times higher than that collected in the same area *Ixodes persulcatus* [3].

These circumstances were the cause of the beginning of the development of an interactive information system (IS) *"Genomics of tick-borne pathogen"* [2] [4]. You can use it to fill up, store and process field data for resettlement, migration of ticks and the pathogens they carry. In addition to specifying pathogens modern diagnostic tools based on sequencing algorithms it had yet to build an interactive map displaying locations of field work. For experts it became necessary to realize the possibility of viewing the number of ticks in the field of observation dates and geographical locations of the work, the number of ticks view by type and gender and the ability to view the occurrence of infections and genes.

Controlling the spread of the main tick vectors and their Borrelia infection, carried by a regular analysis of the state of natural foci for field observations [2]. The study of natural foci was carried out in ten administrative areas (Omsk, Kurgan, Novosibirsk, Tomsk, Tyumen and Chelyabinsk regions, Altai, Krasnoyarsk and Primorsky regions and the Altai Republic), located in different landscape-geographical zones.

2   Statement of the problem and the method of description.

In order to ensure effective prevention requires a spatial and temporal analysis of the spread of mites, including infection by different pathogens. In this regard, one of the most promising ways to control infectious agents can be a system of ongoing monitoring.

The technology of determining the sequence of DNA nucleotides entire genome (sequencing) provides the ability to analyze the relationship of polymorphism of hundreds of thousands of SNP (Single Nucleotide Polymorphism) — markers scattered throughout the genome, with a set of tick-borne pathogens.

The test procedure involves the taking of biological material, DNA isolation, genotyping on chips and statistical analysis of the data.

The first step towards the creation of such a system is a spatial and temporal analysis, on the basis of geoinformation technologies, contamination of certain territories of Siberia, Altai and Kazakhstan pathogenic viruses transmitted by ticks [2, 3, 5].

---

[2]http://tick1.ict.sbras.ru/

To work with the collected modern interactive information system (IS) "Genomics of tick-borne patho-gen"[3] was developed by the material [4]. With it came the possibility of replenishment, storage and processing of field data for dispersal, migration of ticks and the pathogens they carry. In addition to specifying pathogens modern diagnostic tools based on sequencing algorithms, algorithms with an interactive map was designed with the ability to display spots insect collection and information about them, including the publication of research materials. For experts it became necessary to realize the possibility of viewing the number of ticks in the field of observation dates and geographical locations of the work, the number of ticks view by type and gender and the ability to view the occurrence of infections and genes.

2.1 The information system's architecture.

The architecture of the IP identify its components, their functions and interactions. The system is based on the "client – server" technology and consists of a client-side, server and MySQL database. The customer describes the architecture stands browser (user) and server - web server. The logic of the system is distributed between the server and client data storage is carried out in the MySQL database, information is exchanged over the network. An important advantage of this approach is the fact that customers do not depend on a particular user's operating system, so the system is a cross-platform service.

An important component is the client part of the application (see Figure 1). It is based on the use of map service based on Leaflet library. This is an innovative, open source, JavaScript library. With its help, vector map is displayed, which is loaded with service MapBox[4]. Service MapBox offers a large selection of different maps, which may differ in design, language titles on the map and other parameters. As a source for the formation of accurate maps, MapBox uses OpenStreetMap[5] service. OpenStreetMap — a non-profit, open source project that provides the exact coordinates of all the objects that are on the map. Our service uses OpenStreetMap to determine the areas of polygons that form a visual interface to the user.

Showing information on a geographical map is supplemented by elements of the statistical analysis of the data accumulated over several years. For this we use Google Charts library[6]. It is written in JavaScript, for constructing combined histograms, bar charts, calendar schedules, pie charts.

2.2 The information system's basic modules.

The functional information system IS provides a set of software implementations made in the form of individual modules. The most important of them:

1. The data import module loads the data from the format `*.csv` file to the database;
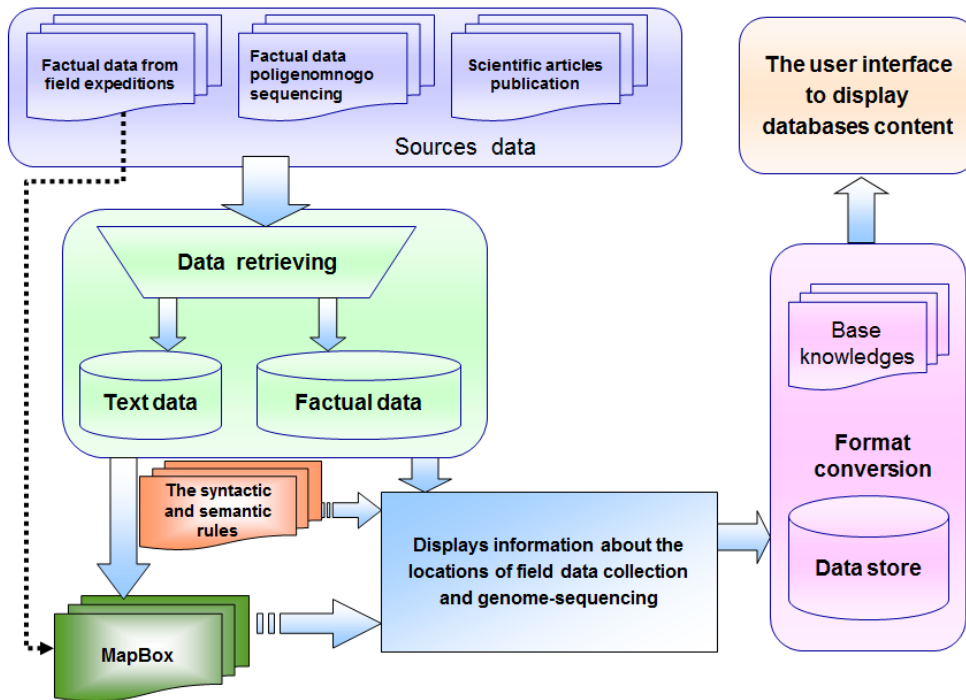

Figure 1: Functional diagram of the information system.

2. MySQL — database management system, all data is stored in the database acarids data;

3. The data processing unit on the server is responsible for the unloading of the data from the database, and integration of data changes in the database;

4. Modules for tracking users — responds to a user action and depending on the logical value selects the desired action;

5. The imaging module is responsible for displaying information on the screen;

6. Edit the module — the component responsible for the editing of information;

7. The module loading new data;

8. Requests module — component responsible for displaying information on the variability of genes and infections.

Each module performs a separate function. If necessary, make changes to one or the other module just need to change a specific function. Each module can be expanded and improved, adding new functionality.

3   Display data and analysis results.

To launch the browser user enters the URL-address of information system[7]. On the client side browser performs rendering the resulting code and present the user with a set of visual controls: interactive maps, navigation tools and zoom and switching card type instruments (see Figure 2).
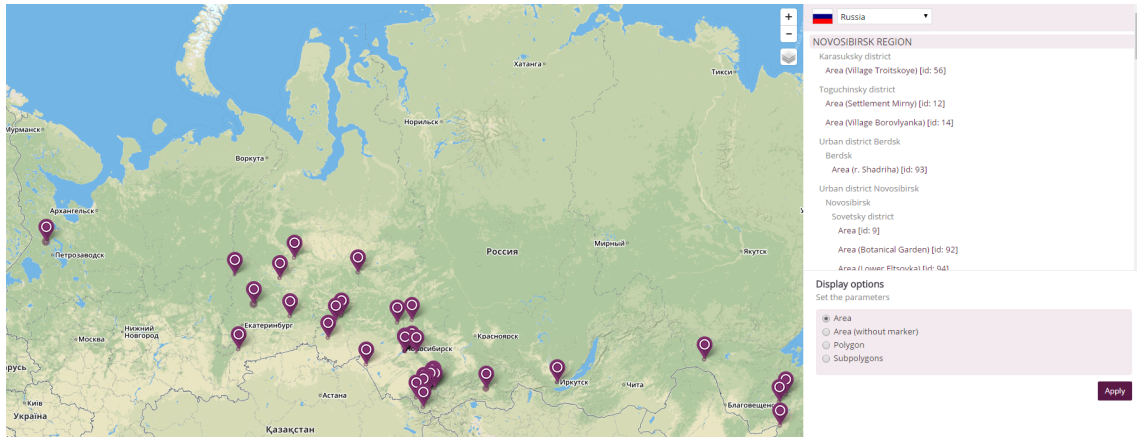

Figure 2: The user interface.

Interactive map — is the main component of the system interface. Interactive mode allows you to easily move around the map and zoom.

On the left is a window that displays a map and the location of her field. It occupies a large part of the interface. The map can zoom, delete. You can change the map view, this creates a corresponding button in the upper right corner of the window. On the map are located markers that point out the places where fieldwork was conducted. Click on the marker, leads to recommend measures The appearance information on the data obtained on the site.

At the top right of the interface is a window, which presents a hierarchical list of all the areas. Here you can select the country, areas in which we want to see. In the hierarchy list, you can select an area, if it's just the area, you will see lots of research on the territory of this region, if this is an area of вЪ<вЪ<research, it opens the statistics for a given site.

List hierarchy receives a request to table fields, then recursively generated processing function.

On the map markers displayed muster field studies mites. Navigation tools and scalability — consists of various buttons that provide navigation, and the map zooms.

Objects on the map have different attribute information (see Figure 3), which pops up a window when the marker is clicked as shown in Figure 2. It comprises: a physical name, administrative name, the research period, the climate, the coordinates detected mites, publication number of ticks, mites sex population, the incidence of infections and genes.
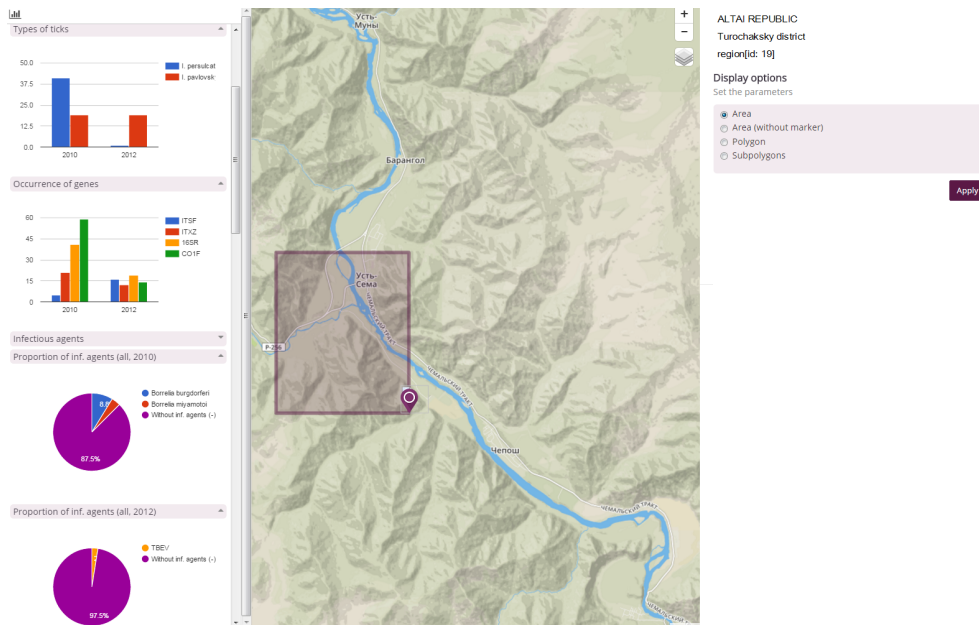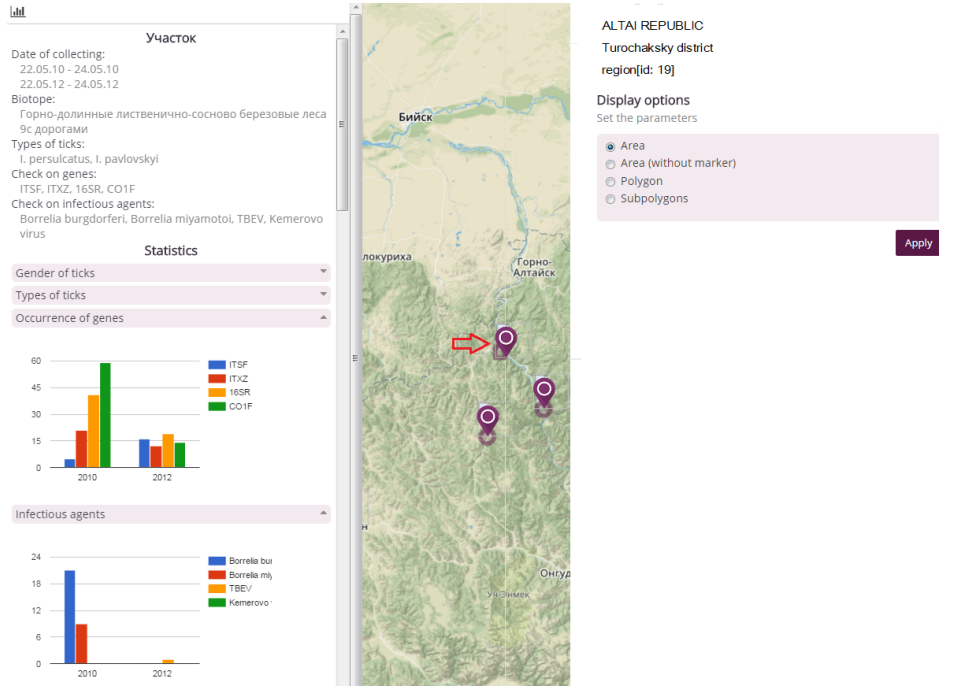
---

[7]http://ixodes.ict.nsc.ru

Figure 3: Windows with attribute information.

4   Conclusion.

Developed an interactive information system (IS), to work with the results of field work, including the resettlement of data migration and ticks they carry viral pathogens. EC contains a database with tables containing information on the data of field work. Designed server and client parts of the information system, built an interactive map displaying locations of field gathering and information about them. The possibility of updating and editing of data on local field training camp and found ticks, developed the ability to view the number of ticks on the floor. Developed the ability to view the occurrence of infections and genes.

References

[1] Ruzjnikov G. and other. *Modern technologies of information and analytical evaluation* // SB RAMS Bulletin, Volume 32, number 6, 57 2012, p. 55–59. (In Russ.)

[2] N.N. Livanova, Borgoyakov V.Y., Livanov S.G., Fomenko N.V. *Characteristics of natural foci of tick borreliosis. Novosibirsk Scientific Center and the Novosibirsk Region* // Siberian Journal of Medicine, 2012 V.111, N. 4, pp 20–23. (In Russ.)

[3] Tkachev S., Panov V., Dobler G., Tikunova N. *First detection of Kemerovo virus in Ixodes pavlovskyi and Ixodes persulcatus ticks collected in Novosibirsk region.*// Russia. Ticks tick-borne dis. 2014, 5:494–496.

[4] Maltsev V.Y., Molorodov Yu.I., Skachkov D.M. *Extraction technology in-formation about the natural habitat of species of bacterial pathogens transferability-pendent ticks* // XV Russian conference with international participation "The distributed information — computing resources" 2 – 5 December 2014, Novosibirsk. — `http://konf.ict.nsc.ru/dicr2014/reportview/249374`. (In Russ.)

[5] Rar V., Epikhina T., Yakimenko V., Malkova M., Tancev A., Bondarenko E., Ivanov M., Tikunova N. *Genetic variability of Anaplasma phagocytophilum in ticks and voles from Ixodes persulcatus/Ixodes trianguliceps sympatric areas from Western Siberia.* // Russia. Ticks tick-borne dis. 2014, 5:854–863.

Molorodov Yu.I.,
Institution, Institute of Computational Technologies SB RAS
Address, 6 Acad. Lavrentjev av., 630090 Novosibirsk, Russia
Email: `yumo@ict.sbras.ru`,
Chernenko V.V.,
Novosibirsk State University
Address, 2 Pirogova str., 630090 Novosibirsk, Russia
Email: `vlavlad.chernenko@gmail.com`,
Fedotov A.M.
Institution, Institute of Computational Technologies SB RAS
Address, 6 Acad. Lavrentjev av., 630090 Novosibirsk, Russia
E-mail: `fedotov@sbras.ru`