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GENETIC DETERMINANTS CHARACTERISTIC FOR *YERSINIA PSEUDOTUBERCULOSIS* STRAINS ISOLATED FROM PATIENTS WITH FAR-EAST SCARLETT-LIKE FEVER

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The illness caused by *Yersinia pseudotuberculosis*, which was firstly described in Russia (Vladivostok, 1959) and named Far East Scarlett-like Fever (FESLF), is manifested via fever, rash and injury of liver and joints. Our study was aimed to reveal phylogenetic relationships of the FESLF isolates with the *Y. pseudotuberculosis* population. Totally, 64 *Y. pseudotuberculosis* strains including 37 isolates from 6 FESLF outbreaks and 19 sporadic cases were used. A previously described MLST scheme was used to characterize clonal diversity. MLST analysis was extended by sequencing virulence genes *inv, yadA*, *yopE, cnf*. We found three MLST types among FESLF isolates: ST2 (n = 33), ST26 (n = 5), and ST32 (n = 3; specific for serotype O3). All but 1 vegetable isolate belonged to ST2, which was also found in 9 (60%) of 15 rodent isolates. ST2 prevailed among isolates from all sources. The ST2/ST26/ST32 sequence types formed a cluster at the eBURST scheme with ST2 and ST32 belonged to separating subclusters descended from ST26. Combining MLST with virulence gene sequence typing gave rise to 6 MVLST types. The concatenated sequences of 10 MVLST genes were used to build a maximum likelihood tree that divided into 2 subclades. One subclade united MVLSTs found in FESLF isolates and MVLST6, which was found in rodent isolates only. The second subclade united MVLSTs found in rodent and vegetable isolates. The analysis of virulence gene diversity revealed predominance of nonsynonymous substitutions among virulence genes, whereas basic parameters of nucleotide diversity were similar in virulence and housekeeping genes. Notably, unique *yopE* and *inv* alleles and a deletion of 946 bp in the *cnf* gene encoding cytonecrotizing toxin were found in all FESLF isolates independently on MLST type. The deletion in *cnf* resulted in a loss of the Rho-binding domain and toxin inactivation. The plasmid pYV was found in all strains. Additional plasmid pVM82 was found in all but 4 ST2 strains but not in other genotypes. The fact that full FESLF symptomatology is caused by several distinct genotypes supports the view that specific virulence traits are characteristic of FESLF-associated strains and suggests that the dominance of the ST2 genotype could be caused by its epidemiologic advantages rather than its pathogenic traits. This suggestion was supported by evolutionary analysis that rejected the hypothesis of equality of evolutionary rates for ST2 and other genotypes ($p < 0.05$).

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DYNAMICS OF MORBIDITY OF THE WEST NILE FEVER IN THE ASTRAKHAN REGION

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The variety and wide prevalence of arbovirus infections, the possibility of adverse outcomes determine the relevance of their study. In the territory of the Astrakhan region the epidemic focus of West Nile Fever is registered. The purpose of this study was to analyze the dynamics of the morbidity of the West Nile Fever in the Astrakhan region from 2014 to 2017. The analysis of "Data on infectious and parasitic diseases" (Form 1) in the Astrakhan region was carried out.

As our research has shown, West Nile Fever in the Astrakhan region is currently characterized by a low intensity of the epidemic process. 5 people in the Astrakhan region were affected by the West Nile Fever in 2014, the morbidity rate per 100 000 of the population was 0.5. The number of cases increased by 3.0 and 4.8 times respectively in 2015 and 2016. 15 people fell ill with West Nile Fever in 2015, and 24 people — in 2016. The mortality rate per 100 000 of the population was equal to 1.5 and 2.4 respectively. It should be noted that the number of people with West Nile Fever in Russian Federation as a whole increased by 1.5 and 4.9 times in 2015 and 2016, compared to 2014. The source of infection in West Nile Fever is mainly wild birds. The increase in the incidence rate in 2015 and 2016 in the Astrakhan region and in Russia may be associated with increased infection of migratory birds during their seasonal migration from the natural foci of West Nile Fever. Only one case of West Nile Fever was registered in the Astrakhan region in 2017, the mortality rate per 100 000 of the population decreased in 24 times compared to the previous year and amounted to 0.1. Children under the age of 14 years were 11.1% of all the patients with this arbovirus infection from 2014 to 2017.

Thus, the natural focus of the West Nile Fever remains in the Astrakhan region, which activity depends on both the sources of infection and its vectors influenced by the intensity of the epidemic process in endemic foci, seasonal migration of sources of infection and climatic conditions.

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POSSIBILITIES OF NON-INVASIVE METODS APPLICATION FOR DIAGNOSIS OF YERSINIOSIS IN CHILDREN

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The term "*Y. enterocolitica* and *Y. pseudotuberculosis* infections" or "yersiniosis" is applied for two infectious diseases caused by Yersinia. These are pseudotuberculosis and intestinal yersiniosis followed by intoxication, injuries to the gastrointestinal tract and multiple organ disorders in case of miscellaneous and multi-disorder disease types. According to course duration of the disease it is classified as an acute (lasts for one month), a protracted (no longer than 3 months) and a chronic form (longer than six months). Nowadays in the acute period and at relapse of the disease bacteriological and PCR methods are used for diagnosis. Sokolova and co-authors (2016) analysed data of the diagnosis procedure of infants with acute diarrhea treated in an infectious diseases unit and proved 3 times more of yersiniosis to be dected by the PCR technique than by using bacteriological tests. Thus, non-invasive PCR technique should be used more widely for acute form *Y. enterocolitica* and *Y. pseudotuberculosis* infections diagnosis.

During the winter rise in the incidence of yersiniosis we investigated the appendix tissue (n = 60) taken from a surgical unit in the acute period of the disease of the children and demonstrated 20% of positive results obtained by PCR (11 DNA of *Y. pseudotuberculosis* and 1 DNA of *Y. entero-*