[Analysis of the Moscow population of Neisseria meningitidis strains by the method of multilocus sequencing-typing].

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Keywords: Cerebrospinal Fluid - microbiology
          DNA, Bacterial - genetics
          Humans
          Meningococcal Infections - microbiology - prevention & control
          Molecular Epidemiology
          Moscow - epidemiology
          Neisseria meningitidis - classification - genetics
          Sequence Analysis, DNA
          Serotyping
          Species Specificity

Abstract: The analysis of meningococcal strains of different serogroups, isolated from the liquor of patients in Moscow, which was carried out with the method of multilocus sequencing-typing (MLST), was presented. At the periods of epidemic morbidity rises in Moscow the prevalence of group A meningococcal strains, belonging to subgroups III with sequence-types 5 (in the 1970s) and 7 (in 1996), was noted, and at a period between epidemics strains of genetic subgroups VI and X were isolated. Meningococcal strains, groups B and C, isolated in 1995 - 2002, had, as a rule, unique sequence-types, differing both one from another and from N. meningitidis sequence-types detected in other countries. Among group B meningococci the prevalence of strains belonging to clonal complex ST-18 was noted, while for group C meningococci strains belonging to clonal complex ST-41/44 were most typical. Such genetic variability of circulating meningococci was regarded as characteristic of the period between epidemics, observed in Moscow since the end of the 1980s.

PubMed ID: 16758895 View in PubMed
The aim of the study was to perform molecular genetic analysis based on multi-locus sequence typing in order to identify source of Legionnaires' disease outbreak in town Verkhnyaya Pyshma in July 2007 and genetic profile of the causative agent. Sequence-based typing protocol recommended by European Working Group on Legionella infection (EWGIL) was used. It was not possible to obtain satisfactory results of Fla gene sequencing for all samples. Obtained allelic profiles of other genes were typical for L. pneumophila. Allelic profiles of L. pneumophila isolated from patients were identical and matched with L. pneumophila DNA detected in water from hot water supply of domestic building, but differed from cooling tower’s isolates and isolates from showerhead in apartment of one patient. Identity of 5 genes of L. pneumophila isolated from autopsy samples and from hot water of central hot water supply of domestic building confirms aspiration route of infection through hot water contaminated by the microorganism. L. pneumophila detected in water from cooling tower, showerhead in apartment of one patient, and from drainage canal of hot water supply station belonged to other allelic variants and, therefore, are not related with the outbreak.
The astroviral infections are considered among the most common pathogens of gastroenteritis in children. The incidence, molecular epidemiology and clinical manifestations of the astrovirus infection in children hospitalized with acute gastroenteritis, in various areas of the Russian Federation from 2004 to 2010 was determined.
The burden of tick-borne diseases in the Altai region of Russia.

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Keywords: Coinfection - epidemiology - microbiology - parasitology
Humans
Incidence
Lyme Disease - epidemiology - microbiology
Prevalence
Risk
Siberia - epidemiology
Spotted Fever Group Rickettsiosis - epidemiology - microbiology
Tick-Borne Diseases - epidemiology - microbiology - parasitology

Abstract: This article presents the results of a comprehensive survey of the burden of tick-borne infectious diseases (TBIDs) in the Altai region of Russia. Official data for TBID incidence were analyzed and 201 samples from patients with suspected TBID were studied. Furthermore, questing ticks and ticks recovered from humans were examined to estimate prevalence of TBID-causative agents. The Altai region was determined to have a heightened risk for TBIDs in Russia. The most epidemiologically significant tick-borne illness in this area is spotted fever group rickettsiosis, while nationally in Russia, the leading TBID is Lyme borreliosis. The prevalence of mixed infection was 12.4% among the studied cases. Additionally, the prevalence of poorly studied pathogens - Kemerovo virus (KEMV) and Rickettsia tarasevichiae - in ticks from the Altai region was determined.

PubMed ID: 28648773 View in PubMed
Sapoviruses were found, for the first time, to be circulating in children with acute gastroenteritis in the city of Moscow. On the basis of a genetic analysis, they were classified as belonging to genotypes 1 and 2. Two groups of sapoviruses that are essentially different from the strains presented now at the GenBank NCBI were described within the case study.

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Keywords: Africa, Western - epidemiology
Democratic Republic of the Congo
Disease Outbreaks - prevention & control
Ebolavirus - genetics - isolation & purification
Guinea - epidemiology
Hemorrhagic Fever, Ebola - diagnosis - epidemiology
Humans
RNA, Viral - genetics
Real-Time Polymerase Chain Reaction - methods
Reverse Transcriptase Polymerase Chain Reaction - methods
Russia
Sensitivity and specificity

Abstract: In early February 2014, an outbreak of the Ebola virus disease caused by Zaire ebolavirus (EBOV) occurred in Guinea; cases were also recorded in other West African countries with a combined population of approximately 25 million. A rapid, sensitive and inexpensive method for detecting EBOV is needed to effectively control such outbreak. Here, we report a real-time reverse-transcription PCR assay for Z. ebolavirus detection used by the Specialized Anti-epidemic Team of the Russian Federation during the Ebola virus disease prevention mission in the Republic of Guinea. The analytical sensitivity of the assay is $5 \times 10^{2}$ viral particles per ml, and high specificity is demonstrated using representative sampling of viral, bacterial and human nucleic acids. This assay can be applied successfully for detecting the West African strains of Z. ebolavirus as well as on strains isolated in the Democratic Republic of the Congo in 2014.

PubMed ID: 26597659 View in PubMed
Development and evaluation of the RT-PCR kit for the rabies virus diagnosis.

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Language: English

Publication Type: Journal Article

Keywords:
Animals
Cats
DNA Primers - chemical synthesis - genetics
Deer - virology
Dogs
Foxes - virology
Humans
RNA, Viral - genetics
Rabies - diagnosis - epidemiology - transmission - veterinary
Rabies virus - genetics - isolation & purification
Real-Time Polymerase Chain Reaction - methods - standards
Reverse Transcriptase Polymerase Chain Reaction - methods - standards
Russia - epidemiology
Sensitivity and specificity

Abstract: To improve the diagnosis, surveillance, and control for the rabies virus, a kit for hybridization-triggered fluorescence detection of rabies virus DNA by the RT-PCR technique was developed and evaluated. The analytical sensitivity of the kit was 4*10 GE per ml. High specificity of the kit was shown using representative sampling of viral, bacterial, and human nucleic acids.

PubMed ID: 29323857 View in PubMed
Development and evaluation of the RT-PCR kit for the rabies virus diagnosis.

https://arctichealth.org/en/permalink/ahliterature289725

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Language: English

Publication Type: Journal Article

Keywords: Animals
          Cats
          DNA Primers - chemical synthesis - genetics
          Deer - virology
          Dogs
          Foxes - virology
          Humans
          RNA, Viral - genetics
          Rabies - diagnosis - epidemiology - transmission - veterinary
          Rabies virus - genetics - isolation & purification
          Real-Time Polymerase Chain Reaction - methods - standards
          Reverse Transcriptase Polymerase Chain Reaction - methods - standards
          Russia - epidemiology
          Sensitivity and specificity

Abstract: To improve the diagnosis, surveillance, and control for the rabies virus, a kit for hybridization-triggered fluorescence detection of rabies virus DNA by the RT-PCR technique was developed and evaluated. The analytical sensitivity of the kit was 4*10 GE per ml. High specificity of the kit was shown using representative sampling of viral, bacterial, and human nucleic acids.

PubMed ID: 29323857 View in PubMed

[Development and use of the assay for Legionella pneumophila detection based on fluorescent real-time/endpoint polymerase-chain reaction].

https://arctichealth.org/en/permalink/ahliterature157285
Abstract: The aim of the work was to develop a PCR-based assay for detection of L. pneumophila and L. micdadei in environmental samples as well as in clinical samples from low respiratory tract and to assess its analytic characteristics. The assay was used during investigation of the outbreak developed in July 2007 in town Verkhnyaya Pyshma (Sverdlovsk region). Polymerase-chain reaction (PCR) with fluorescent detection, sequencing and cloning of DNA fragments were used. Developed assay based on the PCR with fluorescent real-time/endpoint detection is able to detect L. pneumophila in clinical and environmental samples and to quantify amount of bacterial DNA in water. Specificity of analysis (100%) was assessed using the panel of bacterial strains and samples from healthy individuals. Analytic sensitivity of assay and quantitation limit was 1000 GU in 1 ml. Sensitivity of the assay of artificially contaminated biological samples was 1000 bacteria in 1 ml. During outbreak investigation L. pneumophila DNA was detected in 4 lung samples from 4 fatal cases, from 1 of 2 sputum samples, 1 of 2 bronchoalveolar lavage samples with X-ray confirmed pneumonia. Legionella’s DNA was found in samples from cooling towers, central hot water supply as well as from showerheads in apartments of 3 patients. Fountain and drinking water samples were PCR-negative. Specificity of PCR-positive results was confirmed by sequencing. Use of the assay during outbreak investigation allowed to confirm the diagnosis in fatal cases and quickly identify the possible source of infection.

PubMed ID: 18464537 View in PubMed
Genetic characterization of Haemophilus influenzae type B strains isolated in Russian regions.

Author: K O Mironov
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Keywords: Bacterial Typing Techniques
Genes, Bacterial - genetics
Haemophilus Infections - epidemiology
Haemophilus influenzae type b - classification - genetics
Humans
Molecular Epidemiology
Russia - epidemiology
Sequence Analysis

Abstract: Genotyping of Hib strains isolated in regions of Russia as well as characterization of genetic relations of typed strains with strains isolated in other areas.

Genetic characterization of 31 strains of Hib isolated in Russian regions during 2005-2008 was performed by multilocus sequence typing.

Studied strains belonged to 11 variants of sequence types, 6 of which were described in previous studies, whereas other 5 were isolated for the first time during this study. The most common isolated strains were ST-92 (13 strains or 42%) and ST-6 (6 strains or 19%). Typed strains were distributed to two clonal complexes. Clonal complex "A1/A2" ("ST-6") incorporates all typed strains except ST-93 strain belonging to clonal complex "B1b" ("ST-93"). The majority of studied strains (19 or 61%) had difference from "central" sequence type of clonal complex, A1/A2 ("ST-6") on not more than one allele.

Clonal structure of isolated strains is analogous to the one observed in Moscow and foreign strains.

PubMed ID: 20218340 View in PubMed