



Bacillus anthracismolecular diversity in Russia and some CIS countries

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Abstract:

Anthrax is a dangerous zoonotic disease with global distribution presenting a problem for public health and veterinary medicine in many countries, including Russia. The phylogenetic structure of the global *Bacillus anthracis* population is based on the clonal nature of the pathogen and data obtained from multiple-locus analysis of variable number of tandem repeats (MLVA) and analysis of single nucleotide polymorphisms (SNPs) of isolates. It is determined by three main genetic lineages (clades) - A, B, C, 12 subclades including 4 main monophyletic subclades and several "canonical" SNP groups. These data are consistent with the idea that members of TEA subclade are most commonly observed. 8 isolates from Russia, Georgia and Azerbaijan made up the group A.Br.014 (subclade Aust94). 3 isolates from Russia, Uzbekistan and Ukraine were part of group A.Br.034 (Ancient A subclade). It is interesting to mention that Ukrainian strain was isolated from patient who contracted anthrax due to contact with leather imported from Ethiopia. 2 isolates from Russia inherited to the group A.Br.081 (subclade Ames). Both isolates from Turkmenistan belonged to the group A.Br.074 (subclade Vollum). 11 isolates from Russia and one from Georgia were part of the group B.Br.002 (B.Branch), 7 strains were isolated in Asian part and 4 in European part of Russia.

A vast territory of Russia with different environmental conditions and several historical and modern trade routes connecting it with adjacent countries could explain high genetic diversity of anthrax pathogen strains isolated in this territory.

Biography:

Prof Eugene Eremenko is working in Federal Government



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Recent Publications:

1. E.I. Eremenko, et al; Genotype diversity of *Bacillus anthracis* strains isolated from the Caucasus region; 2012
2. E.I. Eremenko, et al; Genotyping and phylogenetic location of one clinical isolate of *Bacillus anthracis* isolated from a human in Russia; 2019
3. E.I. Eremenko, et al; Phylogenetic analysis of *Bacillus anthracis* strains from Western Siberia reveals a new genetic cluster in the global population of the species; 2019
4. E.I. Eremenko, et al; Comparative Analysis of Genotyping Methods for *Bacillus anthracis*; 2019
5. E.I. Eremenko, et al; A *Bacillus anthracis* system for acquisition of heme-bound iron; 2017

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