

Conservation of genetic material of various variola virus strains from the Russian Collection

I.N. Babkina, S.N. Shchelkunov, L.S. Sandakhchiev

According to the recommendations of the WHO Advisory Committee on Variola Virus Research and in connection with the need for studying variola virus DNA, a Laboratory “Repository of DNA of Variola Virus and Other Poxviruses” has been established at SRC VB Vector. Reconstruction of the variola virus DNA repository is in progress.

An “Instruction on Organization of Storage and Keeping of Records on the Movement of Variola Virus DNA Preparations when Performing Research in Departments of SRC VB Vector” has been developed and came into force.

The method of long polymerase chain reaction (LPCR), providing the ability to create a library of amplicons of complete VARV genomes, was used to conserve VARV genetic material. In this form, the genomic VARV sequences may be stored for a long time in a biologically safe form to provide research into genetic organization of this unique virus and development of the state-of-the-art methods for rapid diagnostics of VARV and other orthopoxviruses.

The scheme of primer location used for LPCR allows for production of 28 overlapping amplicons that comprise the nucleotide sequence of complete VARV genome. Amplicons of the predicted lengths (from 2.4 to 11.6 kbp) were produced by LPCR using preparations of several VARV strains. All amplicons were deposited for long-term storage with the repository, which is supplied with the comprehensive characterization.

The collection of amplicons formed the background for the creation of libraries of hybrid plasmids containing DNA fragments of complete genomes of three VARV strains from the Russian Collection. This work is in progress now.