

Abstract

8th meeting of the WHO Advisory Committee on Variola Virus Research, 16-17 November
2006, Geneva, Switzerland

Sequencing and computer-assisted analysis of variola virus DNA at the WHO Collaborating Centre for Orthopoxvirus Diagnosis and Repository for Variola Virus Strains and DNA

S.N.Shchelkunov, I.V.Babkin, T.S.Nepomnyashikh

FSRI State Research Center of Virology and Biotechnology VECTOR, Rospotrebnadzor
630559 Koltsovo, Novosibirsk region, Russian Federation

The previous restriction fragment length polymorphism analysis of the complete genomes of several VARV strains from the Russian collection identified regions carrying distinctions between various VARV strains. Two of such regions from the left and right terminal genomic regions were chosen for sequencing. We calculated primers for LPCR amplification of these VARV DNA fragments with a length of 12.9 and 10.5 kbp as well as for amplification of DNA subfragments of these genomic regions and for their sequencing.

As a result of work accomplished to date, we sequenced DNA fragments for 22 VARV strains. The sequencing data was subjected to a comprehensive computer analysis. The nucleotide sequences obtained were aligned and analyzed for their phylogenetic relationships.