Virus DNA Sequencing

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Strains of variola virus (VARV) display a high degree of homology between their genomic nucleotide sequences. However, they are different with respect to the severity of the diseases they cause. Sequencing of VARV DNA allows the degree of distinctions between various VARV strains to be determined.

The earlier performed restriction fragment length polymorphism analysis of the complete genomes of 21 VARV strains from the Russian Collection detected a region carrying differences between various VARV strains. This region comprises ORFs A57R to B8R (according to the nomenclature of VACV strain Copenhagen). We calculated the primers for LPCR amplification of this VARV DNA fragment with a length of 8236 bp as well as for amplification of six DNA subfragments of this fragment and their sequencing.

At this stage of work, we sequenced the corresponding fragments for 14 VARV strains. The sequencing data were subjected to a comprehensive computer analysis. The obtained nucleotide sequences were aligned and analyzed for their phylogenetic relationships.

We were first to discover a deletion with a size of approximately 1.9 kbp in the region of VCP gene in the DNA of West African monkeypox virus (MPXV) strains. We sequenced this region of four Central African and two West African MPXV strains. Analysis of the sequencing data demonstrated that the deletion of 1953 bp long removed from the genome not only VCP gene, but also the ORFs *D15L–D17L*, encoding fragments of a kelch-like protein. VCP is an important virulence factor of orthopoxviruses, and its deletion in the West African MPXV strains may result in a considerable decrease in their pathogenicity for susceptible animals and humans. Presumably, this is precisely the feature that underlies a small number of human monkeypox cases recorded in West Africa as well as the absence of lethal outcomes.