

Metagenomics-Based Molecular Epidemiology of Viral Diseases

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Abstract : Molecular epidemiology and environmental surveillance are parts of a rational strategy to control infectious diseases. They have been widely used in the worldwide campaign to eradicate poliomyelitis, which otherwise would be complicated by the inability to rapidly respond to outbreaks and determine sources of the infection. The conventional scheme involves isolation of viruses from patients and the environment, followed by their identification by nucleotide sequences analysis to determine phylogenetic relationships. This is a tedious and time-consuming process that yields definitive results when it may be too late to implement countermeasures. Because of the difficulty of high-throughput full-genome sequencing, most such studies are conducted by sequencing only capsid genes or their parts. Therefore the important information about the contribution of other parts of the genome and inter- and intra-species recombination to viral evolution is not captured. Here we propose a new approach based on the rapid concentration of sewage samples with tangential flow filtration followed by deep sequencing and reconstruction of nucleotide sequences of viruses present in the samples. The entire nucleic acids content of each sample is sequenced, thus preserving in digital format the complete spectrum of viruses. A set of rapid algorithms was developed to separate deep sequence reads into discrete populations corresponding to each virus and assemble them into full-length consensus contigs, as well as to generate a complete profile of sequence heterogeneities in each of them. This provides an effective approach to study molecular epidemiology and evolution of natural viral populations.

Keywords : poliovirus, eradication, environmental surveillance, laboratory diagnosis

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