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Abstract

The study of the origin and evolution of viruses presents several challenges related to their biology and diversity in nature. In recent years, several approaches have been developed to analyze the dynamics of the temporospatial dispersion of viruses using molecular data.

We have been using these new methods, integrating molecular, epidemiological, geographical and historical data, on several animal and human viruses from Argentina and South America, such as rabies virus, norovirus, polyomaviruses, and others.

Different strategies for virus surveillance have been implemented, including clinical and environmental sampling, and viral genomes were sequenced. Phylogenetic and phylodynamic analyses were used to study their evolutionary history, population dynamics and geographical dispersion.