



Genetic Diversity of Viruses: From Source Tracing to Treatment Tailoring

Guest Editor:

Dr. Ivana Grgic

Department of Immunological
and Molecular Diagnostics,
University Hospital for Infectious
Diseases “Dr. Fran Mihaljevic”,
10000 Zagreb, Croatia

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Message from the Guest Editor

Every year, new viruses are being identified as etiologic agents of human diseases as they adjust to the new host.

In the process, genetically divergent variants are formed. Determining the genetic sequence of the virus can be a crucial step in battling infection as an understanding of how different variants can affect the clinical outcome and direct the development of new drugs. Direct-acting antivirals have changed the way we deal with viral infections. These lessons could be useful to further improve research for treating many other viral diseases in the future since the development of new antiviral drugs is very much a work in progress, with active drug discovery programs for filoviruses, coronaviruses, dengue, and others. Viruses can easily adapt to any therapy; therefore, resistance to antiviral drugs should be intensely studied.

In this Special Issue, our aim is to emphasize the need to explore how genetic diversity can affect treatment outcomes, whether research discusses viruses developing drug resistance mutations or different genotypes and subtypes of causing a diverse spectrum of symptoms to improve the diagnostic methods available.

