ANDREA GAMARNIK

Academia Nacional de Farmacia y Bioquímica

Instituto de Investigaciones Bioquímicas de Buenos Airres (CONICET)

GENERATING TOOLS AND KNOWLEDGE FOR DENGUE VIRUS CONTROL

Abstract: Dengue virus (DENV) continues to pose a major public health threat across Latin America and other tropical and subtropical regions of the world. Recurrent epidemics cause hundreds of millions of infections each year, imposing severe health and socioeconomic burdens. There are four DENV serotypes (1 to 4), and infection with any of them can lead to clinical outcomes ranging from mild febrile illness to severe hemorrhagic disease. Individuals experiencing a secondary infection with a different serotype are at increased risk of severe disease due to a phenomenon known as antibody-dependent enhancement. Therefore, to provide effective protection, vaccines must be tetravalent, targeting all four serotypes simultaneously. Despite decades of research, the development of an effective vaccine remains elusive, and no specific antivirals are currently available.

Our work aims to dissect the molecular mechanisms of DENV infection and replication to identify novel antiviral targets and guide the design of improved vaccines. A major challenge in vaccine development lies in the differences in infection dynamics, replication rates, and host-virus interactions among the four serotypes. By integrating proteomic studies using human infected cells with technology to genetically manipulate the four DENVs, we have uncovered serotype-specific strategies to subvert human antiviral defenses and drive pathogenesis. This mechanistic information is now being used for rational design of balanced tetravalent vaccines. In parallel, we have established a platform for development of diagnostic tools for detection of all four DENV serotypes, which are currently available for clinical use.

About the speaker: Dr. Andrea Gamarnik obtained her Ph.D. in biochemistry studying plant-pathogen interactions at the University of Buenos Aires in 1993. After a postdoc at the University of California, San Francisco, and working in the biotechnology industry in California, she returned to Argentina at the end of 2001. She is currently the Director of the *Instituto de Investigaciones Bioquímicas de Buenos Aires* (IIBBA) of CONICET at the Fundación Instituto Leloir, where she leads the Molecular Virology Laboratory.

The goal of her lab is to study infectious diseases that are relevant to the country and the region. Given the public health impact of dengue virus in Latin America, she focused her research on this pathogen. Her laboratory has made seminal contributions on the mechanism of dengue virus replication. These achievements led to her incorporation in the American Academy of Microbiology in 2014 and the American Academy of Arts and Sciences

in 2021. She has received numerous national and international awards including the L'Oréal-UNESCO International Award for Women in Science representing Latin America, the Konex Platinum Award in Science 2013–2023, the Award *Investigador de la Nacion* 2022, and she was a member of the Infectious Diseases Program of the Howard Hughes Medical Institute (HHMI).

During the COVID-19 pandemic, she created the COVIDAR group, which developed the first national kit for measuring antibodies against SARS-CoV-2. More recently, her team developed the **DetectAR Dengue** kit for dengue diagnostics through the detection of viral antigens. This kit was approved by ANMAT in 2024 and is now available for clinical use.