

# Zika Virus Pathogenesis

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ZIKV (Zika virus) is a mosquito-borne, positive-sense single-stranded RNA virus belonging to the family *Flaviviridae* (genus *Flavivirus*). ZIKV is further classified by homology to the Spondweni virus (SPONV) in the Spondweni viral clade or serogroup, both viruses were first characterized in Africa in 1947 and 1952, respectively.

Keywords: Zika virus (ZIKV) ; immune evasion ; infection ; tissue propagation ; congenital and neurological disorders

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## 1. Introduction

Apart from the congenital Zika syndrome (CZS) that covers the pathogenic events associated with maternal-fetal ZIKV transmission and the Guillain-Barré syndrome (GBS) <sup>[1]</sup>, primary ZIKV infection is generally asymptomatic or mild in adults <sup>[2][3][4][5][6]</sup>. Factors determining asymptomatic or mild ZIKV infection, and severe manifestations, as well as chronic sequelae, are still to be determined. Understanding the importance of being infected by a particular ZIKV lineage, the influence of comorbidities and previous flavivirus infections (i.e., Dengue virus (DENV)), as well as viral load and the molecular mechanisms underlying severe infection, such as host genetic susceptibility to infection, immunosuppression and/or failure of the innate immunity are key to improving the overall knowledge of the complex ZIKV disease, diagnosis, prophylaxis and treatment <sup>[7][8][9][10][11][12][13][14][15][16][17][18]</sup>.

The interplay between ZIKV and immune responses is initiated once the virus invades different cells, tissues and organs from the early infection. In infected individuals and non-human primates, the virus is fast cleared from blood, but persisting in saliva, urine, semen, breast milk and the central nervous system (CNS) for months <sup>[19][20][21][22][23]</sup>. Several *in vitro* and *ex vivo* studies indicate that ZIKV replicates in human endothelial and epithelial cells <sup>[24]</sup>, peripheral blood mononuclear cells (PBMCs) <sup>[24]</sup>, astrocyte and microglial cells <sup>[25][26]</sup>, different placenta cells, such as trophoblasts <sup>[27]</sup>, Hofbauer cells in chorionic villi and amniotic epithelial cells <sup>[28]</sup>, as well as fibroblasts (placental, uterine, pulmonary) <sup>[29]</sup>. Moreover, ZIKV has a broad cell tropism *in vitro*, infecting human skin cells (i.e., dermal fibroblasts and epidermal keratinocytes), human myeloid cells (i.e., dendritic cells (DCs) and macrophages), and human progenitor cells of neuronal, placental and testicular origin (reviewed in <sup>[30][31]</sup>).

It is important to understand how ZIKV interacts with these cells and tissues, as well as with the host immune system to cause severe disease. The following sections describe the mechanisms underlying interferon (IFN) immune response against flavivirus, and the available knowledge concerning the events triggered by the ZIKV genome and proteins to escape or neutralize the antiviral IFN functions to infect and induce pathogenesis in immune privileged organs such as the brain and eye <sup>[11][32][33][34]</sup>.

## 2. Mechanisms of ZIKV Immune Evasion

ZIKV persistence and pathogenesis involve a complex immune-evasion strategy to facilitate ZIKV trafficking, infection and spread through different cell types and tissues to finally cross protective barriers to the immune-privileged fetus, affecting the development of the fetal brain and eyes.

ZIKV uses its own viral proteins, gRNA and sfRNA elements to evade antiviral immunity, particularly the anti-ZIKV IFN response and associated signals and factors, as mentioned above. Hence, multiple NS proteins of ZIKV negatively modulate the antiviral response at various levels by inhibiting type I IFN production and the expression of downstream ISGs, acting on the IFN-associated cGAS-STING pathway, targeting with TBK1 and therefore impairing IRF3 promoters, or modulating RIG-I- and MDA5-directed type I IFN induction, as well as different steps of the antiviral type I IFN system against RNA viruses such as ZIKV. The NS proteins could cooperate to overcome the INF antiviral functions, limiting immune-protection and the understanding of ZIKV immune-evasion and pathogenesis. Moreover, gRNA-associated modifications that function as an antagonist of the innate type-I IFN response, and sfRNA stability against XRN-1, 5'-3' exoribonuclease, which help to efficiently suppress RIG-I- and MDA-5-mediated IFN have been identified as an important

proviral pathway, abrogating IFN neutralization of ZIKV infection during the early-phase of the viral life cycle. Moreover, ZIKV infection modifies the miRNA landscape of host cells in order to evade innate and adaptive immune responses and promote viral replication and survive. Although the involvement of viral antigen specific CD4<sup>+</sup> T cells in the control of ZIKV infection and disease is still controversial, the CD8<sup>+</sup> T cell response is associated with the control of the ZIKV infection and pathogenesis. This protective action has been more clearly demonstrated by cross-immune reactions of human DENV-elicited CD8<sup>+</sup> T cells [35] which react against ZIKV-NS (i.e., mainly recognizing NS3 protein [36][37]). Anti-ZIKV vaccines are therefore focused on generating protective CD8<sup>+</sup> and CD4<sup>+</sup> T cells in order to control ZIKV infection and promote virus clearance, thereby avoiding harmful ADE effects with potential reinfection events by ZIKV or other flaviviruses [38][39][40][41][42].

In order to reach the human fetus, ZIKV must cross the placenta barrier which develops within days of conception and is indispensable for pregnancy [43][44]. Furthermore, fetal damage by ZIKV infection can be observed after the first trimester, and persistence infection, late during pregnancy, results in fetal disease or adverse pregnancy outcomes [45][46].

Recently, as a result of the global impact of ZIKV and its teratogen effects, such as microcephaly in newborns to infected mothers along with neurological abnormalities and GBS, and comparison with previous congenital pathogens such as *Toxoplasma gondii*, other (e.g., syphilis, human immunodeficiency virus (HIV) or parvovirus B19), rubella virus, cytomegalovirus (CMV) and herpes simplex virus (HSV) (i.e., all of which are grouped under the term of TORCH pathogens) [47]. ZIKV has been proposed as a new TORCH pathogen but more complex in the associated pathogenesis [47]. ZIKV-induced congenital microcephaly abnormality alarmed the whole of the planet [48] together with other developmental abnormalities that determine the CZS (i.e., severe microcephaly with partially collapsed skull, thin cerebral cortices with subcortical calcifications, macular scarring and focal pigmentary retinal mottling, congenital contractures and marked early hypertonia) [49][50], and placental insufficiency and fetal loss [51]. ZIKV is able to infect, traffic and spread through several cells and tissues during fetal differentiation, just after overcoming/crossing several protective barriers such as those mentioned above. ZIKV is able to infect eye and brain immune-privileged organs, avoiding innate IFN defenses and provoking neuroinflammation and cytokine release that halt neurogenesis [52], thereby favoring viral spread and tissue damage.

Therefore, understanding how ZIKV interacts with the INF system and influences the outcome of infection in barrier tissues such as the placenta, eyes and brain during pregnancy may help in the development of therapeutic strategies to clear ZIKV from the organism, based on the action mechanism of the IFN system, and keeping immune-privileged organs safe during both fetal development and in adults.

Moreover, determining the molecular interplay between the ZIKV genome and viral proteins with the IFN and T cell responses and antiviral signals is also crucial to improving vaccine strategies based on mutant live-attenuated viral candidates that need to induce adaptive cellular and humoral immune protective responses, also helping type-I IFN antiviral responses [39][53][54][55].

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