Molecular Mechanisms of Vertical Transmission in Chagas Disease

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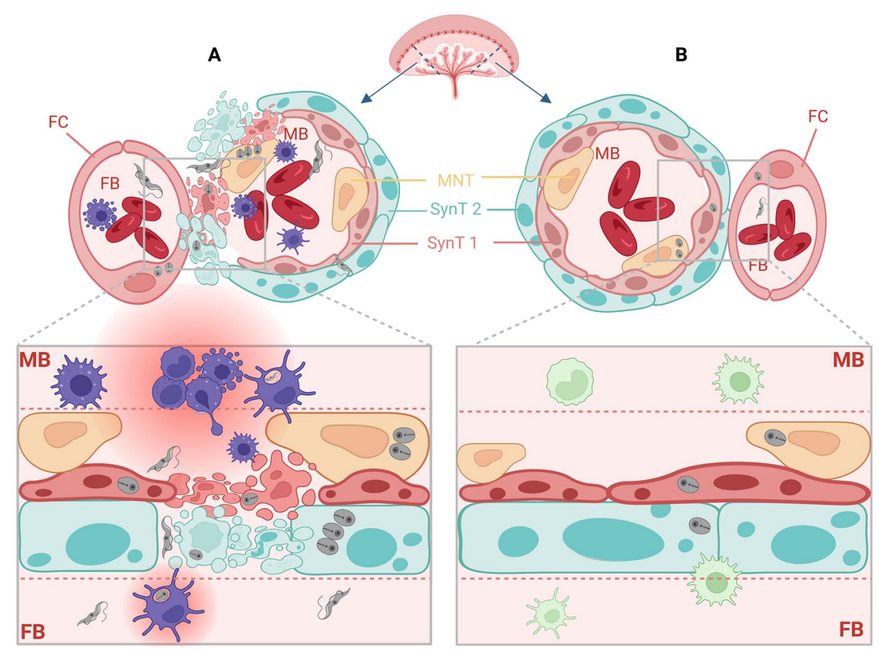
Background

Our recent research focused on characterizing *T. cruzi* strains vertically transmitted (TcVT) in Uruguay. These strains exhibited low virulence and specialization for vertical transmission, differing substantially from commonly used laboratory reference strains. Murine model experiments revealed that TcVT isolates employed a distinct mechanism of transplacental transmission compared to highly virulent strains, resulting in changes in placental gene expression. Notably, TcVT strains modulated genes related to the host immune response, facilitating a "silent" passage of parasites through the transplacental barrier without causing tissue damage. Conversely, highly virulent strains, even when vertically transmitted, activated the immune response, causing cellular damage and inflammation. Furthermore, not all reference strains were vertically transmitted *(Faral-Tello et al., 2023).*

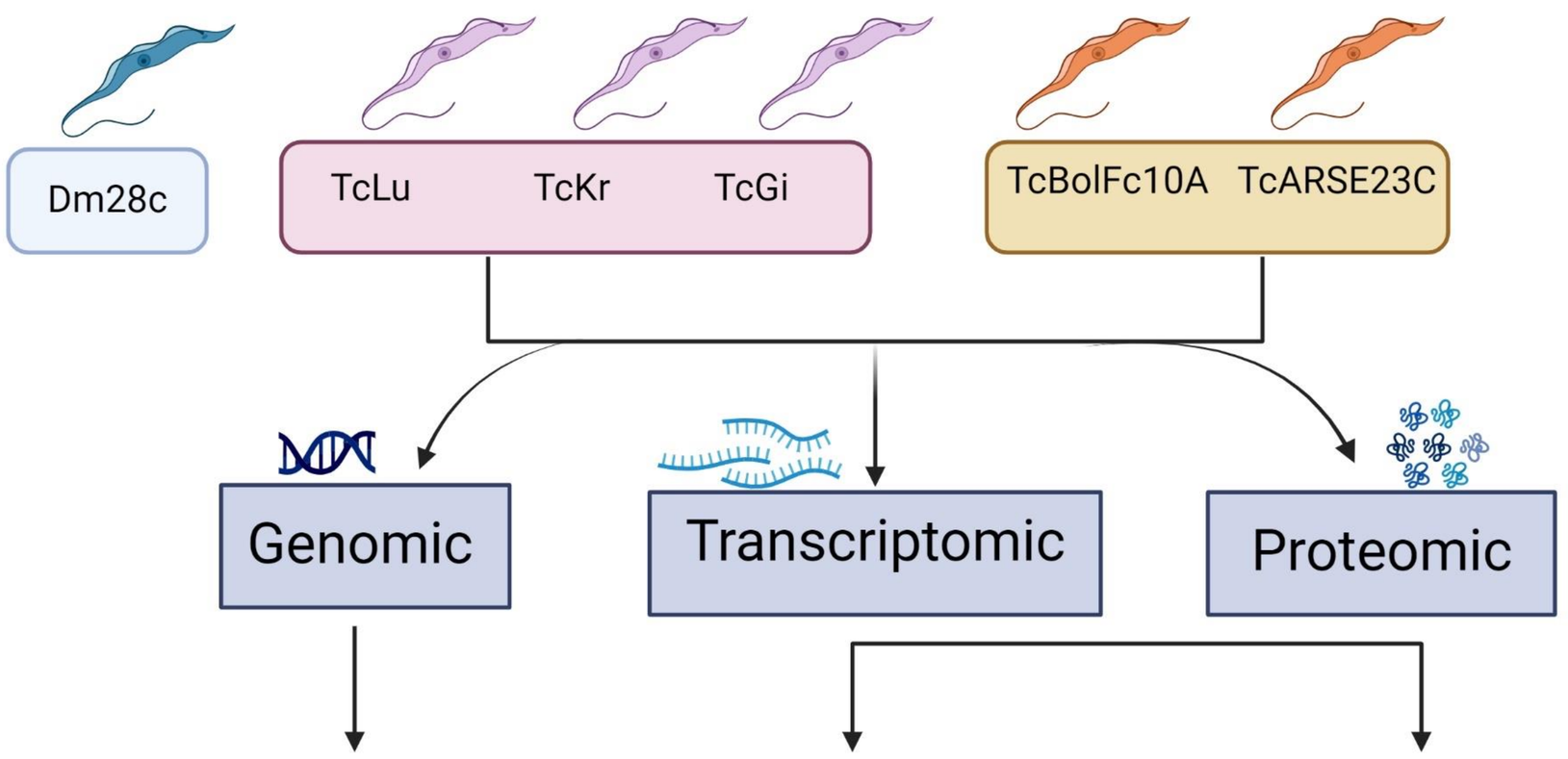
Objective

Our primary goal is to realize a a comparative analysis involving with TcVT isolates (TcGi, TcLu and TcKr) share common characteristics related to infection and transplacental passage, the strain Dm28c, which lacks vertical transmission capability, represents our reference genome (negative control), and possesses a complete genome sequenced (Berná et al., 2018); and isolated from chronic patients through vector transmission, TcBolFc10A and TcAR-SE23C.



Two vertical transmission strategies at the murine maternal-fetal interphase. (A) As observed for the highly virulent strain Garbani, *T. cruzi* is vertically transmitted, unspecifically and without preferential tropism toward the placenta, inducing tissue damage and a Strong proinflammatory placental response. (B) As observed for VT isolates, *T. cruzi* is vertically transmitted, specifically and with a placentotrophic strategy, in a silent manner, without causing damage and without inducing a proinflammatory response. Figure created with biorender.com *(Faral-Tello et al., 2023).*

Methodology



To identify structural variations (insertions, deletions), chromosomal rearrangements and variations in the number of gene copies, repeats and multigene families among diferente genomes.

To unveil a set of genes/proteins associated with metabolic pathways, molecules involved in parasite-host interactions, immunological processes, and other transcriptomic signatures, these findings will be correlated with the phenotype exhibited by different strains.

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