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E**Dr Mohamed-Ali Hakimi**

Team « Toxoplasmosis & Host-parasite coevolution »

IAB- Institute for Advanced Biosciences

Université Grenoble Alpes

INSERM U1209 - CNRS UMR5309

Decoding the Epigenetic Blueprint Behind *Toxoplasma* (Pre)sexual Commitment and Chronic Persistence**MERCREDI, 12 AOÛT 2026 à 12h30**

Pavillon Charles-Eugène-Marchand, salle Hydro-Québec (1210)

Abstract:

Toxoplasma gondii, a widespread apicomplexan parasite, navigates a complex life cycle in which it switches back and forth between tachyzoites and bradyzoites to balance acute infection and persistence while also undergoing an often-overlooked one-way commitment to the sexual stage. Emerging evidence suggests that *Toxoplasma*'s developmental trajectories are orchestrated by an interconnected network of transcriptional switches and chromatin remodeling mechanisms, acting in concert to ensure robust stage transitions. This review outlines an updated epigenetic framework for stage transitions and highlights the functional synergy between an ISWI-family chromatin remodeler and the MORC/HDAC3² repressor complex, which together modulate chromatin accessibility to maintain or shift developmental states. We also spotlight recent findings showing that simultaneous depletion of AP2XII-1 and AP2XI-2 transcription factors reactivates the presexual program in vitro, eliminating the need for cat hosts and allowing ethical, scalable exploration of sexual stages. Strikingly, the knock-down of these transcription factors also reveals a previously unrecognized hybrid zoite co-expressing bradyzoite and merozoite markers, suggesting a transitional state that defies classical stage definition. This hybrid form, as well as more recent data on bradyzoite development, support a new model in which *T. gondii* development unfolds along a continuum of epigenetically primed states rather than a rigid sequence of binary fate decisions. These findings provide a powerful conceptual and experimental framework for dissecting parasite transmission and persistence and have far-reaching implications for the biology of other parasites in the phylum.

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