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## Understanding the History of the Domestic Cycle of *Toxoplasma gondii* in South America

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A growing body of evidence supports the significant role of *Toxoplasma gondii* genotype in determining disease severity. However, isolating and characterizing *T. gondii* strains infecting humans remains challenging. Clinical severity of toxoplasmosis varies geographically, with South America experiencing the highest burden, coinciding with the continent's remarkable *T. gondii* genetic diversity. In our study, we analyzed 156 *T. gondii* genomes and we provide the first direct estimates of *T. gondii*'s mutation rate and generation time. Our findings offer insights into the epidemiology, ecology, and evolutionary history of South American *T. gondii* populations. We identified three distinct categories: (1) wild populations, transmitted through the sylvatic cycle involving wild felids and likely poorly adapted to domestic cats. This includes the "Amazonian" population, linked to various clinical forms in immunocompetent individuals, and the "Pan-American" population, isolated from

wildlife and not yet associated with severe disease forms, (2) domestic intercontinental clonal lineages (types I, II, III, and Africa 1), introduced to the continent with the domestic cat and house mouse by European sailors. (3) hybrids of the first two categories, probably well adapted to domestic cats, and representing the majority of strains found in South America's domestic environment. We discuss how hybridization events and strong selection for a unique haplotype comprising only 0.16% of the *T. gondii* genome on chromosome 1a are likely driving the public health challenge associated with toxoplasmosis in South America.

**Galal, L., Ariey, F., Gouilh, M. A., Dardé, M. L., Hamidović, A., Letourneur, F., ... & Mercier, A. (2022). A unique *Toxoplasma gondii* haplotype accompanied the global expansion of cats. *Nature Communications*, 13(1), 5778.**