

## **GENETIC DIVERSITY IN THE NATURAL *TRYPANOSOMA CONGOLENSE* POPULATION**

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*Trypanosoma congolense* is one of the major parasites responsible for Animal African Trypanosomiasis (AAT), a disease affecting about 10 million km<sup>2</sup> of the sub-Saharan region and considered as one of the principal causes of hunger and poverty in those countries. A key step in the fight against AAT is to monitor the level and distribution of genetic diversity in *T. congolense* populations, to reveal the biologically relevant structural variations present in their genomes that influence pathogenesis, virulence, and mechanisms leading to drug resistance. Using Next-Generation Sequencing technology, we sequenced 50 Savannah and 4 Forest strains sampled between 1971 and 2010 in 9 countries where the disease is endemic. A total of 614859 SNPs were identified and long deletions were detected in both coding and non-coding regions, revealing a high genetic diversity. Interestingly, analyses of linkage disequilibrium decay indicated that genetic recombination and complex genetic exchanges are frequent between *T. congolense* parasites. Additional phylogenetic and structure analysis highlighted a geographically asymmetric distribution of genetic diversity across Africa. Parasites collected within a short period of time in Zambia showed a greater diversity compared to the strains sampled over a period of 30 years in the other countries. The factors resulting in this asymmetric diversity remain speculative but we suggest that the close proximity to wildlife observed in this region and the particular tsetse fly distribution are playing a key role. This last hypothesis is currently being tested by studying the capability of several tsetse species to develop a mature *T. congolense* infection.