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Identification of Villages at Risk (VAR) of Human African Trypanosomiasis: a geographical approach to assess the risk of reemergence of HAT in historical foci

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Human African Trypanosomiasis (HAT) is a neglected tropical disease caused by a trypanosome, transmitted to humans through the blood meal of an infected tsetse fly. During the 19th and 20th centuries, it was a major public health problem, requiring the creation of dedicated control services. From just over 25,000 cases in 2000 to less than 1,000 cases detected in 2020, HAT is on the way to being eliminated as a public health problem, as desired by the WHO. However, some historical foci (sometimes country-wide) where tsetse is present have not been investigated for more than 30 years, for example in Sierra Leone, Liberia, and The Gambia. The IVR method is based on a geographical approach to the HAT pathogen system, which makes it possible, via the construction of a Geographic Information System fed by historical, geographical, entomological and parasitological data, to have an overview of the HAT situation and to assess the risk of re-emergence over a large area. The results obtained provide useful elements for the implementation of a targeted epidemiological surveillance system, allowing the detection of any risk of re-emergence, with a view to achieving the objective of elimination. This oral communication aims to present the method itself, as well as the results obtained by the application of this method in the countries investigated: Burkina Faso, Chad, Côte d'Ivoire, Guinea, Senegal, Guinea-Bissau and Niger.