Surveillance on the fly: point-of-need molecular xenomonitoring for tsetse in a low-resource setting

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Abstract

Background

Tsetse flies (*Glossina sp.*) are the primary vectors of trypanosomes causing human African trypanosomiasis (HAT) and animal African trypanosomiasis (AAT). Disease surveillance can be carried out by detecting *Trypanosoma* DNA in tsetse, also known as molecular xenomonitoring. Whilst molecular methods can increase the efficiency and sensitivity of pathogen detection, trained staff and a well-equipped laboratory are required. In many cases, DNA extraction and screening is outsourced to a central laboratory in a major city either in-country or abroad, far removed from original tsetse collection sites. This increases results turnaround time, incurs transportation costs, and can lead to sample loss or damage.

Methodology/Principle Findings

We set out to develop, optimise and trial methods for tsetse xenomonitoring in a low-resource point-of-need setting. A low-cost protocol was developed consisting of rapid alkali-based DNA extraction and *Trypanosoma* detection qPCR assays using air-dryable reagent mixes. A minimally-equipped laboratory was established in a field station in Arua, Uganda. Following a training workshop, three entomology technicians carried out screening on 286 tsetse collected over a nine-week study period. The technicians consistently extracted high quality DNA (98% success rate) and were able to successfully detect *T. brucei sensu lato* in 4.3% (95% confidence interval (CI) [2.23 - 7.37]), *T. congolense* in 3.6% (95% CI [1.73 – 6.47]) and *T. vivax* in 3.9% (95% CI [1.98 – 6.92]) of total tsetse, representing a total *Trypanosoma sp* detection prevalence of 10.7% (95% CI [9.6 – 11.8]).

Conclusions/Significance

This study demonstrated that sensitive molecular xenomonitoring of HAT and AAT pathogens can be carried out without the need for cold-chain storage or high-powered equipment. Further improvements to the system might be achieved by modifying the DNA extraction protocol to enable high-throughput or pooled samples, increasing the sensitivity of the *T. b. gambiense* DNA detection assay and exploring more sustainable power sources.