Abstract

The polymerase chain reaction (PCR) was used to identify trypanosomes in Glossina pallidipes and G. longipennis caught in Kenya. Of 3826 flies dissected, 188 (4.9%) were parasitologically positive overall. The infection rate in G. pallidipes was 5.7% (187 of 3301 flies), but only one of 525 G. longipennis was infected (infection rate 0.2%). There was a higher infection rate in female G. pallidipes flies than male flies (chi(2) = 18.5, $P < 0.001$) and odds ratio = 2.5 (95% 1.6, 3.7). The infected flies were analysed by PCR using 10 sets of primers specific for species and subgroups within the subgenera Nannomonas, Trypanozoon and Duttonella. Of 188 parasitologically positive samples, PCR identified 137 (72.9%), leaving 51 (27.1%) non-identified. We recorded infection rates of 47.2% for Trypanosoma congolense savannah, forest and kilifi subgroups, 20.9% for T. simiae/T. simiae tsavo/T. godfreyi, 14.9% for T. brucei ssp. and 13.8% for T. vivax. Thirty-nine (26.7%) flies had mixed infections, with a minor association between T. congolense savannah/T. simiae tsavo/T. godfreyi (chi(2) = 6.93, d.f. = 1, $P < 0.05$). The relative proportion of each trypanosome species or subgroup varied between fly belts with T. congolense (all subgroups) being the most abundant and T. godfreyi the least. Statistical analysis showed that dissection method and PCR test classified infections independently (chi(2) = 10.5, d.f. = 1, $P < 0.05$ and kappa = 0.38). This study shows that pathogenic trypanosomes are widespread in all sampled testes fly belts with G. pallidipes as the main vector. Further, PCR test is more reliable in detecting and identifying trypanosomes than dissection method.