1 INTRODUCTION

Tsetse flies (Diptera: Glossinidae) are obligatory haematophagous arthropods, feeding only on vertebrate blood. They are responsible for the transmission of Human Sleeping Sickness (HSS) and African Animal Trypanosomosis (AAT) in large areas of sub-Saharan Africa.

Information on the feeding behaviour of the arthropod vectors of diseases is essential in understanding the relationship between hosts and vectors, and their respective roles in a disease transmission cycle (Tempelis, 1975). Recent models proposed to describe the epidemiology of African Trypanosomosis include the biting rate and the probability of tsetse feeding on different hosts as key parameters for understanding the transmission of these infections. The feeding preferences of tsetse reflect a complex endpoint in a series of linked behavioural responses to hosts. Identification of the host preferences of tsetse would be valuable in the design and implementation of disease and vector control strategies (Bauer et al., 1995).

The source of a tsetse bloodmeal provides important information relating to the epidemiology of trypanosomosis and natural feeding habits of different species of Glossina. For this purpose, serological techniques have been developed using host-specific antisera to identify the source of vertebrate blood from the intestinal tract of flies caught in the wild (Weitz, 1963; Staak et al., 1981; Clausen et al., 1998). Repeated absorption of antisera with the most cross-reacting antigens will yield highly host-specific antisera. Cross-reactivity between members of different groups of animal families can be eliminated after repeated absorptions, while a slight cross-reactivity between phylogenetically closely related species will remain (Clausen et al., 1998).

Since the invention of the polymerase chain reaction (PCR) by Mullis and Faloona (1987), it has been adapted for a range of applications such as characterisation of genes, detection of pathogens, identifying mutations responsible for inherited diseases and DNA fingerprinting for medical and forensic purposes. Polymerase chain reaction-restriction fragment length polymorphism analysis (PCR-RFLP) is used in food analysis, e.g. for the detection of pig, cattle, wild boar, buffalo, sheep, goat, horse, chicken and turkey meat in food products (Allmann et al., 1993; Meyer et al., 1994; 1995). DNA based techniques were also developed for bloodmeal identification in haematophagous insects (Kirstein and Gray, 1996; Boakye et al., 1999). These new approaches might be alternatives to immunological methods for the identification of bloodmeals from arthropod vectors.

The general aim of this work was to develop a DNA based assay for the identification of bloodmeals from tsetse flies.

The specific objectives were as follows:

1. Establish a DNA bank from potential vertebrate hosts of tsetse flies.
2. Evaluate the detection limit and the stability of host DNA in tsetse.
3. Assess the efficacy of cytochrome b (*cytb*) as a discriminatory molecular marker for identification of host DNA of the vertebrate family Bovidae.