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## Detection of infections of *Trypanosoma grayi* in Glossina fuscipes fuscipes in the Central African Republic

DNA probes have become frequently used tools for the identification of trypanosome infections in wild tsetse flies (McNamara et al., 1989, 1995; Bourzat and Gouteux, 1990; Majiwa and Otieno, 1990). Such probes are particularly useful for the identification of infections that are indistinguishable by conventional dissection and microscopy (Lloyd and Johnson, 1924), such as immature infections of parasites in the Trypanozoon or Nannomonas subgenera and mature infections of parasites within the Nannomonas subgenus. Initially, radioactively labelled DNA probes were used for hybridization of dot- or touchblots of tsetse midguts on nitrocellulose filters (Kukla et al., 1987; Gibson et al., 1988). More recently, PCR amplification of the target DNA sequences has allowed greater levels of sensitivity to be reached, enabling the low numbers of trypanosomes in the proboscis or salivary glands to be identified (Masiga et al., 1992, 1996; Majiwa et al., 1994).

Despite these technical improvements, field surveys of tsetse flies continue to produce many unidentifiable trypanosome infections in midgut samples. In particular, flies of the *palpalis* group take a high proportion of bloodmeals from reptiles and may therefore have infections of Stercorarian trypanosome species such as *Trypanosoma grayi*, which may be confused with immature infections of Salivarian trypanosomes (Dirie *et al.*, 1991; McNamara and Snow, 1991). The results of the present study are a case in point.

The study was carried out in the Commune d'Élevage d'Ouro-Djafon, Bambari, Central African Republic, on 25–28 September 1992 (Mission 1) and 9–12 January 1993 (Mission 2); 2 months prior to Mission 1, a trial of pour-on insecticide had been carried out (Gouteux *et al.*, 1996). A total of 355 *Glossina fuscipes fuscipes* was dissected and samples taken for bloodmeal and touch-blot analysis (see Table). Infections of Stercorarian trypanosomes could be distinguished from those of Salivarian trypanosomes by the parasites' form (long and spindly) and their characteristic, rapid vibratory movements during microscopical examination of mid- and hind-gut sections. Such infections were by far the most common (85%); the combined prevalence of salivary gland infections (T. brucei ssp.) and infections of both proboscis and midgut (Nannomonas) was <1% and no proboscis-only infections (T. vivax) were found. Touch blots were subsequently hybridized with a DNA probe comprising sheared total DNA from T. grayi ANR4, a stock isolated from G. palpalis gambiensis in The Gambia, experimentally transmitted through crocodiles and characterized by isoenzyme and DNA probe analysis (Dirie et al., 1991; McNamara and Snow, 1991). At high stringency  $(0.1 \times \text{standard saline-citrate})$ at 65°C) this T. grayi probe hybridizes specifically with T. grayi and not with other trypanosome species (of the subgenera Trypanozoon or Nannomonas) (McNamara and Snow, 1991). Overall, 18 of the 355 touchblots gave a positive hybridization with the T. gravi probe; only seven other touch-blots could be identified with any of the other available DNA probes (for T. brucei, savannah or forest T. congolense, T. simiae and T. godfreyi).

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The results of the microscopical examinations showed low concordance with those obtained using the DNA probe for identification of T. grayi, particularly for Mission 2 (see Table). For Mission 1, of nine infections identified by microscopy as pure T. grayi or mixtures including this species, five were also found positive for this species using the DNA probe. For Mission 2, however, only six of the 40 infections thought to comprise or include T. grayi after the microscopy were positively identified by hybridization. The difference observed in the level of concordance between

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The numbers of infected flies amongst the 355 Glossina fuscipes fuscipes examined by microscopy and by use of a DNA probe specific for Trypanosoma grayi

	Result of using probe during:			
	Mission 1		Mission 2	
	Positive	Negative	Positive	Negative
RESULT OF MICROSCOPICAL EXAMINATION		· · · · · · · · · · · · · · · · · · ·		
Pure T. grayi infection	4	4	6	28
Mixed infection including T. grayi	1	0	0	6
Infection with unidentified trypanosome	1	4	0	3
Uninfected	2	102	4	190
Totals	8	110	10	227

the results of the two identification methods in Missions 1 and 2 may have been the result of a higher prevalence of infections with reptilian trypanosomes other than T. gravi during the latter period; there was a considerable increase in the prevalence of monitor lizard (Varanus) bloodmeals between Missions 1 and 2 (18% v. 83%; Gouteux et al., 1996). These trypanosomes are unlikely to have been T. varani, which infects sandflies rather than tsetse (Dirie et al., 1991), and presumably belong to other, as yet uncharacterized species. Several of the T. grayi infections detected by DNA-probe hybridization had not been identified by microscopy, emphasizing the utility of the DNA-probe methodology.

In conclusion, the present results show that infections with reptilian trypanosomes may reach high levels in the tsetse population and these may give a misleading impression of the actual numbers of immature, Salivarian infections present. ACKNOWLEDGEMENT. We are grateful to T. Njoroge for assistance with the DNA-probe analysis during a training attachment from KETRI.

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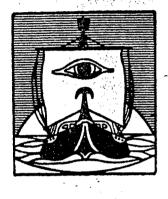
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