

1 Running title: Molecular dipstick for sleeping sickness

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4 **A molecular dipstick test for the diagnosis of sleeping sickness**

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16 **Summary**

17 Human African trypanosomiasis (HAT) or sleeping sickness, is a neglected disease that
18 affects poor rural populations across sub-Saharan Africa. Confirmation of diagnosis is based
19 on detection of parasites in either blood or lymph by microscopy. Here we present the
20 development and the first phase evaluation of a simple and rapid test (HAT-PCR-OC) for
21 detection of amplified *Trypanosoma brucei* DNA. PCR products are visualised on a dipstick
22 through hybridisation with a gold conjugated probe (oligochromatography). Visualisation is
23 straightforward and takes only 5 minutes. Controls for both the PCR reaction and for DNA
24 migration are incorporated in the assay. The lower detection limit of the test is 5 fg of pure *T.*
25 *brucei* DNA. One parasite in 180 μ l of blood is still detectable. Sensitivity and specificity
26 for *T. brucei* were calculated at 100% when tested on blood samples from 26 confirmed
27 sleeping sickness patients, 18 negative controls (non-endemic region) and 50 negative
28 control blood samples from endemic region. HAT-PCR-OC is a promising new tool for
29 diagnosis of sleeping sickness in laboratory settings and the diagnostic format described here
30 may have wider application for other infectious diseases.

31 **Introduction**

32 Human African trypanosomiasis (HAT) is a complex of protozoan infections, fatal if
33 untreated, which can be caused by infection with either *Trypanosoma brucei* (*T. b.*)
34 *gambiense* (chronic HAT) or *T. b. rhodesiense* (acute HAT). Both human infective sub-
35 species are cyclically transmitted by tsetse flies (genus *Glossina*). HAT is a severely
36 neglected disease, typically affecting rural populations of poor people across sub-Saharan
37 Africa (23). Over 60 million people are at risk of contracting the disease with an estimated
38 50-70,000 persons newly infected annually (2). In the absence of treatment, HAT patients
39 inevitably die after a more or less prolonged period of grave illness. Disease control for *T. b.*
40 *gambiense* relies heavily on accurate diagnosis and effective treatment of patients and for *T.*
41 *b. rhodesiense* on treatment of patients and of the animal reservoir (24). Classical diagnosis
42 requires demonstration of parasites in blood or lymph which for *T. b. gambiense* infection is
43 problematic due to extremely low parasitaemias in infected people. It is estimated that 20 to
44 30% of the patients remain undiagnosed by standard parasitological techniques (20). New
45 molecular techniques based on the polymerase chain reaction (PCR) have been developed as
46 surrogate for parasite detection. Applications of PCR for detecting *T. brucei* and its
47 subspecies have been reported, which can be highly effective for detection of *T. b.*
48 *rhodesiense* and for distinguishing *T. b. rhodesiense* from *T. b. gambiense* (7, 16, 17, 18, 22,
49 25). The use of these highly specific and sensitive PCR methods is however only suitable for
50 screening for disease prevalence and for research purposes and are not commonly used to
51 inform diagnosis of HAT (5). This is partly due to the cumbersome methods of PCR product
52 detection. Amplicons are normally identified using UV trans-illumination after being
53 electrophoresed in the presence of ethidium bromide (a carcinogen). Alternative methods for

54 PCR product detection such as real-time PCR, PCR-ELISA or mass spectrometry have been
55 developed (3, 10, 21) but are complex, expensive, equipment, recourse and personnel
56 hungry. There is a demand for a simplified method of amplification and product detection
57 which would make these tools useable in the facilities available in regional sleeping sickness
58 diagnostic laboratories.

59 Oligochromatography (OC) provides a simple and rapid dipstick format for detection of
60 amplified PCR products (Coris BioConcept, Gembloux, Belgium; Patent n° WO
61 2004/099438A1) (12, 13, 15, 19). PCR products are visualised by hybridisation with a gold
62 conjugated probe. This PCR product detection format takes only 5 minutes and no other
63 equipment than a dry heating block and a pipette are needed. An internal control (IC) for the
64 PCR reaction and a control for the chromatographic migration are incorporated in the assay.

65 We present here the development and phase I evaluation of a *T. brucei* specific PCR-
66 Oligochromatography test, called HAT-PCR-OC (Human African Trypanosomiasis-
67 Polymerase Chain Reaction-Oligochromatography). We have chosen the 18S ribosomal
68 RNA gene (rDNA) as the target for the HAT-PCR-OC since it is a multi copy gene that
69 contains sequences conserved within *Trypanosomatids* and species specific sequences (11).

70

71 **Methods**

72 **Parasite DNA**

73 DNA was obtained from *T. b. gambiense* (LiTat 1.3) and *T. b. rhodesiense* (STIB 382)
74 parasites amplified in HsdCpb:WU rats (Harlan, the Netherlands). Trypanosomes were
75 separated from the blood using di-ethyl-amino-ethyl (DEAE) chromatography (9), followed
76 by repeated centrifugation (20 minutes, 2000 g) and sediment washes with Phosphate

77 Buffered Saline Glucose (PSG) (38 mM Na₂HPO₄·2H₂O, 2 mM NaHPO₄, 80 mM glucose,
78 29 mM NaCl, pH 8.0). Trypanosome pellets were stored at –80°C. Twenty µl of
79 trypanosome pellet (approximately 2 × 10⁷ cells) were resuspended in 200 µl of Phosphate
80 Buffered Saline (PBS) (8.1 mM Na₂HPO₄·2H₂O, 1.4 mM NaHPO₄, 140 mM NaCl, pH 7.4)
81 and the DNA was extracted with the QIAamp DNA mini kit (Qiagen, Hilden, Germany),
82 resulting in pure DNA in 200 µl TE elution buffer. The typical yield of DNA extracted from
83 a 20 µl pellet was 150 ng/µl or 30 µg of total DNA. The extracts obtained were diluted 200
84 times in water and divided into aliquots of 2 ml in microcentrifuge tubes for storage at –
85 20°C. Purified DNA from other pathogens, *i.e. Leishmania donovani*, *Trypanosoma cruzi*,
86 *Mycobacterium tuberculosis*, *Plasmodium falciparum* and *Schistosoma mansoni* was
87 obtained from other research groups.

88

89 **Blood samples**

90 Informed consent was obtained from patients, or their parents or guardians and from non-
91 diseased persons. The human and animal experimentation guidelines of the Institute of
92 Tropical Medicine (Antwerp, Belgium) were followed.

93 *Non endemic controls*

94 Venous blood on EDTA from 28 healthy human Belgian blood donors who had never visited
95 a HAT endemic country (6).

96 *Endemic controls*

97 Venous blood on EDTA from 50 healthy human volunteers in Kinshasa, D.R. Congo.

98 *Sleeping sickness patients*

99 Venous blood on heparin from 26 *T. b. gambiense* patients enrolled in a clinical study
100 performed in D. R. Congo and with confirmed presence of parasites in the blood.

101 *Spiked blood*

102 Blood on EDTA spiked with *T. b. gambiense* (LiTat 1.3) parasites was used throughout the
103 development of the assay and for the estimation of its lower detection limit. Bloodstream
104 form trypanosomes were grown in rats. At day 3 post infection, tail blood was taken and
105 diluted in PSG and the number of parasites per ml was counted in a KOVA cell counting
106 chamber (Hycor Biomedical Inc., California, USA). A 10-fold dilution series of parasites
107 was made in freshly taken naive human blood, ranging from 10,000 parasites/180 µl to 1
108 parasite/180 µl blood. Non-spiked blood was used as negative control.

109

110 **DNA extraction from blood samples**

111 As recommended by Qiagen, 180 µl of blood were mixed with an equal volume of AS1
112 buffer (Qiagen, Hilden, Germany) and stored at ambient temperature until DNA extraction.
113 Blood can be stored in this stabilising buffer for up to three months in the dark without loss
114 of DNA quality. DNA was extracted with the QIAamp DNA mini kit (Qiagen, Hilden,
115 Germany) according to the manufacturer's instructions and stored at -20°C. Briefly, DNA is
116 adsorbed onto the silica-gel membrane in the QIAamp Spin Column, washed by two
117 centrifugation steps and eluted in 50 µl elution buffer. 180 µl sample of whole blood will
118 yield an estimated 3 - 12 µg of DNA. The internal control line in the oligochromatography
119 (see below) showed the presence of inhibitory factors in the extracted DNA in some samples
120 (1). In such cases, DNA was further purified as follows: 1/10 volume of 3 M sodium acetate
121 pH 5.2 and 2 volumes of ice-cold 100% ethanol were added, followed by overnight DNA
122 precipitation at -20°C. The suspension was centrifuged at 16,100 g for 15 minutes and the

123 DNA resuspended in 500 µl of 70% ethanol. The suspension was again centrifuged for 10
124 minutes at 16,100 g and the ethanol was removed. DNA was dried in a vacuum chamber for
125 at least 30 minutes and finally resuspended in 50 µl of water and stored at -20°C.

126

127 **Primers and probes (Fig. 1)**

128 Primers, biotinylated primers, internal control DNA and probes were synthesised by Sigma
129 (Bornem, Belgium).

130 *Primers*

131 Sequences of the 18S ribosomal RNA gene (rDNA) of the *Trypanosomatidae* parasites *T.*
132 *brucei gambiense* (GenBank accession number AJ009141), *T. brucei rhodesiense* (GenBank
133 accession number AJ009142), *T. cruzi* (GenBank accession number AF303660) and *L.*
134 *donovani* (GenBank accession number X07773) were aligned and primers (18S-F and 18S-
135 R) were designed to amplify a sequence of the *Trypanosomatidae* 18S rDNA using the
136 'DNAMAN' software (Lynnon Corporation, Quebec, Canada). Primers are situated in
137 *Trypanosomatidae* conserved sequences that surround a *T. brucei* conserved sequence. The
138 reverse primer 18S-R was biotinylated at the 5' end.

139 *T. brucei gold probe*

140 The alignments described above were used to design a 17 bp DNA probe that can hybridise
141 with a *T. brucei* specific sequence situated between the *Trypanosomatidae* conserved primer
142 sequences. Absence of putative secondary structures within the expected PCR amplicon was
143 checked via mfold version 3.1. (26). The probe was conjugated with gold particles using the
144 procedure described in Patent WO 2004/099438A1 (19).

145 *Internal control DNA*

146 The internal control DNA (IC DNA) was constructed to be of the same length as the *T.*
147 *brucei* sequence (106 bp). Its sequence is identical to the *T. brucei* sequence except for the
148 17 bp central part. This central part was designed to have the same GC content as the *T.*
149 *brucei* 17 bp sequence (Patent WO 2004/099438A1) (19).

150 *IC gold probe*

151 A DNA probe was designed that can hybridise with the 17 bp IC specific sequence within
152 the IC DNA. This IC probe was conjugated with gold particles as described above.

153 *Migration control probe*

154 The migration control probe is identical to the 17 bp central sequence of the IC DNA.

155

156 **PCR amplification**

157 An asymmetric PCR was designed using 4 fold more biotinylated reverse primer than
158 forward primer. The 50 µl reaction mixture contained 10 mM Tris-HCl (pH 8.3 at 25°C), 50
159 mM KCl (PCR buffer, Sigma, Bornem, Belgium), 200 µM of each deoxynucleotide
160 triphosphate (Roche, Mannheim, Germany), 2.5 mM MgCl₂ (Sigma, Bornem, Belgium), 0.2
161 µM forward primer 18S-F, 0.8 µM biotinylated reverse primer 18S-R, 0.1 mg/ml acetylated
162 bovine serum albumine (Promega, Madison, USA), 3.2 aM IC DNA, 1 U of HotStar *Taq*
163 polymerase (Qiagen, Hilden, Germany) and 5 µl of sample DNA. An initial denaturation step
164 of 94°C for 15 min to activate the HotStar *Taq* polymerase was followed by 40 cycles of
165 94°C for 30 s, 60°C for 30 s and 72°C for 30 s, with a final extension at 72°C for 5 minutes.
166 Amplification was conducted in 200 µl thin-wall PCR tubes (Abgene, Epsom, UK) in a T3
167 thermocycler 48 (Biometra, Göttingen, Germany).

168

169 **Oligochromatography**

170 *Preparation*

171 The Oligochromatography (OC) dipstick is constructed with polymer backing faced on each
172 side with a lower absorbent pad which overlaps a nitrocellulose membrane (in the middle)
173 and an upper absorbent pad (Fig. 2). The facing side represents the test for *T. brucei* and the
174 back is the control. The lower absorbent pad at the test side is impregnated with the *T. brucei*
175 gold probe and the lower absorbent pad at the control side is impregnated with the IC gold
176 probe. On the membrane at the test side, a line of Neutralite avidin (Belovo SA, Bastogne,
177 Belgium) is coated. On the membrane at the control side, two control lines are coated. A first
178 line of Neutralite avidin (control for PCR) and a second line of a probe that is
179 complementary to the IC gold probe (migration control). The OC conditions for the phase I
180 evaluation were as follows. The PCR product was denaturated at 94°C for 30 seconds and
181 kept on ice. Forty µl were mixed with an equal volume of migration buffer preheated at 55°C
182 followed by dipping the OC dipstick into the solution.

183 *Principle*

184 After amplification of a sample containing *T. brucei* DNA, the PCR product solution
185 contains both IC amplicons and *T. brucei* amplicons. During migration at 55°C through the
186 lower absorbent pad, the solution takes up the impregnated gold probes. The *T. brucei* gold
187 probe hybridises with the biotinylated strands of the *T. brucei* amplicons during migration.
188 These complexes accumulate on the Neutralite avidin line at the test side resulting in a
189 visible red line. On the back side the IC gold probe hybridises with the biotinylated strands
190 of the IC amplicons and these complexes accumulate on the Neutralite avidin line. Unbound
191 IC gold probe migrates further and is trapped by the complementary migration control probe

192 line. Both control lines determine whether the HAT-PCR-OC is valid or invalid (Fig. 3). The
193 migration control line should always be visible to validate the test. A test is invalid when
194 both the IC amplicon control line and the *T. brucei* test line are invisible (Fig. 3d) indicating
195 that the PCR reaction failed possibly due to inhibitory factors in the extracted DNA. When a
196 sample contains very high concentrations of *Trypanosomatidae* DNA, competition between
197 this target DNA and the IC template DNA for the primers can result in an invisible IC
198 amplicon control line combined with a strongly visible *T. brucei* test line (Fig. 3c). In the
199 latter case, the test is considered valid.

200

201 **Results**

202 **Analytical sensitivity**

203 The detection limit of the HAT-PCR-OC was evaluated on a serial dilution of *T. b.*
204 *gambiense* DNA in water. The lower detection limit was 5 fg of parasite DNA which is
205 about 1/40 of the DNA content of one parasite (Fig. 4a). Moreover, the test was able to
206 detect ten times less DNA compared to agarose gel electrophoresis (data not shown). The
207 lower detection limit was also evaluated on DNA extracted from a blood sample series
208 spiked with decreasing numbers of living *T. b. gambiense* parasites. HAT-PCR-OC was
209 consistently able to detect one single parasite in 180 μ l of blood (Fig. 4b). The assay
210 remained negative when non-spiked control blood samples were tested.

211

212 **Analytical specificity**

213 The species specificity of the HAT-PCR-OC was assessed on purified DNA from *T. b.*
214 *gambiense*, *T. b. rhodesiense*, *Leishmania donovani*, *Trypanosoma cruzi*, *Mycobacterium*

215 *tuberculosis*, *Plasmodium falciparum* and *Schistosoma mansoni*. Positive results were only
216 obtained with the two *T. brucei* subspecies (Fig. 4c).

217

218 **Diagnostic sensitivity and specificity (Fig. 5)**

219 HAT-PCR-OC was positive with the blood samples from all 26 *T. b. gambiense* sleeping
220 sickness patients and negative with blood samples from all 28 healthy Belgian blood donors.

221 With the 50 endemic negative control blood samples, 47 tests were valid and negative in

222 HAT-PCR-OC. Three test results were invalid since the IC for PCR was negative, indicating

223 the presence of PCR inhibitory factors in the extracted DNA. Therefore, DNA of these

224 samples was ethanol precipitated and resuspended in water. When re-tested, valid negative

225 test results were obtained. Thus, HAT-PCR-OC results corresponded fully with the infection

226 status of the sampled persons indicating 100% sensitivity and specificity.

227 **Discussion**

228 A major constraint for effective sleeping sickness control is imperfect diagnosis. Reliable
229 and fast diagnostic tools are desperately needed. The HAT-PCR-OC test described here has
230 been developed as a simplified molecular test for rapid and sensitive detection of *T. brucei*
231 parasites in blood samples. HAT-PCR-OC combines both the sensitivity and specificity of
232 PCR with the simplicity and speed of membrane chromatography (visible after 5 minutes by
233 the naked eye). OC, in contrast to conventional amplicon detection techniques, doesn't
234 require post-amplification preparation, neither sophisticated equipment. The data presented
235 here show that the assay is able to detect one single parasite in a 180 µl volume of blood.
236 When evaluated using both trypanosome positive patient and control trypanosome negative
237 samples, HAT-PCR-OC results corresponded 100% with the infection status of the tested
238 persons.

239 HAT-PCR-OC shows clear potential for implementation as a reference diagnostic test in mid
240 level equipped laboratory facilities (clean laboratories with power and cold storage) and will
241 be of particular value for evaluation of cure assessment during clinical trials of new drugs or
242 drug combinations. The simple detection methodology described here may facilitate PCR
243 application in HAT endemic countries. Further refinement of this assay will widen its
244 application. New simple nucleic acid extraction techniques together with novel isothermal
245 nucleic acid amplification methods such as loop-mediated isothermal amplification (LAMP)
246 (8, 14) and nucleic acid based amplification (NASBA) (4) will mean that the constraint to
247 field PCR (namely the need for thermocycling reactions) could be eliminated.

248 A further application of the HAT-PCR-OC test format would be for diagnosis of all
249 *Trypanozoon* infections since the detection probe is specific for all *Trypanozoon* taxa

250 including *T. b. brucei*, *T. evansi* and *T. equiperdum* that affect cattle, buffaloes, small
251 ruminants, camel and horses and that are responsible for severe losses in the agricultural
252 sector. This is of particular value for *T. b. rhodesiense* HAT in which case the disease is
253 maintained in the domestic animal reservoir (24).

254 A common drawback of PCR is the risk of sample contamination with PCR products leading
255 to false positive results. When implementing HAT-PCR-OC, one should take measures to
256 avoid this risk. The oligochromatography procedure should be performed in closed test tubes
257 and pre- and post-PCR manipulations should be physically separated, preferably in separate
258 lab spaces. Finally, used dipsticks should be thrown away after reading the result or should
259 be archived in a post amplification room.

260 To our knowledge this is the first nucleic acid based diagnostic test in dipstick format for
261 vector-borne diseases. The proof of principal for HAT-PCR-OC presented in this study
262 opens perspectives for its use in laboratories within countries where sleeping sickness is
263 endemic. The same format can be applied for other infectious diseases such as malaria,
264 tuberculosis, leishmaniasis, Chagas' disease, schistosomiasis, *etc.* for which more simple and
265 applicable molecular diagnostic tools are needed.

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276 **References**

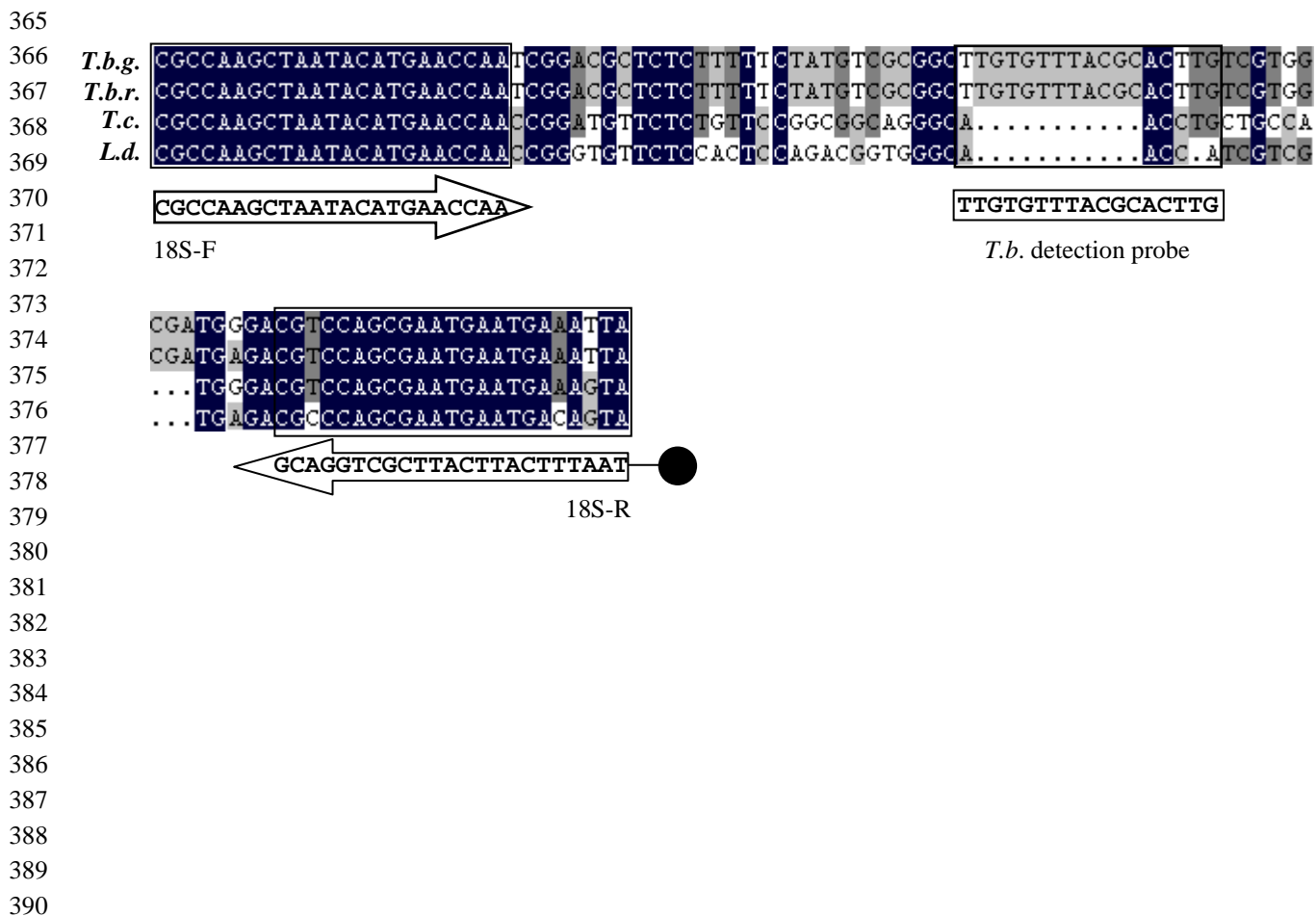
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358 Figure 1. Alignment of the HAT-PCR-OC target sequence within the 18S rRNA gene of the
 359 *Trypanosomatidae* parasites *Trypanosoma brucei gambiense* (*T.b.g.*) (GenBank accession
 360 number AJ009141), *Trypanosoma brucei rhodesiense* (*T.b.r.*) (GenBank accession number
 361 AJ009142), *Trypanosoma cruzi* (*T.c.*) (GenBank accession number AF303660) and
 362 *Leishmania donovani* (*L.d.*) (GenBank accession number X07773). Situation of the forward
 363 primer 18S-F, the biotin labelled reverse primer 18S-R, and the *T. brucei* (*T.b.*) detection
 364 probe. Gaps in the sequence are presented by dots.

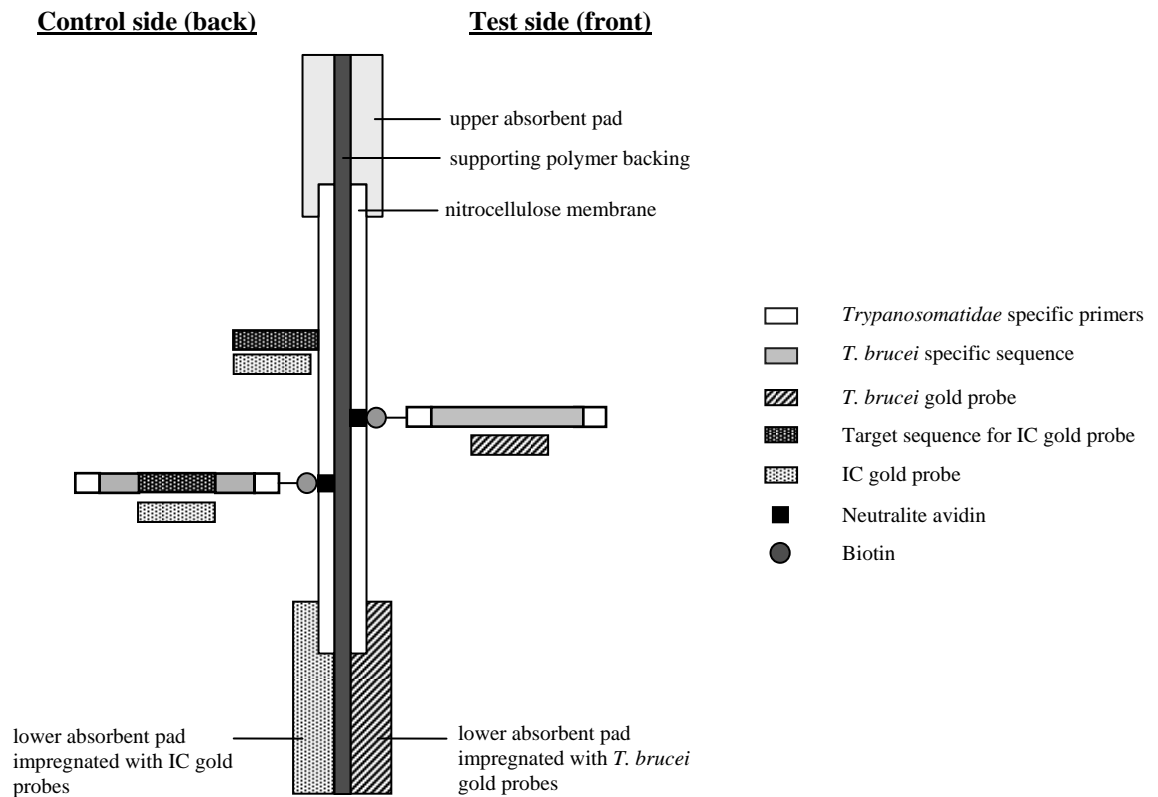


391 Figure 2. HAT-PCR-OC test principle

392 *Test side.* In case of a positive sample, during migration, the *T. brucei* gold probes hybridise
393 with the *T. brucei* amplicons that will accumulate on the Neutralite avidin line on the test
394 side of the stick.

395 *Control side.* During migration the internal control (IC) gold probes hybridise with IC
396 amplicons that will accumulate on the Neutralite avidin line on the control side of the stick
397 (control for PCR). The unbound IC gold probes hybridise with the complementary migration
398 control probes (migration control).

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402 Figure 3. Possible HAT-PCR-OC test result. a. valid test, positive result, b. valid test,
 403 negative result, c. valid test, positive result of a sample with high *T. brucei* DNA content, d.
 404 invalid test

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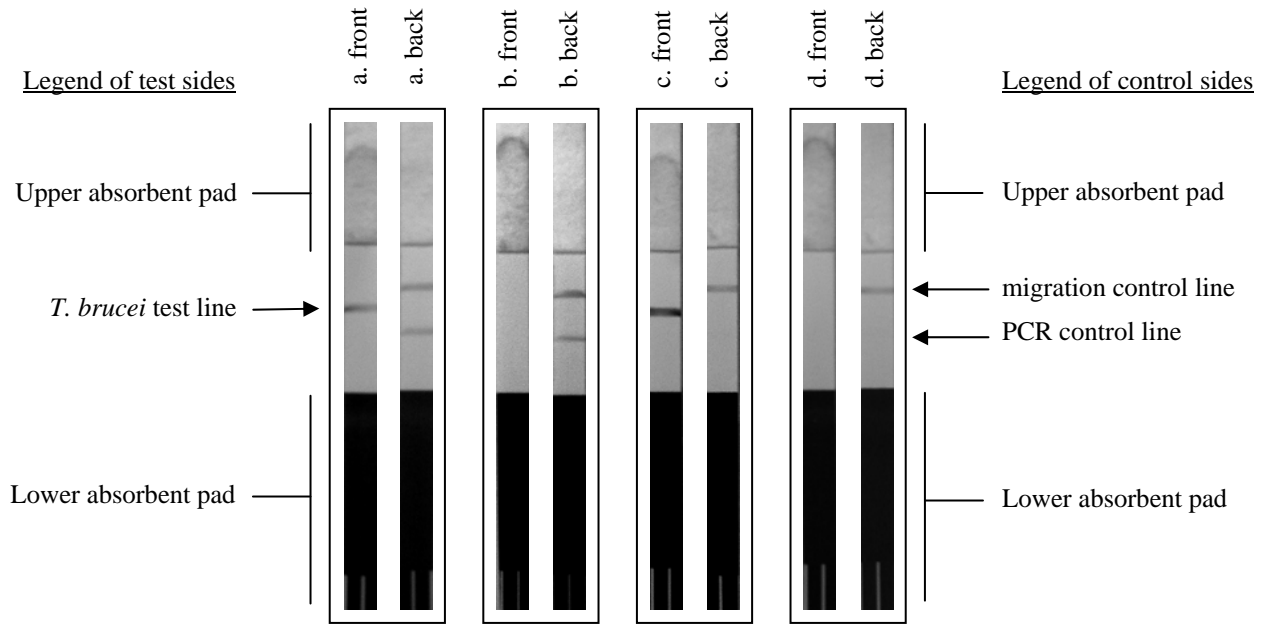
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423 Figure 4. Analytical sensitivity and species specificity of the HAT-PCR-OC test

424 a. Serial dilution of *T. b. gambiense* DNA in water. Dipstick 1 - 7: 500 pg, 50 pg, 5 pg, 500

425 fg, 50 fg, 5 fg, 0.5 fg per PCR reaction

426 b. Serial dilution of living *T. b. gambiense* bloodstream form parasites in naïve human

427 blood. Dipstick 1 - 6: 10,000, 1,000, 100, 10, 1, 0 parasites in 180 µl of blood.

428 c. HAT-PCR-OC results obtained with DNA from *T. b. gambiense* (dipstick 1), *T. b.*

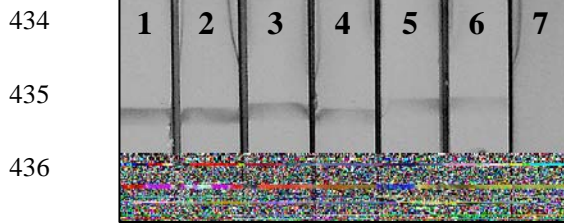
429 *rhodesiense* (dipstick 2), *Leishmania donovani* (dipstick 3), *Trypanosoma cruzi* (dipstick

430 4), *Mycobacterium tuberculosis* (dipstick 5), *Plasmodium falciparum* (dipstick 6) and

431 *Schistosoma mansoni* (dipstick 7).

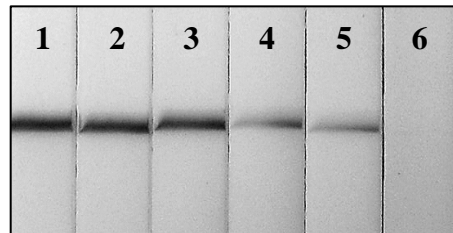
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433 a.

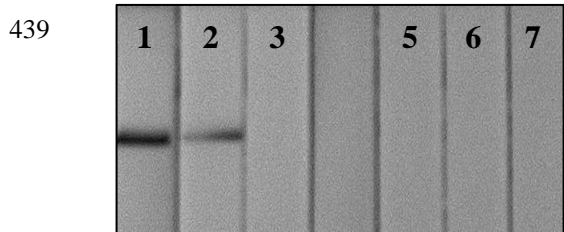


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b.



438 c.



440 Figure 5. Diagnostic sensitivity and specificity of the HAT-PCR-OC.

441 a. HAT-PCR-OC results for 26 blood samples from confirmed *T. b. gambiense* sleeping
442 sickness patients (dipstick 1 – 26) and one negative control (-).

443 b. HAT-PCR-OC results for one positive control (+) and for 5 blood samples from endemic
444 negative controls (dipstick 1 – 5).

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