

Performance of ParaHIT® HRP2-Based Rapid Diagnostic Test and Proportions of Plasmodium falciparum Histidine-Rich Protein 2/3 Gene Deletions in Togo

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1	Performance of the ParaHIT [®] HRP2-based rapid diagnostic test and
2	proportions of <i>Plasmodium falciparum</i> histidine-rich protein 2/3 gene
3	deletions in Togo
4	
5	Running title: Performance of ParaHIT® for malaria diagnostic in Togo
6	
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48 Abstract

49	In areas where malaria is endemic, and microscopes are unavailable, rapid diagnostic
50	tests (RDTs) are essential tools for early diagnosis and prompt and effective treatment.
51	However, HRP2-based RDTs are threatened by the emergence of Plasmodium
52	falciparum parasites that do not carry the pfhrp2 or pfhrp3 genes, leading to false-
53	negative results. Therefore, the aim of this study was to evaluate the performance of the
54	ParaHIT® RDT together with the proportion of pfhrp2/3 gene-deleted P. falciparum
55	parasites in Togo.
56	The performance of RDT compared with microscopy and PCR was determined using
57	capillary blood collected by finger prick during a cross-sectional study conducted from
58	September 2021 to January 2022, in children aged 6–59 months at two sentinel sites.
59	Blood spots were collected for molecular analysis. Amplicons from the target regions
60	(exon 2 of <i>hrp2</i> and <i>hrp3</i> genes) were generated by multiplex nested PCR and
61	sequenced using Illumina's MiSeq protocol.
62	A total of 278 samples were analyzed for ParaHIT® RDT evaluation. The sensitivity and
63	specificity of the RDT test compared to microscopy were 96.4% and 85.7%, respectively,
64	which increased to 97.9% and 90.7%, respectively, when compared to PCR. Of the
65	microscopically and PCR-positive P. falciparum samples, 138 were sequenced to detect
66	pfhrp2/3 deletions. None of the parasites had a single pfhrp2 deletion or a single pfhrp3
67	deletion.

68 The ParaHIT[®] RDT demonstrated an acceptable level of performance in this evaluation,

69 confirming the use of HRP2-based RDTs for the detection of *P. falciparum* infection in

70 areas where microscopy is not available in Togo.

71 Keywords: RDT, malaria, *Plasmodium falciparum*, diagnostic performance, *pfhrp2*,
72 *pfhrp3*, Togo.

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- 74

76

75 Background

577 burden of malaria. The incidence of malaria (*i.e.,* cases per 1000 population at risk)

Over the past two decades, recent reports have shown a significant decline in the global

decreased from 81 in 2000 to 57 in 2019, before increasing to 60 in 2020[1]. However,

the African Region of the World Health Organization (WHO) has a higher burden of

80 malaria cases, accounting for 94% of global malaria cases (233 million) and 95% (580

81 000) of malaria deaths in 2022. Children under five years of age are the most affected,

82 accounting for about 80% of all malaria deaths in the region [2].

83 WHO recommends that all suspected cases of malaria should be confirmed by

84 microscopy or rapid diagnostic tests (RDTs) before treatment. Although microscopy of

85 Giemsa-stained thick/thin blood smears (TTBS) remains the reference method for

86 malaria diagnosis [3], it requires a trained microscope technician, meticulous

87 preparation, and a constant power supply to operate the equipment. These conditions

are not always available in most remote malaria-endemic areas, limiting its use [4].

89 Therefore, RDTs have been proposed as an alternative for malaria diagnosis. These tests 90 can be used by staff, including laypersons, but not necessarily by laboratory technicians 91 after limited training [5]. Their use has increased significantly in recent years with an 92 estimated 412 million RDTs distributed worldwide in 2018 [6]. The majority of these tests 93 (64%) detected only P. falciparum and were supplied to sub-Saharan Africa, with HRP2 94 being the predominant target. HRP2-based RDTs tend to be more sensitive and heat 95 stable than RDTs that detect lactate dehydrogenase (LDH) or aldolase [7]. Although the 96 antibodies on the test strip are designed to recognize the HRP2 antigen, they may also 97 cross-react with another antigen in the HRP family, namely HRP3, due to strong 98 similarities in the amino acid sequences. However, their performance is affected by a 99 number of factors, including low parasite density (DP) infections, particularly below 100 100 parasites/µL, and parasites with *pfhrp2* and *pfhrp3* gene deletions, which can lead to 101 false-negative results in infected individuals. Indeed, these deletion cases have been 102 reported in several West African countries, such as Mali, Senegal, Ghana, Nigeria, and 103 Burkina Faso [8–12]. This situation could contribute to an increase in the risk of malaria-104 related morbidity and mortality and poses a challenge for individual patient management 105 and for control and elimination efforts [13]. WHO has therefore recommended that 106 countries conduct representative baseline surveys of suspected malaria cases to 107 determine whether the prevalence of parasites with pfhrp2/3 deletions has reached a 108 threshold for RDT change (>5% *pfhrp2* deletions causing false-negative RDT results 109 [14]). Since 2004, Togo has introduced RDTs into its diagnostic arsenal, initially in health 110 facilities without microscopy and in the community by health workers, and more recently

in health facilities with microscopy because of their ease of use and rapid availability ofresults.

Several brands of RDTs have been used and evaluated with acceptable levels of
performance according to the WHO criteria. In 2021, ARKRAY Healthcare's PARAHIT[®]
RDT was introduced in Togo and made available to providers. Therefore, this study was
conducted to evaluate the performance of this RDT compared to microscopy and PCR
for the diagnosis of malaria in children aged 6–59 months seeking antimalarial treatment.
Detection of *Plasmodium falciparum* parasites with deletions in the *pfhrp2/pfhrp3* gene
was also carried out.

- 121

122 Methods

123 Study design and sites

124 This cross-sectional analytical study was conducted in Togo from September 14, 2021, 125 to January 29, 2022. Togo is a West African country with stable malaria transmission and 126 two predominant facies: sub-equatorial with two rainy seasons in the southern part of the 127 country and the tropical with a single rainy season in the northern part. The evaluation 128 used two sentinel sites to monitor the effectiveness of ACTs were used: The "la 129 Providence" hospital in Kouvé, a religious institution in the Maritime region, about 76 km 130 from the capital Lomé, and the Anié district hospital in the Plateaux region, 188 km from 131 Lomé. The two sites were sub-equatorial and were located in rural and urban areas, 132 respectively.

133 Study population and sampling

134 The target population was children aged 6–59 months, with an axillary temperature \geq 135 37.5°C, and/or a history of fever in the previous 24 hours, suspected of having malaria, 136 consulted at one of the two participating sentinel sites, and prescribed TTBS. 137 The calculation methods of Buderer et al. (1996) [15] were used to define the size of our sample. To estimate sensitivity and specificity, the formulae, Np= $\frac{Z_{a/2}^2 se(1-se)}{E^2}$ and 138 Nn= $\frac{Z_{a/2}^2 \text{sp}*(1-sp)}{F^2}$ were used to determine the total number of positive cases to be 139 140 included and the number of negative cases in the control group. Thus, for an estimated 141 sensitivity and specificity of 90%, with a tolerated margin of error (E) of 5% and an 142 accepted risk of error (α) of 5% (Z α /2 of 1.96), 139 blood smear-positive patients for P. 143 falciparum and an additional 139 blood smear-negative patients were required, for a total 144 sample size of 278 children. 145 The sensitivity of RDTs varies with parasite density [16,17]. When in good condition, 146 some products can achieve sensitivities similar to those typically obtained by field 147 microscopy (~100 parasites/µL) and may vary from product to product [18]. Thus, 148 malaria TTBS-positive patients were divided into two groups: a low parasite density 149 group (patients with asexual parasitemia counts per microliter between 50 and 1000) 150 and a high parasite density group (patients with asexual parasitemia per microliter 151 between 2000 and 10,000) [19-21]. The control group included patients who were 152 negative for all Plasmodium species. 153

155 Inclusion and exclusion criteria

156	Inclusion criteria were as follows: (a) a monospecific P. falciparum infection detected by
157	microscopic examination; (b) inclusion of patients with 50 to 1000 asexual parasites per
158	microliter in the low parasitemia group; 2000 to 10000 asexual parasites per microliter in
159	the high parasitemia group; individuals with a negative blood smear in the control group
160	and (c) signed written consent obtained from the parent/guardian of the children.
161	Children who did not meet the above criteria and whose parents/guardians voluntarily
162	refused to participate were not included in the study.
163	
164	Data collection
165	A structured questionnaire was used to collect socio-demographic characteristics of the
166	enrolled children, clinical symptoms, medical history and presence of other diseases, if
167	any.
168	
169	Laboratory tests
170	Each patient had a capillary blood sample taken for TTBS. Once the microscopy results
171	were known (parasitemia within a certain range or malaria negative), a second sample
172	was taken from the enrolled children for RDT evaluation and dried blood spots (DBS) on
173	Wattman type III paper for molecular analysis.
174	
475	This has a date to be a damage of

175 Thick and thin blood smears

176 Thick and thin blood smears were made on the same slide stained with 3% Giemsa for 177 45 minutes after fixing the thin blood smear with methanol for a few seconds [22]. The 178 slides were dried and examined under an immersion microscope at 100× magnification. 179 Thick smears were used to determine positivity and for parasite density counting, and 180 thin smears were examined to confirm the parasite species for positive samples. Parasite 181 density was calculated as: number of parasites counted × 6000/number of leukocytes 182 counted using the WHO method [22].

183

184 **Rapid diagnostic test**

185 ParaHIT[®] f ver. 1.0 de ARKRAH Healthcare Pvt. Ltd., which is a WHO pregualified RDT 186 for the diagnosis of *P. falciparum* malaria [21], is based on the principle of 187 immunochromatography, in which a nitrocellulose membrane is coated with an anti-HRP 188 Il antibody (capture antibody) specific for *P. falciparum*. The test was performed in the 189 laboratory by the study staff for each enrolled subject according to the manufacturer's 190 instructions and the results were interpreted. Eight µl of capillary blood from the finger 191 prick was immediately transferred with the micropipette, to the square window "A" of the 192 test device, and then four drops of reaction buffer were transferred to the round window 193 "B." The results were read after 20 to 30 minutes.

194

195 **Real-time PCR assays**

196 DBS was cut into small pieces and transferred to 2 mL microtubes. Genomic DNA was 197

extracted using the QIA amp DNA Mini Blood Kit according to the manufacturer's

198 protocol with some minor modifications [23]. Elution plates containing the extracted DNA 199 were stored at - 80 °C until use. Samples were screened for the presence of 200 *Plasmodium* DNA using a qualitative real-time PCR assay targeting the *cytochrome b* 201 gene. DNA samples identified as positive for *Plasmodium* were then diluted 1:10 and 202 analyzed using a nested real-time PCR assay with primers targeting the same gene 203 fragment and specific for *P. falciparum*. All real-time PCR assays were performed using 204 SYBR green ready-to-use PCR mix (Solis Biodyne, Tartu, Estonia) on a 5 µL DNA 205 template on a BioRad CFX96 real-time PCR system (BioRad) [24]. Details of the PCR 206 program, mix composition, and primer sequences were previously described by Canier 207 et al. [25].

208

209 Detection of pfhrp2/3 gene deletions

210 TTBS- and PCR-positive samples for *P. falciparum* were selected for testing in the 211 absence of the phrp2 and phrp3 genes [8]. Amplicons from the targeted regions (exon 2 212 of the *hrp2* and *hrp3* genes) were generated using multiplexed nested PCR assays with 213 indexed primers containing specific tags (barcodes) [26,27]. A total of 4 µl of PCR 214 reactions from each sample were pooled (96 samples) to increase the sample volume 215 and minimize sample consumption for downstream protocol steps. For each pool, 216 amplicons were purified using AMPure XP beads (Beckman Coulter) according to the 217 manufacturer's protocol to remove dNTPs, salts, primers, and primer dimers. The quality 218 of the purified PCR products was assessed by analysing the eluates containing the 219 purified amplicons on a Bioanalyzer Agilent 2100 (Agilent). The concentrations of the

220 pooled fragments were assessed by fluorometric quantification (Qubit, Thermo Fisher). 221 The pooled libraries were denatured with NaOH to a final concentration of 0.1 N and 222 diluted with hybridization buffer prior to sequencing. Sequencing was performed using 223 the MiSeg v2 reagent and a 300-cycle kit (Illumina) according to the manufacturer's 224 recommendations. Raw sequences were demultiplexed and quality trimmed to a Phred 225 score of 30. Primer sequences were trimmed from the 5'-end of the sequences to avoid 226 primer bias in the sequenced fragments. Base calling was performed by comparing the 227 reads to a custom database consisting of the 3D7 reference sequence (PlasmoDB v45). 228 Bioinformatic analyses were performed using the CLC Genomics Workbench 24 229 software (Qiagen). To detect a deletion of the hrp2 or hrp3 genes, we compared the 230 coverage of each target gene with the coverage of the amplicons generated for hrp2 and 231 hrp3. If the coverage of the hrp2 or hrp3 gene was zero or <1% relative to the coverage 232 of the other target genes, we considered the gene to be deleted. 233 For each plate, we tested DNA from laboratory reference parasite strains for which the 234 presence or absence of hrp2 and hrp3 deletions was known, as controls: a Cambodian

strain 3601 and 7G8 without deletions, Dd2 with an hrp2 deletion and HB3 with an hrp3deletion).

237

238 **Quality control**

Duplicate readings were performed on each slide by two experienced microscopists
[28], one of whom is WHO level 2 accredited for malaria diagnosis, and the other is from
Togo National Reference Laboratory (Institut National d'Hygiène). If the coefficient of

242	variation of the estimated parasitemia was > 5% [29], a third reading was performed by
243	an independent microscopist [22]. If there was a difference between the study site
244	parasitemia and the results found by quality control, parasitemia of the quality control
245	was considered. The estimated parasitemia was used to create the three groups.
246	To ensure the reliability of the RDT results, the kit instructions were followed. The control
247	band should appear regardless of whether the sample is reactive or non-reactive.
248	Visualization of the control band indicated the successful migration of the
249	reaction mixture.
250	For the real-time PCR screening runs, a set of four controls (two DNA positive controls: a
251	high positive control, Pf 3D7 DNA extract at 0.1 ng/ μ l and a low positive control, Pf 3D7
252	DNA extract at 0.001 ng/ μ l and two negatives: water) were added to the 96-well plate
253	before performing the real-time PCR run. Laboratory reference parasite strains (Dd2,
254	7G8, HB3, and the 3601 strain, a Cambodian culture-adapted parasite) with known
255	alleles of each gene were used as controls for the analysis of <i>pfhrp2</i> and <i>pfhrp3</i> gene
256	deletions [27].
257	Training of field team members and supervisors was conducted to standardize working
258	methods and ensure the smooth running of the activity, especially for completing
259	questionnaires and conducting RDT, TTBS, and filter paper sampling.
260	
261	Endpoints
262	Thick/thin blood smear and PCR results were used as reference methods for this

263 evaluation against which RDT results were compared. Sensitivity, specificity, positive

264	predictive value (PPV), and negative predictive value (NPV) are the estimated
265	performance indicators of RDT. Sensitivity and PPV were calculated for low and high
266	parasitemia, respectively.
267	
268	Data management and analysis
269	Data were recorded on registration forms, entered into a Microsoft Excel database
270	(Microsoft Corp, Redmond, Washington, USA), and analyzed using $MedCalc^{\circ}$ version
271	20.218 (MedCalc Software Ltd, Ostende, Belgium; https://www.medcalc.org ; 2023). The
272	sensitivity, specificity, and positive and negative predictive values of the RDTs were
273	determined by microscopy or PCR using 2×2 contingency tables. Exact 95%
274	confidence intervals (95% CI) were calculated for each of the above measures.
275	Bioinformatic analyses were performed using CLC Genomics Workbench 22 software
276	(Qiagen).
277	
278	Ethical considerations
279	The study protocol was approved by the Bioethics Committee for Health Research
280	(CBRS) of Togo (N°021/2021/CBRS of May 27, 2021) before its implementation. In
281	addition, signed informed consent was obtained from the parents or guardians of the
282	children. Any patient testing positive by at least one of the methods was referred to the
283	site clinicians for free treatment with an antimalarial drug available through the National
284	Malaria Control Program.
285	

287 **Results**

288 Characteristics of the study participants

- 289 Of the 369 children screened at the 2 sites, 287 were included in the study, for an
- inclusion rate of 77.8%. Nine patients were excluded for quality control (parasitemia
- 291 outside the accepted range). The final number of patients for analysis was 278 (*Figure*
- 292 1). The mean age of the included patients was 31 (± 1) months, and the sex ratio (M/F)
- was 0.9. Children with a body temperature ≥ 37.5 °C represented 79.5%, and the others
- reported having had a febrile episode in the previous 24 hours. The socio-demographic
- characteristics of the children are summarized in *Table 1*.
- 296 The evaluation of the ParaHIT[®] RDT compared to microscopy included 278 patients, of
- which 140 were in the control group, 41 in the low parasitemia group, and 97 in the high
- 298 parasitemia group (*Table 2*).
- 299

300 Performance of RDT evaluated compared to microscopy

- 301 The sensitivity and specificity of the ParaHIT[®] RDT compared with TTBS for the
- 302 detection of *P. falciparum* were 96.4% [CI = 91.7-98.8] and 85.7% [CI = 78.8-91.1],
- 303 respectively; the PPV and NPV values were 86.9% [CI = 81.6-90.9] and 96.0% [CI = 91.0-
- 304 98.3], respectively (*Table 3*).

305 Performance of evaluated RDTs compared to PCR

- 306 For the PCR analysis, plasmodial DNA was not successfully amplified in five samples
- 307 due to the poor quality of the DBS, leading to DNA degradation; these were microscopy-
- 308 negative samples. Therefore, the estimation of the performance of the evaluated RDT

309	compared with PCR was estimated for a total of 273 patients divided into 129 for the
310	PCR-negative group and 144 for the <i>P. falciparum</i> PCR-positive group (<i>Table 2</i>). The
311	sensitivity of the ParaHIT [®] RDT compared to PCR for the detection of <i>P. falciparum</i>
312	infection was 97.9% [CI = 94.0-99.6], and the specificity was 90.7% [CI = 84.3-95.1]. The
313	PPV and NPV values were 92.2% [CI = 87.3-95.3] and 97.5% [CI = 92.7-99.2],
314	respectively (<i>Table 3</i>).
315	
316	Detection of <i>pfhrp2/3</i> gene deletions
317	All 138 microscopy-positive samples were positive by P. falciparum species-specific
318	PCR and were analyzed for <i>pfhrp2</i> and <i>pfhrp3</i> deletions (<i>Figure 1</i>). The extracted DNA
319	isolates were successfully sequenced to detect phrp2 and phrp3 deletions. None of the
320	parasites had a single <i>pfhrp2</i> deletion or a single <i>pfhrp3</i> deletion.
321	
322	Relationship between RDT results and <i>pfhrp2/3</i> gene deletions
323	Five samples were microscopy-positive and RDT-negative, and none showed a deletion
324	of <i>pfhrp2/3</i> . Of these, three had parasite densities of 70, 329, and 781 parasites/µl,
325	respectively, and would likely have been missed by the RDT due to low parasitemia. The
326	other samples had high parasite densities (2,176 trophozoites/µl and 2,187
327	trophozoites/µl).
328	
329	

331 Discussion

332 RDTs have been developed for their ease of use in the early diagnosis of malaria. 333 especially in endemic countries where microscopy is not available [30]. Although the 334 WHO and the Foundation for Innovative New Diagnostics (FIND) conduct detailed 335 performance evaluations of these tests, it is important that field evaluations are carried 336 out in endemic areas. For example, the WHO requires all RDTs to have a minimum 337 sensitivity of 95% compared to microscopy and a minimum specificity of 90% for all 338 malaria species [31]. Therefore, this study evaluated the diagnostic performance of the 339 PARAHIT[®] ver. 1.0 RDT used in health facilities in Togo and the prevalence of associated 340 *pfhrp2/pfhrp3* gene deletions in samples.

341 The results showed a sensitivity of 96.4% and a specificity of 85.7% for the PARAHIT® 342 RDT, using microscopy as the reference method. These performance levels are similar 343 to those found in Uganda, where an evaluation of the same RDT in field use found a 344 sensitivity of 97.4% and a specificity of 88.1% in field use [32]. These values are slightly 345 lower than those reported in the WHO pregualification report for this RDT (sensitivity : 346 99.42%, specificity : 99.59%) [33]. The difference observed between our results and 347 those of the WHO pregualification report may be explained by the difference in the 348 samples used to test the RDT (a series of Plasmodium falciparum wild-type parasites and 349 negative panels in the WHO pregualification study and field isolates in our study). In our 350 evaluation, sensitivity was proportional to parasitemia, reaching 97.9% when parasitemia 351 was up to 2000 parasites/µL, whereas sensitivity was only 92.7% when parasitemia was 352 less than 1000 parasites/µL. Our results corroborate those of an evaluation of the

353 CareStart[™] RDT in an area of unstable malaria, where the highest sensitivity (95.8%) 354 was found for parasite densities > 5000 parasites/ μ L [17,34]. However, another study 355 conducted in a hyperendemic area of *P. falciparum* malaria showed no change in 356 sensitivity with decreasing parasitemia [5]. The specificity observed in our evaluation 357 (85.7%) was slightly lower than that recommended by the WHO (90%). These false 358 positives could be due to the persistence of the HRP2 antigen after treatment. Indeed, 359 Grandesso et al. [35] showed that the median time to become negative for HRP2-based 360 tests was 35–42 days. Another study supporting this finding showed that this persistence 361 can be up to 52 days [36]. It has also been suggested that rheumatoid factor may cause 362 false positives due to binding to IgG [37]. Although the use of IgM is thought to reduce 363 the problem of rheumatoid factor cross-reactions [15], it is not known which type of 364 antibody is used to coat the PARAHIT[®] RDT [31]. 365 Regarding the predictive accuracy of the RDT used for malaria diagnosis in the current

study, the PPV was 86.9%, while the NPV was relatively high at 96.0%. Bouah-Kamon *et*

al. in their study in 2018 showed a similar PPV (87.1%) for "SD Bioline Malaria Antigen Pf

[®] (HRP2)" [38]. However, it should be noted that PPVs are a function of disease

369 prevalence. Indeed, a study conducted in Burkina Faso found that the PPV and NPV of

370 RDT in the dry season were 9% and 99.8%, respectively, compared with 82% and 84%

in the rainy season for infants and over 99% for adults [39].

372 When PCR was used as the reference method, higher performance levels were

373 observed for the PARAHIT[®] RDT. The sensitivity and specificity of the test were 97.9%

374 (96.4% compared to microscopy) and 90.7% (85.7% compared to microscopy),

375 respectively. The same result was reported by Diallo *et al.* in Senegal (sensitivity: 97.3%
and specificity: 94.1) [40]. In our study, some RDT-positive but microscopy negative
377 results could indicate submicroscopic infections. Indeed, PCR can detect parasites at
378 levels as low as 0.002 P/µL, thus detecting submicroscopic infections in the population
379 [17].

380 This study also provides data on parasites with *pfhrp2/3* gene deletions. None of the 381 isolates had a single *pfhrp2* deletion or a single *pfhrp3* deletion. The proportion of false-382 negative RDTs compared with microscopy (3.6%) found in our evaluation was probably 383 not related to the pfhrp2/3 deletion, but rather to their low parasitemia, below the 384 detection threshold of the HRP2-based RDT. Other factors, such as the lot-to-lot 385 variability of the RDT used, operating error or potential epitope variations that could 386 account for these unexpected false negatives in RDT result. [41-44]. In the Democratic 387 Republic of Congo, a study of asymptomatic children did not find parasites with a 388 pfhrp2/3 deletion [45]. In West Africa, several studies have shown the presence of this 389 deletion: Funwei et al. in Nigeria (10.6% pfhrp2 deletion, 6.0% pfhrp3 deletion, and 6.1% 390 combined pfhrp2/3 deletion) [10] and Tarama et al. in Burkina Faso (4.4% pfhrp2 391 deletion) [8]. The variability in prevalence suggests that geographical and 392 methodological differences influence the diversity of pfhrp2 prevalence in malaria-393 endemic regions. In Ghana, Amoah et al. reported pfhrp2 gene deletions in 33.3% and 394 36.2% of microscopically confirmed and PCR-confirmed RDT-positive samples, 395 respectively, in Accra [11], whereas Addai-Mensah et al. found no deletions in the Volta 396 region [46].

397 Our study had several limitations. The sample size was smaller than that recommended 398 by the WHO in the surveillance template protocol for *pfhrp2/pfhrp3* gene deletions, 399 which is 370 confirmed cases of *P. falciparum* malaria per region, although the sample 400 size may vary depending on logistical and budgetary constraints [7]. Nevertheless, it is 401 worth noting that the target population is consistent, i.e., individuals with fever seeking 402 care at health care facilities. Indeed, our study included febrile children with suspected 403 malaria who presented to health facilities. Therefore, another study with a larger sample 404 size would better estimate the proportion of *pfhrp2/pfhrp3* gene deletions in Togo.

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407 **Conclusion**

The PARAHIT[®] RDT showed acceptable levels of performance in this evaluation
compared to TTBS as the reference method. Higher levels of test performance were
observed when PCR was used as the reference method due to its higher sensitivity than
microscopy. In addition, none of the isolates showed a deletion of the *pfhrp2/3* gene in
the samples evaluated. The results of this study support the use of HRP2-based RDTs to
confirm *P. falciparum* infections in Togo.

414

415 Authors' contributions

416 DCT, AMD, EA, and KY conceived of and designed the study. AMD led to training and

417 oversaw its implementation in Togo. AMD, EA, KY, ES, and MH supervised the data

418 collection. DCT, AMD, EA, and DM drafted the analysis plan; provided data analysis and

419 interpretation; and wrote the first draft of the manuscript. All authors have read, revised,420 and approved the final manuscript.

421

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437 All the data used to draw the conclusions of the study are provided in the manuscript.438

439 **Consent for publication**

440 Not applicable.

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609	Figure legend		
610	Figure 1: Flow diagram for the sele	cting samples	
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613	Tables		
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615	Table 1: Patients' sociodemograph	ic characteristics and	clinical signs
	Baseline characteristics (N = 278)		
	Sex, n (%)		
	Female	141 (50.7)	
	Male	137 (49.3)	
	Age in months, n (%)		
	6-59	278 (100)	
	Median temperature, °C (range)	37.8 (36-40.3)	
	Residence, n (%)		
	Rural	100 (36.0)	
	Urban	178 (64.0)	
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Table 2: Total number of samples included by defined site

Sites	Anié, n (%)	Kouvé, n (%)		
Microscopy (TTBS)				
Negative (n = 140)	75 (27.0)	65 (23.4)		
Positive				
Low parasitemia (n = 41)	26 (09.3)	15 (05.4)		
High parasitemia (n = 97)	77 (27.7)	20 (07.2)		
Total (n = 278)	178 (64.0)	100 (36.0)		
PCR				
Negative (n = 129)	66 (24.2)	63 (23.1)		
Positive (n = 144)	110 (40.3)	34 (12.4)		
Total (n = 273)	176 (64.5)	97 (35.5)		

	Positive RDT	Negative RDT	*SE% [95% CI]	*SP% [95% CI]	*PPV% [95% CI]	*NPV% [95% CI]
Місгоѕсору						
Low parasitemia						
Positive (n=41)	38	3	92.7 [80.1-98.5]	-	65.5 [55.7-74.2]	-
Negative (n=140)	20	120				
High parasitemia						
Positive (n=97)	95	2	97.9 [92.8-99.7]		82.6 [76.0-87.7]	-
Negative (n=140)	20	120		-		
Total						
Positive (n=138)	133	5		85.7 [78.8-91.1]	86.9 [81.6-90.9]	96.0 [91.0-98.3]
Negative (n=140)	20	120	96.4 [91.7-98.8]			
PCR						
Positive (144)	141	3	97.9 [94.0-99.6]		92.2 [87.3-95.3]	97.5 [92.7-99.2]
Negative (129)	12	117		90.7 [84.3-95.1]		

Table 3: ParaHIT® performance compared to TTBS and PCR for detecting *P. falciparum*.

628 #: Low parasitemia =50-1000 asexual parasitaemia/µl; high parasitemia=2000-10000 asexual parasitaemia/µl



Figure 1: Flow diagram for the selecting samples