Molecular detection and quantification of Plasmodium falciparum gametocytes carriage in used RDTs in malaria elimination settings in northern Senegal

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Research

Keywords: Malaria, RDT, Gametocytes, DNA extraction, Quantification, Plasmodium falciparum, qPCR

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Abstract

Background: Malaria surveillance requires powerful tools and strategies to achieve malaria elimination. Rapid diagnostic tests for malaria (RDTs) are easily deployed on a large scale and are helpful sources for the parasite's DNA. The application of sensitive molecular techniques to these RDTs is a modern tool for improving malaria case detection and drug resistance surveillance. However, the detection of the parasite with these RDT based tools has so far only concerned asexual forms of P. falciparum. The knowledge of gametocyte carriage in the population is important to better assess the level of parasite transmission in elimination settings. The aim of this study was to develop the quantitative real time PCR technique to detect gametocytes of P. falciparum from RDTs and to provide a new tool for the molecular monitoring of malaria transmission.

Methods: DNA was extracted from 303 RDT devices (SD Bioline Malaria Pf) using the Chelex-100 protocol. qPCR was performed in a 20 µL reaction to detect and quantify transcripts of the pfs25 gene. The cycle threshold (Ct) was determined by the emission fluorescence corresponding to the initial amount of amplified DNA.

Results: We found an overall prevalence of 53.47% with an average Ct of 32.12 ± 4.28 cycles. In 2018, the prevalence of gametocytes was higher in the Ranérou district (76.24%) than in the Saint-Louis district (67.33%) where an increase in the number of gametocyte carriers in 2018 was noted, in comparison with 2017.

Conclusions: RDTs are a good source of DNA for molecular monitoring of gametocyte carriage. This method, described for the first time, is a simple and effective tool to better understand the level of malaria transmission and reach elimination. Keywords: Malaria, RDT, Gametocytes, DNA extraction, Quantification, Plasmodium falciparum, qPCR.

Background

The presence of mature gametocytes (stage V) in the human peripheral blood is the determining factor in the maintenance and increase of malaria transmission [1]. In Senegal, progress in the fight against malaria led the program to become part of the regional elimination of malaria by introducing primaquine in the management of the disease in the north of the country in order to reduce malaria gametocyte carriage in the population and block the transmission of the disease [2,3].

Gametocytes are sexual forms of the parasite that are transmitted from the human host to mosquito vectors and thus perpetuate the transmission of malaria [4,5,6]. The passage of gametocytes to vectors is possible even in sub-microscopic low-density situations in human blood (<4 gametocytes / µl) [1,4,7]. The detection and quantification of specific gametocytes from modern molecular techniques such as the quantitative Reverse Transcriptase Polymerase Chain Reaction (qRT-PCR) have shown a high frequency of sub-microscopic densities [1,7]. Even after treatment with antimalarials, the gametocytes persist for several weeks after the clearance of asexual parasite forms with longevity depending on the nature and dose of the treatment administered as well as the immune response of the host [6]. Treated subjects carrying gametocytes in their blood are potential reservoirs of the parasite [7]. The development of modern tools for the identification of these reservoirs is necessary to achieve the elimination of malaria [4,6,8].

Since mosquito infection requires the presence of gametocytes in humans, knowledge of the epidemiology of gametocyte carriage is an essential parameter for assessing malaria transmission and predicting infectiousness in vectors [1,7,8]. Some molecular techniques are used today for the detection and quantification of gametocytes [9,10]. The complexity and cost of these tests limits their use in resource areas.

Large-scale RDTs in endemic countries are now used as sources of parasite DNA [11,12] and have helped develop molecular tools to improve malaria surveillance [13,14,15]. Recently, numerous studies have detected asexual forms of *P. falciparum* in TDR samples by PCR [16]. However, no study has been conducted to detect and quantify gametocytes from these RDTs.

This study aimed to develop a new tool to determine the gametocyte carriage on RDT samples used by the quantitative real time PCR (qPCR) technique. This is the first study on the detection of gametocytes from collected RDTs that can be applied to the molecular monitoring of malaria in northern Senegal.

Methods

Study area and field samples

RDTs were collected as part of malaria surveillance in northern Senegal where the incidence of malaria is low (<5 ‰). Febrile patients who went to public or private health facilities were tested by RDTs and treated. All TDRs used (negative and positive) were stored in plastic bags at room temperature (Fig 1A).

In Senegal, malaria transmission is closely related to the rate of rainfall and generally increases during the rainy season. The density of vector populations is dependent on rainfall.

For this study, two (2) health districts of two (2) regions were concerned, including that of Saint-Louis in the Saint-Louis region and that of Ranerou in the Matam region. The large shares of malaria cases recorded in the two regions were reported in these two districts. In recent years, the district of Saint-Louis had recorded the majority of malaria cases in the Region. As part of malaria elimination, the program of Senegal began in 2018 to use primaquine combined with the usual treatment of malaria cases in this area to reduce gametocyte carriage and malaria transmission. The 2018 epidemiological data showed that the number of malaria cases in this district had doubled compared to 2017 despite the intensification of control strategies. In order to better appreciate the impact of primaquine on gametocyte carriage, we have chosen to study the gametocyte prevalence in 2018 in the district of Saint-Louis, which will be compared with the prevalence in 2017 before using primaquine and the prevalence in 2018 in the district of Ranérou where primaquine is not used. At the time of testing, patients were informed about the protocol and their consent was obtained.

We randomly selected a total of 303 positive RDTs from different time periods and sites. In Saint-Louis, we chose 101 positive TDRs completed in 2017 and 101 completed in 2018. In Ranérou 101 positive TDRs of 2018 were chosen.

RDT devices

The RDTs used in the northern part of the country for malaria surveillance were SD-Bioline Malaria Ag Pf for the detection of *P. falciparum* specific Histidine-Rich Protein II (HRP-II) antigen. DNA extraction was done by opening the TDR cassettes (Fig. 1C).

RDT-DNA extraction methods

Several methods for extracting *P. falciparum* DNA have been described [11,17]. We used the DNA extraction protocol with Chelex-100 described by Wooden J. et al (1993) which is the result of a combination of several techniques taking into account a variable number of strains of the parasite [18]. The RDTs were opened using a metal spatula to access the nitrocellulose strip. This band was taken using forceps and the blood deposition and absorption filters were cut into small pieces in labeled Eppendorf tubes (Fig. 1C). The migration zone of the blood sample on the nitrocellulose membrane was carefully scraped with a scalpel to collect the maximum amount of DNA from the devices (Fig. 1D). For each sample the material used was cleaned in 96% ethanol, then rinsed with water and dried on clean tissue paper, to minimize cross-contamination during sample preparation.

In each tube, 800 µl of 0.5% Saponin solution containing 0.5 g of saponin and 100 ml of PBS diluted to 1x were added. The tubes were then centrifuged for 10 minutes at 150 rpm and incubated at room temperature overnight. The liquid was completely aspirated from the tubes by using a micropipette and the samples were then washed twice by adding 800 µl of 1xPBS for 5 minutes. We added 150 µL of sterile water and 75 µL of 20% Chelex solution into the tubes, which were tightly closed and vortexed for 15 seconds and incubated with a dry-bath incubator for 8 minutes. After centrifugation at maximum speed for 5 minutes, the supernatant containing the DNA was aspirated with a micropipette and then transferred to sterile tubes leaving the Chelex at the bottom of the tube [18].

qPCR assay

The validation of the technique was done using 6 different samples. Two (2) different RDT samples (Paracheck ™ -Pf and SD Bioline Malaria Ag-Pf) were made by depositing 5 µL of gametocyte culture in the RDT wells. From the same culture 50 µL were deposited on a filter paper. To these samples we added two more positive RDTs whose gametocytes with different densities were identified by microscopy and another sample of filter paper whose PCR was positive for the detection of gametocytes as a positive control. qPCR-steps were done in duplicate for samples. The SYBR Green Master Mix has been standardized to detect and quantify Pfs 25 gene transcripts using the BIO-RAD CFX96™ tool which showed positive results.

Field sample analysis

The real time-PCR was performed in a 20 µL reaction. The reaction was prepared with SYBR Green Master Mix, Forward and Reverse primers used for amplification of *Pfs 25*, DNA template and Nuclease-Free Water. Each 20 µL reaction mixture contained 2 µL of sample cDNA, 10 µL of 2x SYBR Green master mixtures, 2.25 µL of primers at a final concentration of 300 nM and 5.75 µL of Nuclease-Free Water. Amplification included a template denaturation step at 95°C (10 min) followed by 45 cycles of 15 seconds at 95°C, and 1 minute at 60°C, with fluorescence acquisition at the end of each extension step. Reactions were run in 96-well PCR plates on a Bio-Rad CFX Connect real time PCR Detection System. For our study we used 4 plates for 303 samples.

Data analysis

We used the Bio-Rad CFX Manager 3.0 software for the post-amplification data analysis.

Quantification cycle (Cq) or cycle threshold (Ct) determination mode was set to single threshold with baseline-subtracted curve fit and a user defined threshold of 50 relative fluorescence units (RFUs) for analysis of parasite. A cycle threshold value (Ct) <35 was chosen for positive PCRs. Samples with a cycle value greater than 35 Ct were considered negative for PCR. The data was also exported to Excel and analyzed with the Epi Info software.

Results

Amplification of pfs25 gene transcripts by quantitative real-time PCR

We standardized a qualitative and conventional qPCR protocol to detect pfs25 gene transcripts in RDT samples. With this method, 162 of the 303 RDT samples analyzed (53.47%) were positive (Table 1). Negative samples did not show gene amplification or showed amplification after 35 cycles (n=141). (Fig 2A)

The Ct is the threshold point at which the fluorescence signal is significantly greater than the background noise, i.e., the minimum number of cycles for which the amplified DNA is detectable. The average Ct was 32.12 with standard deviation of 4.28. The minimum number of cycles observed for DNA amplification was 8 cycles corresponding to the presence of a very large initial amount of parasite DNA (Fig. 2D).

Gametocyte carriage

Amplification of the Pfs25 gene allowed the detection of gametocytes on each RDT. The fluorescence emission determines a Ct value that reflects the initial amount of DNA (2B). When the Ct is low the initial amount of DNA is large. For the qPCR positive samples (n=162) gene transcription was shown before 35 cycles. The overall gametocyte prevalence was 53.47% (162/303) (table 1).

Table 1 : Gametocyte carriage by study area and by year of samples collection

RESULTS	SITES			TOTAL
	Ranérou 2018	Saint-Louis 2017	Saint-Louis 2018	
Negative	24	84	33	141
%	23,76%	83,17%	32,67%	46,53%
Positive	77	17	68	162
%	76,24%	16,83%	67,33%	53,47%
TOTAL	101	101	101	303

In the year 2018 the gametocyte prevalence was 76.24% (77/101) in the Ranérou district and 67.33% (68/101) in the Saint-Louis district (Table 1). The results of the analysis showed that during the year 2017 gametocyte prevalence in the district of Saint-Louis was lower with 16.83% (17/101). A large increase in gametocyte carriage was observed in 2018, increasing the risk of malaria transmission. During this 2018 year primaquine was combined with antimalarial treatment to reduce the gametocyte carriage. Increased gametocyte carriage despite the use of primaquine makes it necessary to improve the strategy against malaria transmission.

Discussion

We have performed a DNA extraction technique from RDT samples to detect expression of *P. falciparum* Pfs25 gene by qPCR. This study revealed that *P. falciparum* mature gametocytes can also be sourced from used RDTs. In addition to quantifying the number of DNA amplification cycles, SYBR Green makes it possible to estimate the number of gametocyte copies [9,19,20]. The number of copies would have allowed providing more precision on the estimation of the gametocyte density in this study [20]. Expanding the use of molecular techniques for the detection of sexual forms of the parasite and their applicability on the field are effective means to control the epidemiology of gametocyte carriage and to obtain an estimate of malaria transmission [9,21]. The method of extracting DNA from RDTs is simple and can be applied on the field for molecular control of transmission by rapidly estimating the prevalence level of gametocytes.

Overall, qPCR analyzed 96 RDT samples per plate and is of high epidemiological significance. It is a reproducible and easily adaptable method for determining the carriage of gametocytes from large-scale RDTs used for the diagnosis of malaria. Detection of mature *P. falciparum* gametocytes by qPCR was performed only from DNA extracted from filter papers or directly from blood. DNA extracted from RDTs was, to our knowledge, had never been used before. The qPCR is a sensitive technique capable of detecting sub-microscopic densities of mature gametocytes on both filter paper and RDTs [9]. This study revealed an overall gametocyte prevalence of 53.47% (162/303) with a mean Ct of 32.12 cycles with a standard deviation of 4.28. This result expresses the level of parasite transmission from humans to mosquitoes and allows an assessment of the risk of transmission of the disease. In the St. Louis district, gametocyte prevalence was higher in 2018 than in 2017. In recent years, larger population movements in search of work from high-transmission areas (south of the country) to low-transmission areas (in the north) has contributed to an the increased transmission of malaria in this northern part of the country [3].

However, this increase in the level of transmission can also be explained by the duration of strike action on the part of health staff which led to an interruption in the operational implementation of control strategies and an increase in malaria cases. The artemisinin-based combination therapy (ACTs) used in the treatment of malaria cases promote the production of gametocytes. More malaria cases treated entail more gametocyte carriers.

The Saint-Louis region has experienced excessive rainfall in 2018 as compared to 2017 when a deficit in rainfall was recorded depressed [22,23]. This increase in rainfall in 2018 led to an increase in the Anopheles population and the level of malaria transmission.

The increase of gametocyte carriers is a real problem for the parasite reservoir control as an element of the malaria prevention strategy. The analysis of RDTs collected in the Matam area (Ranérou district) showed a gametocyte prevalence of 67.33% (68/101). According to the National Malaria Control Program, this district has for many years recorded the vast majority of reported cases in the region where the transmission of the disease is strong at the local level [3]. Future studies involving asymptomatic patients are needed to evaluate the sensitivity and accuracy of the method and to evaluate the potential benefits of molecular control of transmission [8]. Extension of this study to the 3 regions where the malaria elimination project is operational will provide reliable estimates to better guide malaria control strategies [1]. The use of RDTs as a source of DNA for the detection of mature gametocytes by molecular techniques is relevant for epidemiological studies assessing the efficacy of candidate vaccines against malaria transmission [8,21] and it is, therefore, an important support for controlling the reintroduction of malaria [8,9].

Conclusions

The collection of RDTs in the field is simple and systematic in Senegal for the surveillance of malaria. The use of this tool to determine the prevalence of gametocytes is practical and affordable. Developing this method with a large-scale estimation of gametocyte density, including on asymptomatic individuals, will increase the monitoring power and allow further elimination. PCR has good sensitivity as a tool for the detection of gametocyte genes expression [20]. The pressure of the drugs in the treatment of malaria contributes to the production of the gametocytes responsible for the presence of these sexual forms of the parasite in the treated subjects. Development of effective tools to monitor the carriage of gametocytes is necessary to control parasite pools. The recent use of fluorescence for the detection of gametocyte DNA has led to a better description of the male and female gametocyte genes [24]. We researched the transcription of the Pfs25 gene to determine the prevalence of gametocytes in northern Senegal. Our conclusion is that this method should be put to greater use to determine the level of gametocyte carriage in the larger population by including asymptomatic individuals in order to develop adequate strategies to destroy the parasite's reservoirs and achieve the elimination of malaria [16]. Primaquine has been administered only to malaria cases. A mass administration of primaquine will have an impact on gametocyte carriage and will help curb malaria transmission.

Abbreviations

RDTs: Rapid diagnostic tests for malaria - ***cDNA*** : Complementary DNA **-** ***qPCR***: quantitative real time PCR **-** ***Cq***: Quantification cycle - ***Ct*** : Cycle threshold - ***RFUs***: Relative Fluorescence **–** **ACTs**: Artemisinin-based Combination Therapy

Declarations

· Ethics approval and consent to participate

The study protocol was submitted for approval to Senegal's National Committee for Ethics for Health Research (CNERS) (Reference: 046/2015/CER/UCAD).

· Consent for publication

“Not applicable”

· Availability of data and materials

The datasets used during the current study are available from the corresponding author on reasonable request.

· Competing interests

The authors declare that they have no conflict interests.

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This work was supported by MACEPA for the field survey and sample collection. The Department of Medical Parasitology at Cheikh Anta Diop University supported the analysis of the samples and the interpretation of the results.

· Authors' contributions

KT Guiguemde, A Lam, MP Diouf, IA Manga, M Ndiaye and A Collé Lô developed the DNA extraction protocol and performed the manipulations of the samples in the laboratory. RCK Tine and B Faye supervised the work and validated the results. G Dieng Sow, M Diop, T Souane are the focal points of MACEPA in the northern regions who led the field investigations under the coordination of Y Dieye and taking part in interpretation and analysis of data as well as writing. All authors read and approved the final manuscript.

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· Authors' information

Professor B Faye is the Head of Department of Medical Parasitology at Cheikh Anta Diop University in Dakar where Professor RCK Tine, KT Guiguemde, A Lam, MP Diouf, IA Manga, M Ndiaye and A Collé Lô work. Y Dieye is the coordinator of the Malaria Control and Evaluation Partnership (MACEPA) in Senegal. G Dieng Sow, M Diop and T Souane are the focal points of MACEPA in the northern regions of Senegal.

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Figures

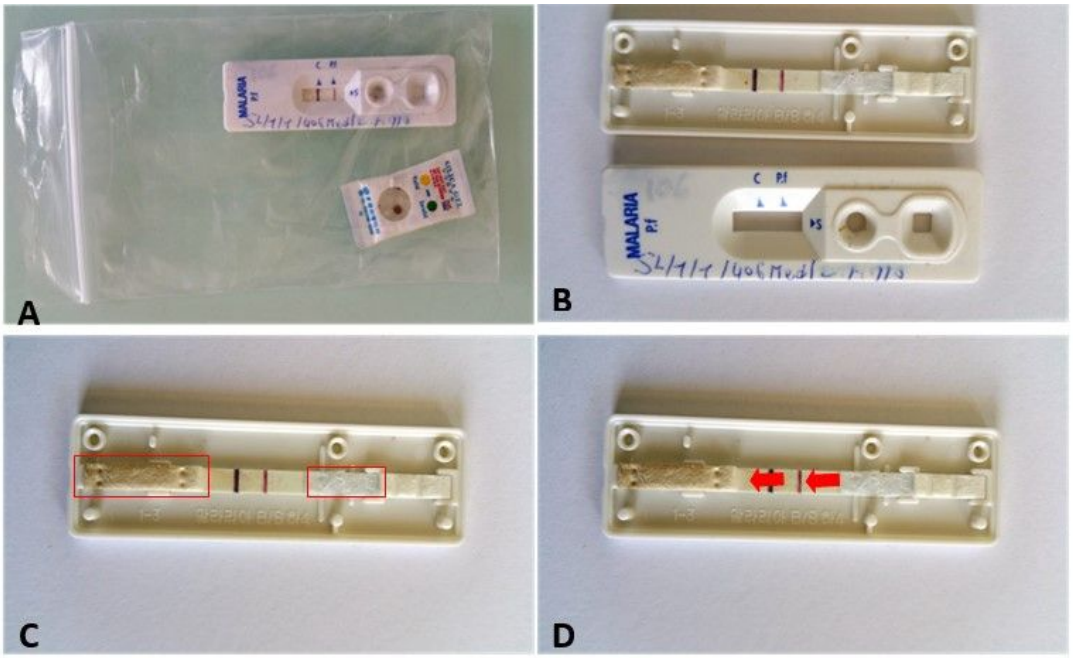

Figure 1

RDT device and fragments used for DNA extraction. (A) SD-Bioline RDT device stored in plastic bag; (B) device opened, (C) absorption filters on nitrocellulose strip, (D) blood migration zone scraped.

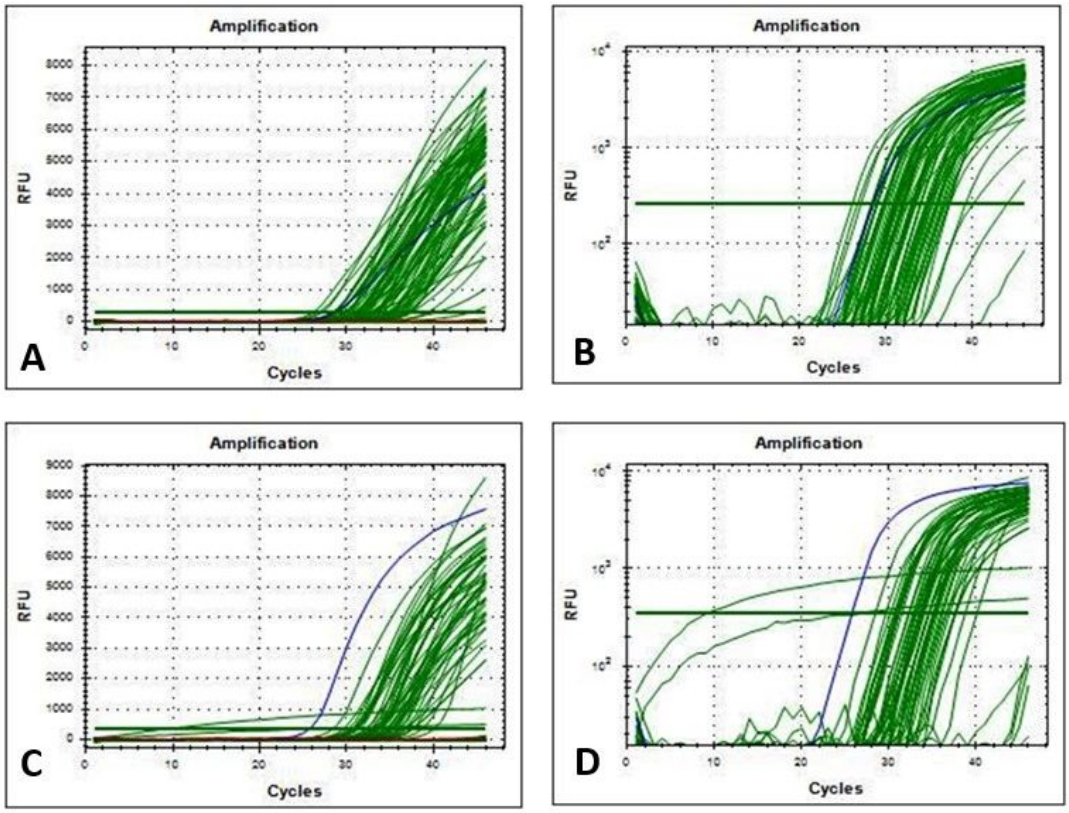

Figure 2

Plasmodium falciparum Pfs25 detection from RDT by direct real time-PCR. (A) DNA amplification kinetics per cycle on plate 1 for each sample (B) logarithmic value of fluorescence and presence of background noise (C) Amplification on plate 2, (D) DNA amplification at 8 cycles. Reactions performed on a conventional RT-PCR instrument (Bio-Rad CFX Connect) with a threshold setting of 50 relative fluorescence units (horizontal line).