Reverse transcription PCR to detect low density malaria infections [version 1; peer review: 1 not approved]

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Abstract
Background: Targeted malaria elimination strategies require highly sensitive tests to detect low density malaria infections (LDMI). Commonly used methods for malaria diagnosis such as light microscopy and antigen-based rapid diagnostic tests (RDTs) are not sensitive enough for reliable identification of infections with parasitaemia below 200 parasites per milliliter of blood. While targeted malaria elimination efforts on the Thailand-Myanmar border have successfully used high sample volume ultrasensitive quantitative PCR (uPCR) to determine malaria prevalence, the necessity for venous collection and processing of large quantities of patient blood limits the widespread tractability of this method.
Methods: Here we evaluated a real-time reverse transcription PCR (RT-PCR) method that reduces the required sample volume compared to uPCR. To do this, 304 samples collected from an active case detection program in Kayin state, Myanmar were compared using uPCR and RT-PCR. To do this, 304 samples collected from an active case detection program in Kayin state, Myanmar were compared using uPCR and RT-PCR.
Results: Plasmodium spp. RT-PCR confirmed 18 of 21 uPCR Plasmodium falciparum positives, while P. falciparum specific RT-PCR confirmed 17 of the 21 uPCR P. falciparum positives. Combining both RT-PCR results increased the sensitivity to 100% and specificity was 95.1%.
Conclusion: Malaria detection in areas of low transmission and LDMI can benefit from the increased sensitivity of ribosomal RNA detection by RT-PCR, especially where sample volume is limited. Isolation of high quality RNA also allows for downstream analysis of malaria transcripts.
Keywords
Low density malaria infection, Plasmodium, quantitative PCR, diagnostic, reverse transcription PCR (RT-PCR)

This article is included in the Mahidol Oxford Tropical Medicine Research Unit (MORU) gateway.
Background

As malaria burden reduces globally, the international community is working toward its elimination. Successful targeted malaria elimination strategies will require increased surveillance and highly sensitive tests capable of detecting asymptomatic and low density malaria infection (LDMI). These infections are often well below 200 parasites per milliliter and are an important disease reservoir capable of transmitting malaria that must be detected and eliminated\(^1\). Light microscopy and antigen based rapid diagnostic tests (RDTs) are the most common tests used in malaria prevalence surveys, and usually assess 5 μL of whole blood per test, a volume which precludes reliable detection of LDMI. Ultrasensitive RDTs improve detection sensitivity of patients with a parasitaemia between 200 parasites/mL and 10,000 parasites/mL\(^2\), but are still limited by their low input volume. Molecular methods using the polymerase chain reaction (PCR) remain the only common and reliable method to detect LDMI. The sensitivity of PCR is due to its ability to detect single, specific nucleic acid molecules and use of concentrated DNA from a large sample. Widespread use of PCR based assays, namely real-time quantitative PCR (qPCR) and reverse-transcription PCR (RT-PCR), have revealed a new landscape of malaria prevalence particularly in low transmission areas\(^3\)\(^,\)\(^,\)\(^4\).

The targeted malaria elimination project (TME) on the Eastern Myanmar border used a high blood volume ultrasensitive qPCR (uPCR) to consistently detect parasitaemia down to 22 parasites per mL\(^5\), and revealed a high proportion of LDMI\(^5\). Major features of uPCR are its 7 copies of gene target, the high volume of blood tested and the ability to accurately quantify low density parasitaemia. Although increasing the blood volume of a PCR leads to higher sensitivity\(^6\), the collection of large numbers of high volume samples have their own specific limitations. These can include, the ethics approval required for venous blood draw, sample logistics, increased nucleic acid extraction cost and increased sample processing time. Another way to increase the sensitivity of PCR is to increase the number of specific nucleic acid targets per parasite by targeting specific RNA and DNA using RT-PCR. As previously reported by Kamau et al\(^3\), the primer set used in uPCR can be made more sensitive by incorporating reverse transcription prior to qPCR, enabling detection of the 7 genes encoding Plasmodium 18S ribosomal nucleic acid (rRNA) and its tRNA transcripts.

In this study, we compare the sensitivity and specificity of high sample volume, low target copy number ultrasensitive qPCRs, with reduced sample volume, high target copy number RT-PCR for the detection and quantification of \emph{Plasmodium} spp. and \emph{P. falciparum}.

Methods

We selected 304 samples with previously reported uPCR results: 21 \emph{P. falciparum} positive and 283 \emph{Plasmodium} spp. negative for comparison to RT-PCR with increased target numbers per parasite but 30% of the sample volume.

Study area and sample collection

Active case detection samples were collected from rural Eastern Kayin (Karen) state of Myanmar between 2014 and 2015 as part of an international malaria elimination project. Full methods have been published\(^4\), briefly, 3 ml of blood was drawn into an EDTA container from each adult, and transported on ice to the Shoklo Malaria Research Unit in Mae Sot, Tak, Thailand. Within 48 hours the samples were processed, and two aliquots of up to 500 μL of packed red blood cells (PRBC) were stored at -80°C. Only 500 μL samples were accepted for Malaria Elimination Task Force (METF) qPCR while RT-PCR included samples with at least 150 μL.

Ultrasensitive qPCR (uPCR)

DNA was extracted from 500 μl of cryopreserved PRBC using QiAamp DNA Blood Midi Kit (Cat. No. 51185, Qiagen\(^\text{TM}\)) according to manufacturer’s instructions. The DNA template was then dried in a vacuum concentrator, re-suspended in 10 μL of PCR grade water and stored at -20°C prior to qPCR. Separate uPCRs specific for \emph{Plasmodium} spp., \emph{P. falciparum} and \emph{P. vivax} were performed over 3 years from 2013 as previously described\(^5\). Briefly, uPCR was done in 10 μL reactions that contained 2 μL of DNA template with 1x QuantiTect Multiplex PCR No ROX mastermix (Cat. No. 204743, Qiagen\(^\text{TM}\)), 0.4 μM each primer, and 0.2 μM Taqman probe. Thermal cycling and signal acquisition was done on an ABI 7500 Fast real-time PCR machine with initial denaturation and enzyme activation at 95°C for 15 min, then 50 cycles of denaturation at 94°C for 15 sec followed by annealing and extension at 60°C for 60 sec. A reaction with exponential signal increase before cycle 40 was considered positive.

Sample selection, nucleic acid extraction and RT-PCR

Within 3 years of sample storage at -80°C, nucleic acid extraction and RT-PCR assays were performed on the second aliquot of PRBC for selected samples: 21 uPCR \emph{P. falciparum} positives and 283 uPCR negatives.

Nucleic acid was extracted using a Zymo Research Quick-RNA Miniprep (Plus) kit (Cat. No. R1058, Zymo Research\(^\text{TM}\)) from manufacturer’s instructions for whole blood were followed with minor changes. These include, extraction from 150 μL of white blood cell depleted PRBC in phosphate buffered saline (PBS) up to 200 μL instead of 200 μL of whole blood, DNase enzyme wasn’t used, and RNA was eluted in 20 μL of molecular grade water. Two RT-PCRs were performed on each extract in duplicate: the \emph{Plasmodium} spp. specific assay using the same primer and probe set as uPCR, and a \emph{P. falciparum} specific set targeting the DNA of the A-18S rRNA genes and its rRNA transcripts\(^5\). Both reactions had a final volume of 15 μL and contained 4 μL of RNA template, 1x Superscript III One-Step RT-PCR System master mix (Cat. No. 12574018, ThermoFisher Scientific\(^\text{TM}\)), 0.4 μM forward and reverse oligo primer and 0.2 μM of MGB Taqman probe. Amplification and signal acquisition were done on an ABI 7500 Fast real-time PCR machine with cycling conditions as follows: reverse
transcription at 45°C for 30 min, enzyme activation at 95°C for 2 min, followed by 50 cycles of denaturation at 95°C for 15 sec and combined annealing and extension steps at 60°C for 60 sec. A reaction with exponential signal increase before cycle 40 was considered positive.

**Primer and probe sequences**

*Plasmodium* spp. specific primer and probe sequences used by uPCR and RT-PCR were published previously by kamau *et al.*. The forward primer sequence was 5'-GCTTCTTCTGATTTCTGGATG-3', reverse primer was 5'-AGCAG-GTTAAGATCTCGTTG-3' and the probe sequence was 5'-ATGCGGTGTTTGTAGTTG-3', labeled with TAMRA as reporter and a TAMRA quencher. The primer and probe sequences used to identify *P. falciparum* infection in uPCR positive samples were published by Perandin *et al.*. The forward primer was 5'-CTTTTGAGAGTTTTGTACTTTGTGAA-3', reverse was 5'-TACCTCCATGCTGGATTTGCACCA-3' and the probe sequence was 5'-TGGCTCAAACAGGGTAGT-CATGATTGAGTTCA-3' with FAM and TAMRA as reporter and quencher respectively. RT-PCR primer sets were taken from the publication by Sumari *et al.*. The forward primer was 5'-TCCGATAACGAAAGAGATCTTAA-3', reverse primer was 5'-ATATAAGTTACTATGTTCAATTTC-3' and the minor groove binding probe sequence was 5'-TAGCGGCAAGTAGTAC-3' labelled with a FAM reporter and BHQ1 quencher.

**Standard curve**

Standard reference curves for the RT-PCR and uPCR were made using aliquots of 10,000 flow cytometry sorted small ring stage *P. falciparum* (3D7) parasites. The method used to extract the nucleic acids from these parasites depended on the assay used (RT-PCR or uPCR). For the uPCR standard curve, Qiagen DNA Blood Mini Kit (Cat. No. 51106, Qiagen) was used to extract DNA, this was eluted in 200 μL of sterile water, dried in a partial vacuum at 30°C for consistency with sample extraction, and re-suspended in 200 μL of Qiagen AE buffer. Nucleic acid for the RT-PCR standard curve was extracted using the Zymo Quick-RNA Miniprep (Plus) (Cat. No. R1058, Zymo Research) kit as above but eluted in 40 μL of water. Serial one in five dilutions were made with these extracts to make 7 standards. The uPCR standard curve ranged from 1000 parasites to 0.064 parasites per reaction.

**Analysis**

*Plasmodium* spp. and *P. falciparum* diagnostic accuracy was calculated by comparing RT-PCR results to the uPCR result in 2 × 2 cross tabulation with uPCR as gold standard in STATA version 15.1 (StataCorp LLC, USA). Results of both RT-PCRs were also combined and compared to uPCR, where a positive test by at least one RT-PCR was considered positive. Continuous non-parametric data were compared with Kruskal-Wallis equality-of-populations rank test. *P* values <0.05 were considered statistically significant. Analyses were performed using STATA version 15.1. Agreement between the two *Plasmodium* specific PCR quantifications (spp RT-PCR and uPCR) was determined using Bland-Altman analysis of log transformed data (difference vs average) using GraphPad Prism version 6.07 for Windows, GraphPad Software (La Jolla California USA).

**Results**

*Plasmodium* spp. RT-PCR

*Plasmodium* spp. RT-PCR confirmed 18 of 21 *Plasmodium* spp. uPCR positives and an additional 9 positive reactions from the 283 uPCR negatives. The sensitivity and specificity of *Plasmodium* spp. RT-PCR was 85.7% and 96.8% respectively when compared to uPCR (Table 1). The positive predictive value (PPV) of this test was 66.7% with a 95% confidence interval (CI) of 46 – 83.5% and negative predictive value (NPV) was 98.9% with a 95% CI of 96.9 – 99.8%.

*P. falciparum* RT-PCR

Using the *P. falciparum* specific RT-PCR, 16 of the 21 uPCR *P. falciparum* positives were confirmed along with 5 extra positives from the 283 negatives. Sensitivity and specificity of this test was 76.2% and 98.2% respectively when compared to uPCR (Table 1). PPV for this PCR was 76.2% (95% CI = 52.8 – 91.8%) and NPV was 98.2% (95% CI = 95.9 – 99.4%).

**Combined *Plasmodium* spp. and *P. falciparum* RT-PCR**

Combining the results of both *Plasmodium* spp. and *P. falciparum* RT-PCRs, all 21 uPCR positives are confirmed positive (100% Sensitivity) with 14 additional/false positives (specificity 95.1%) (Table 1). These combined results gave

| Table 1. Results of three PCRs on 304 malaria survey samples: tabulated results from *Plasmodium* spp. uPCR, *Plasmodium* spp. RT-qPCR and *P. falciparum* RT-qPCR including total positives, total negatives, false positives, false negatives, sensitivity and specificity using *Plasmodium* spp. uPCR results as gold standard. |
|---------------------------------|-------|-------|-------|-------|-------|-------|-------|
|                                  | Positive | Negative | False Positive | False Negative | Sensitivity (95% CI) | Specificity (95% CI) |
| *Plasmodium* spp. uPCR          | 21     | 283    | N/A        | N/A         | 85.7% (63.7 - 97%)   | 96.8% (94 - 98.5%)  |
| *Plasmodium* spp. RT-PCR        | 27     | 277    | 9          | 3           |                 |                   |
| *P. falciparum* RT-PCR          | 21     | 283    | 5          | 5           | 76.2% (52.8 - 91.8%) | 98.2% (95.9 - 99.4%) |
| Combined RT-PCR                 | 35     | 269    | 14         | 0           | 100% (83.9 - 100%)  | 95.1% (91.8 - 97.3%) |
Quantification

No significant differences were found for the calculated parasites/ml ($P = 0.5506$) for the three different methods with geometric means of $2.78 \times 10^4$ (95% CI $4.34 \times 10^3 - 1.79 \times 10^5$), $1.81 \times 10^4$ (1.35 $\times 10^3 - 2.41 \times 10^5$) and $6.85E \times 10^3$ (1.09 $\times 10^3 - 4.31 \times 10^4$) for the *Plasmodium* spp. RT-qPCR, *P. falciparum* RT-qPCR and the *Plasmodium* spp. uPCR respectively (Figure 1).

Bland-Altman analysis of log transformed parasitaemia data did not show any significant systematic bias between uPCR and RT-PCR measurements (Bias = -0.3786 +/- S.D 1.948), 95% of our differences fall between 2 standard deviations or more precisely $1.96 \times S.D (1.948) = 3.82$. This implies a reasonable amount of agreement between uPCR and RT-PCR.

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**Figure 1.** Parasite quantification by *Plasmodium* species ultrasensitive PCR (spp uPCR), *Plasmodium* species RT-qPCR (Spp RT-qPCR) and *Plasmodium falciparum* RT-qPCR (Pf RT-qPCR). Quantification of parasitaemia from three PCRs on 21 uPCR positives from the TME malaria survey of Kayin state, Myanmar.

**Figure 2.** Bland-Altman analysis (difference vs average) of uPCR and RT-PCR quantification data from the TME malaria survey of Kayin state, Myanmar.
Discussion

LDMI detection is essential for effective targeted elimination programs, necessitating the careful selection of a detection assay that is appropriate to the setting and study requirements. Sample volume, storage conditions and transit time are important factors, as well as the required assay sensitivity, specificity and its cost. RNA is generally less stable than DNA, and accurate RNA quantification often requires normalization due to variable transcription rates. It is for these reasons that DNA based qPCR was chosen for the original study as this approach enabled accurate quantification of LDMI in a setting where samples from remote locations would likely experience delays.

The targeted malaria elimination (TME) project on the Eastern Myanmar border used conserved regions of the 18S rRNA genes as the target for qPCR. This high sample volume uPCR assay was modified from the RT-PCR published by Kamau et al., for their detection of low density malaria infections (LDMI). After uPCR detected a high prevalence of LDMI in the region, and with continued surveillance in mind, we wanted a lower sample volume assay with similar LDMI detection sensitivity. As Kamau et al. has shown, using this primer set as a RT-PCR significantly increases the sensitivity of the assay. The increased sensitivity of RT-PCR is due to the increased number of targets per parasite (compared to uPCR). These amplification targets include the 18S rRNA genes, and the structural RNA of each ribosome. Plasmodium genus specific uPCR amplifies type A and S 18S ribosomal RNA genes distributed on chromosomes 1, 5, 7, 11 and 13. A positive qPCR reaction requires at least one of these genes to be included in the assay. Alternatively, RT-PCR can detect these gene loci, and their gene transcripts (rRNA). The increased target copy number per parasite means a smaller fraction of parasite is needed to provide a positive reaction, leading to less false negatives and an opportunity for further downstream applications. The downside to increased sensitivity and target copy is the variable nature of gene expression and relative fragility of RNA molecules. In general this makes accurate quantification of parasitaemia by RT-PCR more challenging, and is one of the reasons for outliers in our inter-assay quantification comparison. In future studies the use of a comprehensive methodology tailored specifically to RNA preservation, extraction and amplification would improve sensitivity and allow for downstream applications involving whole-transcriptome profiling important for studies on transmission, pathogenesis and virulence.

While there were obvious differences in quantification for some samples by each method, these did not reach statistical significance. One reason for these outliers was the use of different stored aliquot volumes between assay types. The uPCR aliquot was fixed at 500 μL while the second aliquot, which was used for RT-PCR ranged from 150 μL to 1 mL prior to freezing. Because RT-PCR targeting rRNA is capable of detecting tiny fractions of a single parasite, the original lysed sample volume becomes an important detail. Assuming a single freeze thaw lysed blood stage Plasmodium and a Plasmodium assay has a hundred thousand targets per parasite, then a single lysed parasite divided into one hundred aliquots can produce one hundred positive reactions, if the parasite wasn’t lysed beforehand then only 1 of 100 would be positive. This can lead to people describing their assay sensitivity well below the sample volume used, a theoretical impossibility unless detecting free circulating nucleic acids outside of parasite cells.

Alternatively, LDMI detection relying on DNA, will have a significant reduction in sensitivity if only a fraction of the DNA template is tested. This is exemplified by the lowest concentration standard used for quantification in uPCR. This standard theoretically contains 0.032 parasites per PCR reaction, at this concentration there is a 1 in 5 chance for the reaction to be positive (7 target genes per parasite x 0.032 = 0.2 copies per reaction). These factors need to be considered when setting up a qPCR standard curve for LDMI quantification. A reliable standard curve for qPCR requires at least one copy of its target at the lowest concentration. In conclusion, the success of any LDMI detection protocol relies on the careful consideration of the following factors: sample volume, elution volume, template volume per assay reaction, primer set target and assay type (uPCR or RT-PCR).

Conclusion

Our experience of the different types of assay suggest that for a LDMI program requiring highly sensitive, accurate quantification and where venous blood collection is possible, uPCR is recommended. In an environment where blood volume is limited (i.e. finger prick sampling) and quantification accuracy of parasitaemia is less important, RT-PCR is a suitable alternative.

Declaration

Ethics approval and consent to participate

First, community engagement teams sought community approval ahead of the survey date. Then, survey participants received individual information in their language, and informed consent was obtained from each individual before they provided a venous blood sample. Appropriate treatment for Plasmodium falciparum or Plasmodium vivax was available for all RDT-positive individuals.

The METF project has ethical approval from the Lower Myanmar Department of Medical Research Ethics’ committee (reference 73/ETHICS2014, dated 25 November 2014, and renewed in November 2015 and 2016 under the same reference).

Data availability

Underlying data

Open Science Framework: Reverse transcription PCR to detect low density malaria infections. https://doi.org/10.17605/OSF.IO/76K9R

This project contains the following underlying data:
- Plasmodium quantifications_Parasites per mL.xls (Contains Plasmodium spp., P. falciparum quantifications (parasite per mL whole blood) and the threshold cycle for all RT-PCRs)
Acknowledgements

The authors would like to thank all the staff and participants involved in the malaria elimination project.

References


Gisely Melo
Tropical Medicine Foundation Dr. Heitor Vieira Dourado, Instituto de Pesquisa Clínica Carlos Borgorema, Manaus, Brazil

Abstract:
What was the target used? Was all PCR targeted to a specific gender? What was the gold standard used? The method is not clear. Why used only *falciparum* used for the manuscript?

Introduction:
What is the target? What is the comparison with methods used as the gold standard of PCR?

Methods:
Why was only *Plasmodium falciparum* used? What chance does the target fail to detect other malaria? Which parasitemia of the people studied to study low parasitemia? If used, was gold pattern used as a thick blood smear or RDT? The target for RT-PCR was for *Plasmodium*? Two RT-PCRs were performed on each extract in duplicate: *Plasmodium* spp. and are they sensitive enough? Using uPCR as a gold standard would not be the most appropriate use of the thick blood smear as a control. It is not clear that he will use a method for gender and species for methodology.

Results:
Using uPCR as a gold standard is not the most suitable. How to be sure of positive positives and false negatives? Why was parasitemia not compared in the studied methods to verify the comparison between the methods to verify the smallest parasitemia that it would detect? In quantification, it is more appropriate to perform correlation analysis to compare a parasitemia between the methods.

Discussion:
The targets should have been described in the methodology as well. What are the limitations of the study?

Is the work clearly and accurately presented and does it cite the current literature?
Partly

Is the study design appropriate and is the work technically sound?
No

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Partly

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Partly

Competing Interests: No competing interests were disclosed.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to state that I do not consider it to be of an acceptable scientific standard, for reasons outlined above.

Author Response 22 Apr 2021
Peter Christensen, Mahidol University, Maesot, Thailand

Thank you for your time reviewing this paper, I appreciate the effort.

Hopefully I can address all your comments in the next draft.

Info on target & sensitivity specificity data:
I will update the paper to include more information about the primer targets earlier and will add the previously published Sens and Spec for the Plasmodium spp. primer set used by uPCR and RT-PCR. It has been done in the original paper for both qPCR and qRT-PCR and then again for high volume uPCR. **Will adding previously published data be satisfactory?**

Why only *falciparum*:
We used Pf only because we can produce very young rings *invitro* that are then FACS sorted for a more consistent standard, and because clinical vivax samples often contain late stages (which may contain more than one nucleus per infected red cell and also contain more ribosomal material). Furthermore, although there is a growing realisation of vivax malaria’s importance; the funder and clinicians at the field site still consider the sensitive and timely diagnosis of Pf a priority. Nonetheless I wish to assure the reviewer that we also would have preferred to have a Pv data set (esp. considering Pv is the most prevalent in the region); however due to the large proportion of sample per reaction (4ul of DNA template per rxn & only 20ul DNA eluted) this means we can only do two PCRs in duplicate. This is a limitation
of this type of high blood volume per reaction assay. I can discuss this limitation.

*Clarify targets:*
Only 2 new RT-PCR results were produced in this study, both target 18S RNA. One was Plasmodium genus specific, the other was *P. falciparum* specific. The original Pf classification given by uPCR used another Pf primer set from Perandin et al. JCM 2004. In hindsight I should have used this same Pf primer set for my RT-PCR assays. The reason I used primers from Sumari et al. is because they had been used in RT-PCR format and we originally included gametocyte data using PfS25 primers from that paper as well. We didn't have enough sample to complete the data set, so it was removed from the paper.

*RDT and Microscopy:*
Microscopy would be better as it is the gold standard. But the LOD is so low it would not be able to detect the majority of samples in this data set (13 of 21 are submicroscopic (<50,000 p/mL)). Unfortunately RDT data from the malaria elimination program, was found to have some important QA issues (the specific batch of PfHRP-2 RDTs provided by Global Fund)).

*Statistics:*
I thought correlation was appropriate here as well, but our statistician sent me this paper (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4470095/). So I used bland-altman for assessing agreement (both similarities and differences) between test measurements. Originally I wanted this assay to be yes/no and semi-quantitative and expected the analysis to not show agreement between tests. The reason thought this is because Kamau et al have already shown this primer set is less accurate at low parasitaemia when used as qRT-PCR.

*Number of LDMI:*
I will add the number of samples that were low density (less than 50 parasites/uL) by uPCR result: 13 of 21 were LDMI.

Again we wish to thank the reviewer for their time and expertise,

Regards,

Peter C

*Competing Interests:* No competing interests were disclosed.