

SHORT REPORT

Open Access



Detecting *wMel Wolbachia* in field-collected *Aedes aegypti* mosquitoes using loop-mediated isothermal amplification (LAMP)

Daniela da Silva Gonçalves^{1*†}, David J. Hooker^{1†}, Yi Dong¹, Nathan Baran¹, Peter Kyrylos¹, Iñaki Iturbe-Ormaetxe¹, Cameron P. Simmons^{1,2} and Scott L. O'Neill¹

Abstract

Background: The World Mosquito Program uses *Wolbachia pipiensis* for the biocontrol of arboviruses transmitted by *Aedes aegypti* mosquitoes. Diagnostic testing for *Wolbachia* in laboratory colonies and in field-caught mosquito populations has typically employed PCR. New, simpler methods to diagnose *Wolbachia* infection in mosquitoes are required for large-scale operational use.

Methods: Field-collected *Ae. aegypti* mosquitoes from North Queensland were tested using primers designed to detect the *Wolbachia wsp* gene, specific to the strain *wMel*. The results were analysed by colour change in the reaction mix. Furthermore, to confirm the efficiency of the LAMP assay, the results were compared to the gold-standard qPCR test.

Results: A novel loop-mediated isothermal amplification (LAMP) colorimetric test for the *wMel* strain of *Wolbachia* was designed, developed and validated for use in a high-throughput setting. Against the standard qPCR test, the analytical sensitivity, specificity and diagnostic metrics were: sensitivity (99.6%), specificity (92.2%), positive predictive value (97.08%) and negative predictive value (99.30%).

Conclusions: We describe an alternative, novel and high-throughput method for diagnosing *wMel Wolbachia* infections in mosquitoes. This assay should support *Wolbachia* surveillance in both laboratory and field populations of *Ae. aegypti*.

Keywords: *wMel*, *Wolbachia*, LAMP, Diagnostics

Background

Arboviral diseases transmitted by the mosquito *Aedes aegypti* such as dengue, chikungunya and Zika constitute a significant burden to human health and economic development worldwide [1, 2]. This is reflected in the nomination by the World Health Organisation of dengue as one of the top ten global health threats in 2019. There is an urgent need for novel and efficient strategies to control these diseases [3].

The World Mosquito Program (WMP, <https://www.worldmosquitoprogram.org>, formerly known as the Eliminate Dengue Program) has developed a novel arboviral disease biocontrol strategy utilising the endosymbiotic bacterium *Wolbachia pipiensis*. This maternally transmitted bacterium [4] is found in 40–60% of insect species worldwide [5–7]. WMP reported the successful introduction of the *wMel* strain of *Wolbachia* into *Ae. aegypti* in northern Australia since 2011 [8]. Subsequently, numerous studies demonstrated that the presence of *wMel* reduces dengue virus [9], Zika [10], chikungunya virus [11] yellow fever [11] and Mayaro virus [12] infection and replication and, in turn the virus transmission potential of the mosquito [13, 14]. *wMel* has been established in field populations of *Ae. aegypti* in five countries and it

*Correspondence: danisgbio@hotmail.com

†Daniela da Silva Gonçalves and David J. Hooker contributed equally to this work

¹ World Mosquito Program, Institute of Vector-Borne Disease, Monash University, 12 Innovation Walk, Clayton, VIC 3800, Australia
Full list of author information is available at the end of the article



has been expanded to more than ten worldwide [15]. The mitigation of local dengue outbreaks in northern Australia [16] following the establishment of *wMel* is consistent with the laboratory and modelling expectations of this intervention [17].

A duplex TaqManTM qPCR assay has been considered the gold-standard reference method for diagnosing *Wolbachia* infection in mosquitoes [5, 18]. The advantages of qPCR are clear: it is able to detect multiple genes of interest, produce quantitative or qualitative data [19] and is scalable. However, these advantages are significantly offset by high initial start-up costs and on-going maintenance of equipment, and the complexity of interpreting threshold values and amplification curves requires extensive training [20]. This is exacerbated in low-resource settings where the sourcing of laboratory equipment can be challenging, and technical expertise is not readily available. Given the rapid expansion of the World Mosquito Program [21, 22], there is a need to develop diagnostic tools suitable for resource limited settings.

Loop-mediated isothermal amplification (LAMP) [23, 24] is a technology potentially suitable for *Wolbachia* diagnostics in resource-limited laboratories [25, 26]. LAMP has been adapted as a nucleic acid test with multiple direct and indirect methods to detect several pathogens [27–30]. Hence the purpose of this study was to develop and validate the diagnostic accuracy of a colorimetric LAMP assay for the *wMel* strain of *Wolbachia*.

Methods

Mosquito samples

Field-collected *Ae. aegypti* mosquitoes ($n=3585$) were collected from BG-Sentinel traps during and after *Wolbachia* establishment in Cairns, Townsville and Innisfail, Australia, over an eight-month period from June 2017. The DNA from each mosquito was individually crudely extracted in the laboratory as previously described [31] before being tested by both TaqManTM qPCR [32] and LAMP assays.

wMel LAMP reactions

LAMP primers (Integrated DNA Technologies, Singapore, Singapore) were designed to detect the *wsp* gene from *wMel* and *wMelPop-CLA* strains using the software LAMP Designer 1.02 (PREMIER Biosoft International, Horsham, UK). Individual reaction consisted of 2X WarmStart[®] Colorimetric LAMP Master Mix (New England BioLabs, Ipswich, USA; Cat# M1800S), primers according to the manufacturer recommendation (Table 1), and 1 μ l of target DNA in a total reaction volume of 17 μ l. Reactions for individual samples were performed in 96-well PCR plates (LabAdvantage, Tingalpa, Australia; 96-well PCR plates, full skirt, clear). Plates were incubated in a thermocycler (BioRad C1000) at 65 °C for 30 min then held at 12 °C until scoring. Within one hour after incubation, colour changes of individual samples were recorded where pink indicates negative, yellow as positive and orange as equivocal (see Additional file 1: Figure S1). Results were interpreted by the naked eye directly from the reaction plates and also captured with a smartphone for data storage.

wMel LAMP assay performance

Target specificity

To assess the specificity of the LAMP assay for *wMel*, multiple *Wolbachia* trans-infected *Ae. aegypti* lines (*wMel*, *wMelPop-CLA*, *wRi*, *wPip* and *wAlbB*) were tested, in addition to two tetracycline-treated lines (*wMel.tet* and *wAlbB.tet*). For each mosquito line, three mosquitoes were tested and three technical replicates were performed, totalling nine reactions per line. Mosquitoes were reared and maintained as described [32], DNA was crudely extracted as previously described [31] and tested in the *wMel* LAMP assay.

Diagnostic performance comparison

Field-collected samples were tested using both the *wMel* LAMP and the reference TaqManTM qPCR assays [32]. The qPCR assay was modified by the use of an LC-640-tagged *wsp* gene probe (fluorescence bandwidth

Table 1 LAMP primers targeting *wMel* and *wMelPop* *Wolbachia* strains

Primer name	Primer sequence (5'–3')	Length (bp)	Final primer concentrations (μ M)
FIP_ <i>wMel/wPop</i>	TGTATGCGCCTGCATCAGCTTCGGTTCTTATGGTGCTAA	39	1.6
BIP_ <i>wMel/wPop</i>	GCAGAAGCTGGAGTAGCGTTGTGTCATGCCACTTAGATGG	40	1.6
F3_ <i>wMel/wPop</i>	TGATGTAACCTCCAGAAGTCA	20	0.2
B3_ <i>wMel/wPop</i>	CTTATTGGACCAACAGGATCG	21	0.2
LpF_ <i>wMel/wPop</i>	AGCCTGTCCGGTTGAATT	18	0.4
LpB_ <i>wMel/wPop</i>	CAGTCTTGTATCCCAAGTGAGT	22	0.4

618–660 nm) to provide improved separation from the FAM-tagged housekeeping gene *Rps17* (fluorescence bandwidth 465–510 nm). Both the qPCR and the LAMP results were analysed in blinded fashion, i.e. the interpretation of each assay was performed blind to the outcome of the other assay. The LAMP assay diagnostic specificity, sensitivity, positive predictive value (PPV) and negative predictive value (NPV) calculations were performed with any equivocal samples (orange colour) being excluded from the calculations. All statistical analysis and calculations were performed using Medcalc (https://www.medcalc.org/calc/diagnostic_test.php).

Results

wMel LAMP assay performance

Target specificity

The wMel LAMP assay consistently detected only the *wsp* target sequence from the wMel strain in *Ae. aegypti*, and did not amplify the other six *Wolbachia* strains tested (Additional file 2: Figure S2).

Diagnostic performance on field-caught mosquitoes

A total of 3585 individual field-collected adult mosquitoes, sampled between June 2017 to February 2018 from Cairns, Townsville and Innisfail, were tested by both TaqManTM qPCR and LAMP and the comparison between the results from each assay is shown in Table 2. Amongst the field-caught mosquitoes, 24 (0.7%) were found to be non-*Ae. aegypti* due to non-amplification of *Ae. aegypti* housekeeping *Rps17* gene in duplex TaqManTM qPCR assay, and hence excluded from the analysis.

Relative to the qPCR reference method, LAMP false positives were more likely ($n=70$) to occur than false negatives ($n=8$). Equivocal LAMP results were more likely to result from qPCR-negative samples than qPCR-positive samples. LAMP increased the estimation of wMel positivity by 2%, with an additional 1% of total samples producing equivocal results. The sensitivity of LAMP assay was close to 100% (Table 3) and this parameter was confirmed when performed in serially diluted field samples up to 1:1000 (data not shown). Also, wMel LAMP diagnostic had high positive and negative

Table 2 wMel LAMP positivity and negativity compared to qPCR

	qPCR-positive	qPCR-negative	Total
LAMP-positive	2327	70	2397
LAMP-negative	8	1128	1136
LAMP-equivocal	2	26	28
Total	2337	1224	3561

Table 3 LAMP diagnostic parameters of LAMP-qPCR parallel testing

Diagnostic parameter	Value	95% CI
Specificity	94.16	92.67–95.42
Sensitivity	99.66	99.33–99.85
Accuracy	97.79	97.25–98.25
Positive predictive value	97.08	96.36–97.66
Negative predictive value	99.30	98.60–99.65

Abbreviation: CI, confidence interval

predictive values in relation to the wMel TaqManTM qPCR (Table 3).

Discussion

TaqManTM qPCR has been a mainstay for diagnosing *Wolbachia* infection in mosquitoes despite utilising expensive reagents and sophisticated equipment that require specialised training and maintenance [20]. Previous work has shown that there is potential to use LAMP for detecting *Wolbachia* in *Ae. aegypti*, either for any strain, targeting the 16S rRNA gene [25], or specifically targeting the *wsp* gene of the strains wAlbB and wPip [26]. Here, we have taken this framework and built on it by utilising a pH indicator that possesses the same characteristics but gives a greater resolution to differentiate between positive and negative results. The colorimetric LAMP assay in this study is an attractive candidate to replace qPCR because it does not require sophisticated equipment, is qualitative in nature, can easily be analysed by visual inspection and can be more cost-effective [33–35]. In addition, LAMP has been shown to be a reliable and robust assay across a range of DNA matrices [36] making it ideal for field-caught mosquito homogenates that can be highly variable. A small number of results were scored as false negatives. These could be explained by pipetting errors, or the presence of inhibitors of DNA amplification. Inhibitors such as EDTA, or human blood in blood-fed female mosquitoes, could block enzyme activity [37]. The frequency of false negatives was very low (0.22%), and does not affect the robustness of our assay.

When considering the implementation of colorimetric LAMP as the primary diagnostic method for monitoring the establishment of wMel, certain trade-offs should be recognised. First, compared to qPCR there may be an increased likelihood of contamination due to the high amplification efficiency of LAMP [23, 38]. Secondly, as the colorimetric LAMP assay is a single target nucleic acid test, it relies on entomologists to accurately identify *Ae. aegypti* mosquitoes from other species and insects that might be collected from the field. Thirdly, despite

its robustness, the LAMP assay can produce equivocal results occasionally, presenting as wells with varying hues of the colour orange. However, equivocal results were rare (typically 1% of the samples) and did not significantly impact on the predictive ability of the assay. In general, this rate of equivocal findings should not adversely affect the chronological and geographical picture of *Wolbachia* establishment. Finally, the *wMel* LAMP assay is scored visually which may be subject to interpretation bias. To avoid possible visual biases, a smartphone application has been developed to conveniently and reliably score positivity and negativity, and this can promote consistency across multiple and international settings.

Conclusions

In conclusion, the *wMel* LAMP assay described here was sensitive, specific and suitable for high throughput application. With these results, we believe the assay is an appropriate tool to monitor the progress of *wMel Wolbachia* establishment in field *Ae. aegypti* populations worldwide in order to protect local communities from mosquito-borne diseases.

Additional files

Additional file 1: Figure S1. Example of colorimetric LAMP result interpretation. Results are scored based on colour change. Samples (1) and (2) in yellow are positive for *wMel Wolbachia*; (3) and (4) in pink are negative; and (5) and (6) in orange are considered equivocal.

Additional file 2: Figure S1. Specificity of the *wMel* LAMP assay. LAMP reactions were performed using a number of *Ae. aegypti* lines transinfected with different *Wolbachia* strains per column, as follows: (1) *wMel*-infected, field-collected; (2) *wMel*, purified gDNA; (3) *wAlbB*; (4) *Ae. aegypti* tetracycline treated (without *wAlbB*); (5) *wMelPop-CLA*; (6) *wPip*; (7) *wRi*; (8) *wMelCS*; (9) *Ae. aegypti* tetracycline treated (without *wMel*); (10) wild type uninfected *Ae. aegypti* from Townsville, Australia; (11) water; and (12) extraction buffer negative control. Eight technical replicates were run for controls.

Acknowledgements

We thank the World Mosquito Program Oceania field deployment team for collecting mosquito samples; NEB for assistance; Luciano Andrade Moreira for providing outstanding technical assistance; Jesse Chapotet for helping to process samples; Heather A. Flores and David C. Hack for critical reading, and Stephanie Tanamas for statistical advice.

Authors' contributions

DSG, DJH, NB and PK participated to the study design, performed experiments, contributed to obtaining the results and drafted the manuscript. YD contributed to the study design and drafted the manuscript. IIO, CPM and SLO participated on the study design. CPM and SLO coordinated the work and critically reviewed the manuscript. All authors read and approved the final manuscript.

Funding

This work was supported by Wellcome trust strategic award.

Availability of data and materials

All relevant data generated or analysed during this study are included in this published article and its additional files.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author details

¹ World Mosquito Program, Institute of Vector-Borne Disease, Monash University, 12 Innovation Walk, Clayton, VIC 3800, Australia. ² Oxford University Clinical Research Unit, Hospital for Tropical Diseases, Ho Chi Minh City, Vietnam.

Received: 25 June 2019 Accepted: 10 August 2019

Published online: 15 August 2019

References

- Hotez PJ. Forgotten people, forgotten diseases: The neglected tropical diseases and their impact on global health and development. Washington, DC: American Society for Microbiology Press; 2008.
- Bhatt S, Gething PW, Brady OJ, Messina JP, Farlow AW, Moyes CL, et al. The global distribution and burden of dengue. *Nature*. 2013;496:504–7.
- Kyle JL, Harris E. Global spread and persistence of dengue. *Annu Rev Microbiol*. 2008;62:71–92.
- Veneti Z, Clark ME, Zabalou S, Karr TL, Savakis C, Bourtzis K. Cytoplasmic incompatibility and sperm cyst infection in different *Drosophila-Wolbachia* associations. *Genetics*. 2003;164:545–52.
- de Oliveira CD, Gonçalves DS, Baton LA, Shimabukuro PH, Carvalho FD, Moreira LA. Broader prevalence of *Wolbachia* in insects including potential human disease vectors. *Bull Entomol Res*. 2015;105:305–15.
- Hilgenboecker K, Hammerstein P, Schlattmann P, Telschow A, Werren JH. How many species are infected with *Wolbachia*? A statistical analysis of current data. *FEMS Microbiol Lett*. 2008;281:215–20.
- Zug R, Hammerstein P. Still a host of hosts for *Wolbachia*: analysis of recent data suggests that 40% of terrestrial arthropod species are infected. *PLoS One*. 2012;7:e3854.
- Hoffmann AA, Montgomery BL, Popovici J, Iturbe-Ormaetxe I, Johnson PH, Muzzi F, et al. Successful establishment of *Wolbachia* in *Aedes* populations to suppress dengue transmission. *Nature*. 2011;476:454–7.
- Moreira LA, Iturbe-Ormaetxe I, Jeffery JA, Lu G, Pyke AT, Hedges LM, et al. A *Wolbachia* symbiont in *Aedes aegypti* limits infection with dengue, chikungunya, and *Plasmodium*. *Cell*. 2009;139:1268–78.
- Dutra HL, Rocha MN, Dias FB, Mansur SB, Caragata EP, Moreira LA. *Wolbachia* blocks currently circulating Zika virus isolates in Brazilian *Aedes aegypti* mosquitoes. *Cell Host Microbe*. 2016;19:771–4.
- Aliota MT, Walker EC, Uribe Yepes A, Velez ID, Christensen BM, Osorio JE. The *wMel* strain of *Wolbachia* reduces transmission of chikungunya virus in *Aedes aegypti*. *PLoS Negl Trop Dis*. 2016;10:e0004677.
- Pereira TN, Rocha MN, Sucupira PHF, Carvalho FD, Moreira LA. *Wolbachia* significantly impacts the vector competence of *Aedes aegypti* for Mayaro virus. *Sci Rep*. 2018;8:6889.
- Ye YH, Carrasco AM, Frentiu FD, Chenoweth SF, Beebe NW, van den Hurk AF, et al. *Wolbachia* reduces the transmission potential of dengue-infected *Aedes aegypti*. *PLoS Negl Trop Dis*. 2015;9:e0003894.
- Carrington LB, Tran BCN, Le NTH, Luong TTH, Nguyen TT, Nguyen PT, et al. Field- and clinically derived estimates of *Wolbachia*-mediated blocking of dengue virus transmission potential in *Aedes aegypti* mosquitoes. *Proc Natl Acad Sci USA*. 2018;115:361–6.
- O'Neill SL. The use of *Wolbachia* by the World Mosquito Program to interrupt transmission of *Aedes aegypti* transmitted viruses. *Adv Exp Med Biol*. 2018;1062:355–60.
- Ritchie SA. *Wolbachia* and the near cessation of dengue outbreaks in Northern Australia despite continued dengue importations via travellers. *J Travel Med*. 2018;25:1–3.

17. Ferguson NM, Kien DT, Clapham H, Aguas R, Trung VT, Chau TN, et al. Modeling the impact on virus transmission of *Wolbachia*-mediated blocking of dengue virus infection of *Aedes aegypti*. *Sci Transl Med*. 2015;7:279ra37.
18. Joubert DA, O'Neill SL. Comparison of stable and transient *Wolbachia* infection models in *Aedes aegypti* to block dengue and West Nile viruses. *PLoS Negl Trop Dis*. 2017;11:e0005275.
19. Smith CJ, Osborn AM. Advantages and limitations of quantitative PCR (Q-PCR)-based approaches in microbial ecology. *FEMS Microbiol Ecol*. 2009;67:6–20.
20. Bustin SA, Nolan T. Pitfalls of quantitative real-time reverse-transcription polymerase chain reaction. *J Biomol Tech*. 2004;15:155–66.
21. Flores HA, O'Neill SL. Controlling vector-borne diseases by releasing modified mosquitoes. *Nat Rev Microbiol*. 2018;16:508–18.
22. O'Neill S, Ryan P, Turley A, Wilson G, Retzki K, Iturbe-Ormaetxe I, et al. Scaled deployment of *Wolbachia* to protect the community from *Aedes* transmitted arboviruses. *Gates Open Res*. 2018;2:36.
23. Notomi T, Okayama H, Masubuchi H, Yonekawa T, Watanabe K, Amino N, et al. Loop-mediated isothermal amplification of DNA. *Nucleic Acids Res*. 2000;28:E63.
24. Mori Y, Notomi T. Loop-mediated isothermal amplification (LAMP): a rapid, accurate, and cost-effective diagnostic method for infectious diseases. *J Infect Chemother*. 2009;15:62–9.
25. Goncalves Dda S, Cassimiro AP, de Oliveira CD, Rodrigues NB, Moreira LA. *Wolbachia* detection in insects through LAMP: loop mediated isothermal amplification. *Parasit Vectors*. 2014;7:228.
26. Bhadra S, Riedel TE, Saldana MA, Hegde S, Pederson N, Hughes GL, et al. Direct nucleic acid analysis of mosquitoes for high fidelity species identification and detection of *Wolbachia* using a cellphone. *PLoS Negl Trop Dis*. 2018;12:e0006671.
27. Calvert AE, Biggerstaff BJ, Tanner NA, Lauterbach M, Lanciotti RS. Rapid colorimetric detection of Zika virus from serum and urine specimens by reverse transcription loop-mediated isothermal amplification (RT-LAMP). *PLoS One*. 2017;12:e0185340.
28. Khan MG, Bhaskar KR, Salam MA, Akther T, Pluschke G, Mondal D. Diagnostic accuracy of loop-mediated isothermal amplification (LAMP) for detection of *Leishmania* DNA in buffy coat from visceral leishmaniasis patients. *Parasit Vectors*. 2012;5:280.
29. Neeraja M, Lakshmi V, Lavanya V, Priyanka EN, Parida MM, Dash PK, et al. Rapid detection and differentiation of dengue virus serotypes by NS1 specific reverse transcription loop-mediated isothermal amplification (RT-LAMP) assay in patients presenting to a tertiary care hospital in Hyderabad, India. *J Virol Methods*. 2015;211:22–31.
30. Quoc NB, Phuong NDN, Chau NNB, Linh DTP. Closed tube loop-mediated isothermal amplification assay for rapid detection of hepatitis B virus in human blood. *Heliyon*. 2018;4:e00561.
31. Yeap HL, Axford JK, Popovici J, Endersby NM, Iturbe-Ormaetxe I, Ritchie SA, et al. Assessing quality of life-shortening *Wolbachia*-infected *Aedes aegypti* mosquitoes in the field based on capture rates and morphometric assessments. *Parasit Vectors*. 2014;7:58.
32. Frentiu FD, Zakir T, Walker T, Popovici J, Pyke AT, van den Hurk A, et al. Limited dengue virus replication in field-collected *Aedes aegypti* mosquitoes infected with *Wolbachia*. *PLoS Negl Trop Dis*. 2014;8:e2688.
33. Goto M, Honda E, Ogura A, Nomoto A, Hanaki K. Colorimetric detection of loop-mediated isothermal amplification reaction by using hydroxy naphthol blue. *Biotechniques*. 2009;46:167–72.
34. Nagamine K, Hase T, Notomi T. Accelerated reaction by loop-mediated isothermal amplification using loop primers. *Mol Cell Probes*. 2002;16:223–9.
35. Mori Y, Kanda H, Notomi T. Loop-mediated isothermal amplification (LAMP): recent progress in research and development. *J Inf Chem*. 2013;19:404–11.
36. Francois P, Tangomo M, Hibbs J, Bonetti EJ, Boehme CC, Notomi T, et al. Robustness of a loop-mediated isothermal amplification reaction for diagnostic applications. *FEMS Immunol Med Microbiol*. 2011;62:41–8.
37. Oscorbin IP, Belousova EA, Boyarskikh UA, Zakabunin AI, Khrapov EA, Filipenko ML. Derivatives of Bst-like Gss-polymerase with improved processivity and inhibitor tolerance. *Nucleic Acids Res*. 2017;45:9595–610.
38. Parida M, Sannarangaiah S, Dash PK, Rao PV, Morita K. Loop mediated isothermal amplification (LAMP): a new generation of innovative gene amplification technique; perspectives in clinical diagnosis of infectious diseases. *Rev Med Virol*. 2008;18:407–21.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Ready to submit your research? Choose BMC and benefit from:

- fast, convenient online submission
- thorough peer review by experienced researchers in your field
- rapid publication on acceptance
- support for research data, including large and complex data types
- gold Open Access which fosters wider collaboration and increased citations
- maximum visibility for your research: over 100M website views per year

At BMC, research is always in progress.

Learn more biomedcentral.com/submissions

