A novel CRISPR-based malaria diagnostic capable of *Plasmodium* detection, species differentiation, and drug-resistance genotyping

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**ABSTRACT**

**Background:** CRISPR-based diagnostics are a new class of highly sensitive and specific assays with multiple applications in infectious disease diagnosis. SHERLOCK, or Specific High-Sensitivity Enzymatic Reporter UnLOCKing, is one such CRISPR-based diagnostic that combines recombinase polymerase pre-amplification, CRISPR-RNA base-pairing, and LwCas13a activity for nucleic acid detection.

**Methods:** We developed SHERLOCK assays capable of detecting all *Plasmodium* species known to cause human malaria and species-specific detection of *P. vivax* and *P. falciparum*, the species responsible for the majority of malaria cases worldwide. We further tested these assays using a diverse panel of clinical samples from the Democratic Republic of the Congo, Uganda, and Thailand and pools of *Anopheles* mosquitoes from Thailand. In addition, we developed a prototype SHERLOCK assay capable of detecting the dihydropteroate synthetase (*dhps*) single nucleotide variant A581G associated with *P. falciparum* sulfadoxine resistance.

**Findings:** The suite of *Plasmodium* assays achieved analytical sensitivities ranging from 2\(^{+}\)/C\(^{15}\) to 18\(^{+}\)/C\(^{18}\) parasites per reaction when tested against laboratory strain genomic DNA. When compared to real-time PCR, the *P. falciparum* assay achieved 94% sensitivity and 94% specificity during testing of 123 clinical samples. Compared to amplicon-based deep sequencing, the *dhps* SHERLOCK assay achieved 73% sensitivity and 100% specificity when applied to a panel of 43 clinical samples, with false-negative calls only at lower parasite densities.

**Interpretation:** These novel SHERLOCK assays demonstrate the versatility of CRISPR-based diagnostics and their potential as a new generation of molecular tools for malaria diagnosis and surveillance.

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1. Introduction

Timely and accurate diagnosis is an important component of malaria control and elimination efforts. The current generation of rapid diagnostic tests (RDTs) that detect *Plasmodium falciparum* histidine-rich protein 2 (PfHRP2) are widely deployed, accounting for 74% of all malaria testing in Africa in 2015, but they have shortcomings...
Research in context

Evidence before this study

CRISPR-based diagnostics are a new family of assays that combine the base-pairing recognition of CRISPR RNAs with the varied function of Cas effector proteins to detect nucleic acid targets with high sensitivity and specificity. SHERLOCK, or Specific High-Sensitivity Enzymatic Reporter UnLOCKing, is one of two major classes of CRISPR-based diagnostics. The initial manuscript characterizing SHERLOCK described it as capable of detecting DNA and RNA from pathogens at attomolar concentrations and detecting single nucleotide variants conferring antimicrobial resistance. We identified 20 publications describing the use of SHERLOCK for molecular diagnosis in PubMed as of January 19, 2021 (search terms: “SHERLOCK CRISPR” and “Cas13a”). The majority involved assays for viral targets including SARS-CoV-2, but proof-of-principle assays for human genotyping and species identification of fish were also described. One manuscript published during review applied a CRISPR-based diagnostic approach to Plasmodium spp. detection and species differentiation using Cas12a.

The majority of malaria diagnostic testing worldwide relies upon rapid diagnostic tests (RDTs) that detect parasite antigens. Widely deployed malaria RDTs fail to detect low density infections, especially in non-falciparum infections, and Plasmodium falciparum parasites with deletions of the P. falciparum histidine-rich protein 2 and/or 3 genes. Parasites with these deletion mutations have now been reported in at least 24 countries worldwide, leading to renewed calls for new malaria diagnostic approaches.

Added value of this study

We developed novel proof-of-concept SHERLOCK assays for malaria that are capable of robust detection, species identification, and drug-resistance genotyping of Plasmodium spp. We validated these assays using diverse clinical samples collected in Africa and Asia. This is one of the first manuscripts describing the SHERLOCK method outside of its original group of authors and its first use for a eukaryotic pathogen in a large cohort of human clinical samples. We demonstrate SHERLOCK’s potential as a sensitive and specific diagnostic for malaria and its versatility for a range of applications.

Implications of all the available evidence

This manuscript demonstrates that SHERLOCK is a sensitive, specific, and highly adaptable nucleic acid detection platform that can be applied for a variety of uses in infectious disease detection and drug resistance surveillance. While additional streamlining and optimization is needed for field-ready implementation, the novel assays described herein have potential as a new generation of malaria diagnostics.

for malaria diagnosis, it is only sporadically available throughout much of Africa because performance is highly operator dependent, it is labor-intensive, and it requires careful, sustained training of personnel. RDTs that detect alternative antigens such as parasite lactate dehydrogenase (pLDH) are less sensitive and heat-stable.

To address the shortcomings of antigen and microscopy-based diagnostics, molecular methods have been developed to detect parasite nucleic acid such as polymerase chain reaction (PCR), loop-mediated isothermal amplification (LAMP), and recombinase polymerase amplification (RPA) [3–5]. These modalities have proven themselves highly sensitive and specific and can detect different Plasmodium species and single nucleotide variants (SNVs), making it possible to monitor the emergence and spread of drug resistance in a timely manner [6–8]. However, most molecular methods have important shortcomings, including relatively expensive instrument requirements and reagent costs. To overcome these challenges, a new generation of field-deployable malaria diagnostics capable of detecting diverse species and drug-resistant variants is needed.

SHERLOCK is a CRISPR-based diagnostic that combines RPA, in vitro transcription, and RNA target detection using custom-designed CRISPR RNA (crRNA) oligonucleotides and Cas13a derived from the bacteria Leptotrichia wadei (LwCas13a) [9]. Briefly, the first step of SHERLOCK is an RPA reaction performed with primers tagged with a T7 promoter sequence to generate short, double-stranded DNA (dsDNA) amplicons of a target sequence. In vitro transcription of the RPA product by T7 polymerase produces single-stranded (ssRNA) targets, which are recognized by base-pairing interactions with LwCas13a:crRNA complex. CrRNA-ssRNA target base-pairing interactions activate collateral RNAse activity of LwCas13a, which cleaves fluorescent or colorimetric RNA reporter molecules in the reaction to produce a detectable signal. SHERLOCK can also detect SNVs; crRNA-ssRNA target base-pairing interactions activate collateral RNAse activity of LwCas13a, which cleaves fluorescent or colorimetric RNA reporter molecules in the reaction to produce a detectable signal. SHERLOCK can also detect SNVs; crRNA-ssRNA target base-pairing interactions activate collateral RNAse activity of LwCas13a, which cleaves fluorescent or colorimetric RNA reporter molecules in the reaction to produce a detectable signal.
nucleotides [15]. We then added a T7 promoter sequence (5'-GAAAT- TAATACGACTCACTATAGGG-3') to the 5' end of one RPA primer in each set to enable in vitro transcription by T7 polymerase during the LwCas13a detection step. All primers with off-target complementarity predicted by BLAST were excluded. Salt-free primers were synthesized by Integrated DNA Technologies (Coralville, Indiana). The full list of oligonucleotides designed and used in this manuscript can be found in Supplementary Table 1.

2.2. crRNA design

Oligonucleotides for crRNA synthesis were designed as two complementary ssDNA oligonucleotides and then in vitro transcribed to produce single-stranded 67 nt crRNAs. Each ssDNA oligonucleotide was composed of three parts: a variable spacer region (to facilitate recognition of the RNA target molecule), a constant region (to facilitate crRNA association with LwCas13a), and a T7 promoter sequence (to facilitate crRNA in vitro transcription).

Spacers are 28 nt long and recognize the in vitro transcribed RNA product of the RPA reaction through complementary base-pairing [9]. For the P. falciparum and P. vivax species-specific SHERLOCK assays, spacers were designed to bind a species-specific region of the 18S rRNA gene previously targeted for amplification during real-time PCR assays [3]. Spacers were selected to have at least three mismatches between species for the P. falciparum and P. vivax-specific assays to minimize off-target activity. For the pan-Plasmodium SHERLOCK assay, a spacer was selected in a region of the 18S rRNA gene conserved between Plasmodium species.

Spacers for dhps SHERLOCK assays were designed to maximize the difference in signal between a specific SNV and alternate motifs as previously described [9]. To accomplish this, spacers were designed so the SNV is recognized at position 3 or 6, and a synthetic mismatch between the spacer and target was present at position 5 or 4, respectively (Supplementary Table 2). The resulting spacer has one mismatch with the SNV of interest and two mismatches with the alternate variant, producing a measurable difference in signal between the two variants (Figure 2). Spacers were queried through BLAST to search for any off-target complementarity [15].

The same constant LwCas13a-associating region was used as described in Gootenberg et al. (2017), 5'-GGGGAUUUAGACUACCCCAAAAACGAAGGGGACUAAAAC-3', and the T7 promoter sequence used was 5'-GAAATTAATACGACTCACTATAGGG-3' [9]. Put together, two 89 nt ssDNA oligonucleotides ( appended to spacer sequences) for each crRNA were designed in the format 5'-GAAATTAATACGACTCACTATAGGGATTTAGACTACCCCAAAAACGAAGGGGACUAAAAC-spacer-3' and 5'-spacer reverse complement-GTTTTAGTCCCCTTCGTTTTGGGGTAGTCTAAATCCCCTATAGTGAGTGGTATTAATTTTC-3'. These oligonucleotides were ordered from Integrated DNA Technologies (Coralville, IA). For each SHERLOCK assay, multiple crRNA designs were screened, and crRNAs with the greatest signal:background and/or SNV signal:alternate signal were selected for all future experiments (Supplemental Figures 1-3).

2.3. crRNA synthesis

Complementary ssDNA oligonucleotides were annealed (final concentration 10 μM each) in 10 mM Tris–HCl, 50 mM KCl, and 1.5 mM MgCl2 pH 8.3 for 5 minutes at 95°C followed by a 5°C/minute temperature decrease to 25°C. Annealed dsDNA templates were then in vitro transcribed using the HiScribe T7 Quick High Yield RNA Synthesis Kit (New England Biolabs, Ipswich, MA) using overnight
incubation as described in the protocol for <0.3kb transcripts (https://www.neb.com/products/e2050-hiscribe-t7-quick-high-yield-rna-synthesis-kit#Protocols%20Manuals%20Usage). CrRNAs were purified using RNAClean XP magnetic bead purification (Beckman Coulter, Indianapolis, IN) and quantified by NanoDrop spectrophotometry (ThermoFisher, Waltham, MA).

2.4. LwCas13a synthesis and purification

LwCas13a protein was synthesized and purified at the University of North Carolina at Chapel Hill (UNC) Protein Expression and Purification Core as previously described with several modifications [9]. Briefly, the pET His6-TwinStrep-SUMO-LwCas13a (NovoPro, Shanghai, China) expression vector was transformed into Rosetta™ 2 (DE3) pLysS Singles Competent Competent Cells (Millipore) in autoinduction media and grown at 37°C until OD0-6, when the temperature was lowered to 18°C and grown overnight. The pellet was harvested and stored at -80°C until purification. For purification, the pellet was resuspended in lysis buffer (50 mM NaPO4, 500 mM NaCl, 20 mM imidazole, 1 mM PMSF, 50 μg/ml lysozyme) and mixed at 4°C for 30 min. The solution was then sonicated on ice and centrifuged for 1 hour at 10,000 x g at 4°C. Clarified supernatant was filtered using a 0.45 micron filter. Filtered supernatant was then loaded over Nickel Sepharose 6 Fast Flow resin (GE). The column was washed with 5 CV buffer A (50 mM NaPO4, 500 mM NaCl, 20 mM imidazole) and eluted with 10 CV Buffer B (50 mM NaPO4, 500 mM NaCl, 500 mM imidazole). Buffer exchange was performed via dialysis to a final solution of 600 mM NaCl, 50 mM Tris-HCl pH 7.5, 5% glycerol, and 2 mM DTT.

2.5. Recombinase polymerase amplification

RPA reactions were conducted as described in TwistAmp Basic Instruction Manual (TwistDx, Cambridge, UK) with several modifications (https://www.twistdx.co.uk/en/products/product/twistamp-basic). Each 50 μL TwistAmp reaction was subdivided by first creating a 45 μL mastermix and aliquoting five 5 × 9 μL reactions before adding 1 μL of sample input. Magnesium acetate was added to the mastermix before adding the sample input. To simulate human background in clinical samples, 40 ng human gDNA from buffy coat (Sigma Aldrich, St. Louis, MO) was added in all experiments except those using clinical isolates. RPA reactions were incubated at 37°C for 30 minutes in a thermal cycler with a 40°C heated lid. After the first 4 minutes of incubation, samples were removed, vortexed briefly, and then returned to the thermal cycler for the remainder of the incubation period.

2.6. Detection using LwCas13a

LwCas13a detection reactions were performed as previously described with several modifications. We chose LwCas13a rather than Lepotrichia shahii Cas13a because LwCas13a has been demonstrated to have higher RNA-guided RNase activity than Lc13a and is better characterized in the context of SHERLOCK assays [11]. Each reaction was performed using 25 μL total volume and contained 45 nM LwCas13, 100-500 ng crRNA, 125 nM fluorescent RNA reporter (RNase Avert v2, ThermoFisher), 0.625 μL murine RNAse inhibitor (New England Biolabs), 31-25 ng background RNA (isolated from Burkitt’s Lymphoma (Raji), ThermoFisher), 1 mM NTP mix (New England Biolabs), 0.75 μL T7 polymerase (New England Biolabs), 3 mM MgCl2, and 1.25 μL of RPA product in nuclease assay buffer (20 mM HEPES, 60 mM NaCl, 6 mM MgCl2, pH 6.8) [10]. Detection reactions were conducted in 96-well black half-area microplates (PerkinElmer, Waltham, MA) and sealed with MicroAmp optical adhesive film (ThermoFisher). Detection reactions were incubated for 3 hours at 37°C on a VICTOR Nivo fluorescent plate reader (PerkinElmer) with fluorescence measurements taken every 5 minutes. Background subtracted average fluorescence intensity of the human gDNA controls at 180 minutes of the human gDNA control from each sample.

2.7. Analytical sensitivity and specificity estimation

To determine the analytical sensitivity of the SHERLOCK assays, we performed each assay in triplicate using serially diluted template DNA from P. falciparum strain Dd2 (MRA-150C) for P. falciparum, P. vivax 18S RNA plasmid DNA (MRA-178), P. ovale 18S RNA plasmid DNA (MRA-180), P. malariae 18S RNA plasmid DNA (MRA-179), and P. knowlesi genomic DNA (MRA-456G) (Beif Resources, Manassas, VA). To facilitate ease of interpretation, we assumed six copies of 18S rRNA targets per genome when calculating parasite genome-equivalents [16]. Parasite DNA ranging from 10^5 and 10^-2 parasite genomes/μL was used to simulate expected parasite densities observed during human infection, including clinical malaria (typically 10^2 to 10^5 parasites/μL) and subclinical infection. Differences in mean background-subtracted fluorescence were assessed using the student’s unpaired t-test. We then performed additional biological replicates using 2-fold serial dilutions near the observed limit of detection to improve the precision of our analytical sensitivity estimates. Positive SHERLOCK calls were made if background-subtracted fluorescence was positive. Finally, we assessed each assay’s analytical specificity using high-concentration DNA for all human-infecting Plasmodium species, including gDNA and 18S RNA plasmid DNA as described above and containing 100,000 parasite genome-equivalents per microliter.

2.8. Clinical sensitivity and specificity estimation

We assessed the clinical sensitivity and specificity of our assays using a panel of dried blood spot (DBS) samples collected in the Democratic Republic of the Congo (DRC), Uganda, and Thailand. Samples were chosen out of convenience; a summary of the sources of clinical samples is provided in Supplementary Table 3. DRC samples were collected from subjects presenting to government health facilities with symptoms of malaria in Kinshasa, South Kivu, and Bas-Uele Provinces in 2017 as part of a separate study of malaria rapid diagnostic test performance [17]. Ugandan samples were collected from febrile children presenting to public health facilities located in the Kasere District of western Uganda over the period November 2017 to June 2018 [18]. Thai samples were collected from patients presenting to public health clinics and found to be smear-positive for P. vivax and as part of ongoing entomological surveillance in the Mae Sod district of Tak Province, northwest Thailand in 2010. All enrolled subjects provided informed consent. Ethical approvals were obtained by the Kinshasa School of Public Health, Mbarara University of Science and Technology, Uganda National Council for Science and Technology, Walter Reed Army Institute of Research, Ministry of Public Health in Thailand, and the University of North Carolina at Chapel Hill.

The presence and species of Plasmodium in each sample was determined using real-time PCR. Prior to DNA extraction, DBS were stored at -20 or -80°C in sealed plastic bags with desiccant. Briefly, DNA was extracted from these 6 mm DBS punches using Chelex-100 and saponin for DRC samples [19] Chelex-100 and Tween for Uganda samples [20], and the QIAamp DNA mini kit (QIAGEN, Hilden, Germany) for Thailand samples prior to storage at -20°C. DRC samples were first subjected to a pan-Plasmodium real-time PCR assay targeting the 18S rRNA gene [21]. Positive samples were then subjected to four species-specific, semi-quantitative 18S rRNA real-time PCR assays for P. falciparum, P. ovale, P. malariae and P. vivax, respectively. Parasite densities for all DRC and Uganda samples were determined using quantitative real-time PCR (qPCR) targeting the single-copy P. falciparum lactate dehydrogenase (pfdh) gene as
previously described [25,26]. *P. vivax* infection was diagnosed and parasite densities determined in Thailand using microscopy at the time of DBS collection and later confirmed using qualitative, species-specific 18S rRNA real-time PCR for *P. vivax* [22,24]. PCR primers, probes, and reaction conditions are described in the Supplementary File.

We first assessed the performance of all three assays using a panel of 11 DNA samples from real-time PCR-confirmed *Plasmodium* infections, including the four major human species (no *P. knowlesi* clinical isolates were available) and a range of parasite densities. We further characterized the performance of the *P. falciparum* assay using a panel of 62 PCR-positive and 50 PCR-negative samples collected in the DRC and Uganda. *Plasmodium* SHERLOCK assays were performed in triplicate for the panel of 11 DNA samples and once for the 112 samples collected in the DRC and Uganda. To improve specificity, positive SHERLOCK calls were made if the absolute fluorescence was at least 20% above background fluorescence. Clinical sensitivity, clinical specificity, and Cohen’s Kappa coefficient were calculated using real-time PCR as the gold standard.

2.9. Parasite DNA detection in mosquito pools using SHERLOCK

Parasite DNA was extracted from insectary-reared *Anopheles dirus* mosquitoes fed on blood from gametocyte-infected *P. falciparum*-infected volunteers in Cambodia. Mosquitoes were saved 9 and 16 days post-feeding to capture oocyst-stage and sporozoite-stage infection, respectively. They were pooled in groups of 10 and preserved in 95% ethanol before undergoing DNA extraction via a simplified Chelex protocol as previously described [27]. SHERLOCK assays were performed on DNA from mosquito pools in triplicate. Comparison of mean background-subtracted fluorescence values was performed using the t-test as described above.

2.10. Deep sequencing of clinical samples and dhps genotyping

We selected 463 DNA samples from the DRC with *P. falciparum* mono-infection by real-time PCR for dhps genotyping using a multiplex real-time PCR assay that discriminates wild-type from 581G mutants (see Supplementary File for details) [7]. We then selected samples for amplicon-based deep sequencing, including a subset of 92 wild-type and 581G mutant DNA samples identified during dhps real-time PCR screening of DRC samples and 92 *P. falciparum* histidine-rich protein 2-based RDT-positive samples from Uganda. Each of these 184 samples was amplified using a barcode-labeled forward and reverse primer (Supplementary Table 4). PCR reactions were carried out in a total volume of 50 µL and using 5 µL of input DNA. The reaction mixture contained 1X Accuprime PCR buffer II (Invitrogen, Carlsbad, CA), 1 unit Accuprime HiFi taq, 1 µL of 0.0025 mg/µL BSA, and 400 nM of forward and reverse primer. The reaction conditions were 95°C for 2 minutes, followed by 40 cycles of 95°C for 30 seconds, 60°C for 30 seconds and 68°C for 1 minute, with a final extension of 68°C for 10 minutes. PCR products were quantified using picogreen on a microplate reader. Amplicons were pooled, prepared for sequencing using Kappa HyperPrep Kits (Roche, Indianapolis, IN) and sequenced on a single MiSeq (Illumina, San Diego, CA) run using 250 bp paired-end chemistry at the UNC High Throughput Sequencing Facility.

Sequencing data was analyzed using Sequel v2.6-5 using default parameters [28]. Briefly, data were demultiplexed using the dhps primers and a dual barcoding scheme, and final haplotypes for each sample were determined by removing low per-base quality scores and low frequency mismatches. Final haplotypes were further filtered by removing haplotypes with <2,000 reads within samples. We then selected DNA from samples containing a single variant consistent with a wild-type or A581G mutant parasite for SHERLOCK SNV testing. Mixed infections were excluded. Wild-type parasites were stratified by sampling location and selected for SHERLOCK testing using a random number generator (Excel, Microsoft, Seattle, WA).

2.11. Dhps SNV detection by SHERLOCK

All dhps SNV-detection SHERLOCK assays were performed in triplicate using the conditions described above. Positive SHERLOCK calls were made if background-subtracted fluorescence was positive. Clinical sensitivity, clinical specificity, and Cohen’s Kappa coefficient were calculated using deep sequencing calls as the gold standard.

2.12. Statistical analysis

Statistical analyses were performed in Prism (RRID:SCR_002798, GraphPad, San Diego, CA) and R (R Core Team, Vienna, Austria). Comparisons were made using the t-test for continuous variables. Probit analysis was used to determine the 95% limit of detection and 95% confidence intervals for each SHERLOCK assay. Samples were not randomized and experimenters were not blinded in conducting these experiments.

3. Results

We translated SHERLOCK to malaria by designing and screening candidate RPA primers and crRNAs, optimizing assay conditions, and validating them on clinical and mosquito samples collected in diverse sites (Figure 1). Assay development included the design and testing of two broad categories of RPA primers and crRNAs. The first design targeted conserved and variable regions of the *Plasmodium* 18S rRNA gene and enabled detection and species identification of *Plasmodium* parasites in clinical samples and mosquitoes. The second design included engineered crRNA-target mismatches to enable detection of the *P. falciparum* A581G mutation associated with resistance to sulfadoxine (Figure 2). A range of reaction parameters were tested during pilot testing. While we were unable to replicate the “one-pot” reaction approach (combining RPA, IVT, and Cas13a detection) previously described for viral targets,[10] we achieved best performance using a two-step reaction format (RPA followed by IVT and Cas13a detection) and 10-50-fold higher crRNA concentrations than those originally described by Gootenberg et al [9].

3.1. Plasmodium SHERLOCK achieves robust analytical sensitivity and specificity

Our SHERLOCK assays demonstrated attomolar analytical sensitivity for *Plasmodium* DNA, equivalent to 95% lower limits of detection (LODs) of 2.5-18.8 parasite genomes per reaction (4.2-31.3 am; Figure 3, Table 1) for all three assays. Using only 1 µL of initial DNA input, this is roughly equivalent to 2.5-18 parasites/µL. These sensitivities approach those of commonly deployed malaria real-time PCR assays,[3] which achieved 0.3-2.5 parasites/µL analytical sensitivities during head-to-head testing in one controlled setting [29]. The pan-*Plasmodium* and *P. falciparum* SHERLOCK assays achieved superior LODs compared to *P. vivax*, but all three assays achieved LODs well below those detected by commonly used malaria RDTs (Table 1).

To test the specificity of our SHERLOCK assays against different *Plasmodium* species, we conducted assays using high concentration 18S rRNA plasmid DNA or gDNA from all five human-infecting *Plasmodium* species (Figure 4). The pan-*Plasmodium* SHERLOCK assay detected all five *Plasmodium* species, while the *P. falciparum* SHERLOCK assay only displayed activity against *P. falciparum* gDNA. The *P. vivax* SHERLOCK assay detected *P. vivax* 18S rRNA plasmid DNA, but also demonstrated low-level cross-reactivity for *P. knowlesi* gDNA.
3.2 SHERLOCK performs well in clinical samples and infected mosquitoes

Our SHERLOCK assays successfully detected and differentiated the four most common Plasmodium spp. known to cause human malaria from clinical samples across a range of parasite densities. When applied to a panel of real-time PCR-positive clinical isolates from the DRC and Thailand, the species-specific P. falciparum and P. vivax assays demonstrated complete clinical specificity (Figure 5). When applied to a larger panel of 62 PCR-positive and 50 PCR-negative samples from the DRC and Uganda, the P. falciparum SHERLOCK assay’s sensitivity and specificity were 94% and 94%, respectively, compared to real-time PCR (Supplementary Figure 4, Supplementary Table 5). The four PCR-positive/SHERLOCK-negative samples had

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**Table 1**

95% lower limits of detection (LOD) for Plasmodium spp. SHERLOCK assays. Input is 1 μL of DNA template per reaction.

| SHERLOCK Assay | LOD (95% CI) | 10^5 | 10^6 | 10^7 | 10^8 | 20 | 15 | 10 | 5 | 2.5 | 1.25 |
|----------------|-------------|------|------|------|------|----|----|----|----|-----|-----|
| Pan-Plasmodium | 2.5 (1.9–21.3) | 3/3 | 3/3 | 3/3 | 3/3 | -  | -  | 20/20 | 20/20 | 19/20 | 14/20 |
| P. falciparum  | 6.8 (5.3–11.6) | 3/3 | 3/3 | 3/3 | 3/3 | -  | -  | 20/20 | 17/20 | 9/20  | 8/20  |
| P. vivax       | 18.8 (13.3–146.3) | 3/3 | 3/3 | 3/3 | 3/3 | 20/20 | 20/20 | 10/20 | 19/20 | -    | -    |

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Fig. 3. Analytical sensitivity of Plasmodium spp. SHERLOCK assays. (a) Pan-Plasmodium assay vs. P. falciparum strain 3D7 gDNA. (b) Pan-Plasmodium assay vs. P. vivax 18S rRNA plasmid DNA. (c) P. falciparum assay vs. P. falciparum strain 3D7 gDNA. (d) P. vivax assay vs. P. vivax 18S rRNA plasmid DNA. N = 3 technical replicates, n = 1 biological replicate. Unpaired student’s T test vs. NTC, ± SEM. Abbreviations: NTC, no template control.

Fig. 4. (a) Pan-Plasmodium SHERLOCK assay can detect all five Plasmodium species in humans, while (b) P. falciparum, and (c) P. vivax SHERLOCK assays can differentiate between Plasmodium species. Input for all species was the equivalent of 100,000 parasites/μL as either species-specific 18S plasmid or gDNA. n (P. knowlesi only). N = 3 technical replicates, n = 1 biological replicate. Unpaired student’s T test vs. NTC, ± SEM. Abbreviations: NTC, no template control.
positive SHERLOCK results upon repeat testing, suggesting operator error or stochastic amplification failure during the initial assay. When SHERLOCK was performed in singleton, Cohen's kappa was 0.87, consistent with excellent agreement between methods.

The P. falciparum SHERLOCK assay also performed well when applied to DNA extracted from pooled, infected mosquitoes (n=4) (Figure 5). In all cases, the P. falciparum SHERLOCK assay was able to detect the presence of parasites, including both the sporozoite and oocyst stages within the sporogonic life cycle.

3.3. SHERLOCK can be used to detect SNVs associated with antimalarial drug resistance

Amplicon-based deep sequencing was performed to distinguish wild-type and A581G mutant dhps P. falciparum infections in 185 samples from the DRC and Uganda collected from patients with symptomatic malaria. The A581G mutation is associated with high-level resistance to sulfadoxine. The median read count per sample was 81,775. After filtering, only two variants were observed across all samples, corresponding to wild-type and A581G mutant dhps. Forty-three samples that were confirmed to be mono-infections bearing only wild-type or A581G mutant dhps mutations were selected for testing by SHERLOCK.

When applied to 22 wild-type and 21 A581G mutant dhps samples from Uganda, the sensitivity and specificity of the P. falciparum dhps SHERLOCK assay were 73% and 100%, respectively, using dhps deep sequencing calls as the gold standard. Cohen's kappa was 0.72, consistent with good agreement between SHERLOCK and amplicon-based deep sequencing. When restricted to field samples with parasite densities of ≥420 parasites/μL, the dhps SHERLOCK assay's clinical sensitivity and specificity were 100% and 100%, respectively. Among these higher parasite density samples, Cohen's kappa was 1.0, consistent with perfect agreement between the dhps SHERLOCK assay and amplicon-based deep sequencing in these samples with higher parasite densities.

4. Discussion

We describe a suite of novel SHERLOCK malaria assays and highlight the versatility of CRISPR-based diagnostics for a range of infectious disease applications. The new assays achieved robust clinical sensitivity and specificity when applied to well-characterized clinical samples and were easily adapted for parasite detection in mosquitoes and for drug-resistance genotyping. New diagnostics that can be used to detect, identify species, and genotype P. falciparum infections rapidly and reliably are especially needed in sub-Saharan Africa, where 94% of malaria deaths occur (https://www.who.int/publications/i/item/9789241565721).

These SHERLOCK malaria assays outperform HRP2-based RDTs, the predominant malaria diagnostic modality deployed throughout Africa, and achieve similar performance to recently developed ultrasensitive HRP2-based RDTs, which have achieved clinical sensitivities of roughly 3 parasites/μL [30,31]. Increasing reports of P. falciparum with deletion mutations of the histidine rich 2 and/or 3 (pfhrp2/3) genes raise concerns about reliance on HRP2 as the primary diagnostic target for RDTs [2]. RDTs that detect alternative antigens such as pLDH are available, but they are less sensitive and less heat-stable than HRP2-based RDTs. Thus, there is a need for novel malaria diagnostics that detect other targets. While both SHERLOCK and other CRISPR-based diagnostic assays currently in development need additional optimization prior to field deployment, we demonstrate that...
they are easily adapted for specific use cases and represent a promising avenue for malaria diagnostic development.

The analytical and clinical sensitivity of these SHERLOCK malaria assays approached that of commonly used real-time PCR assays, but the ability to conduct SHERLOCK without thermocycling allows for reduced laboratory infrastructure requirements and enables simplified isothermal approaches. More recently developed “ultrasensitive PCR” assays that target RNA and/or multicopy genes have achieved analytical sensitivities as low as 0.02 parasites/µL, but their use in low-resource laboratory settings is limited by the need to protect against RNA degradation and/or the requirement for large-volume samples [32,33]. LAMP is an alternative nucleic acid detection method that has been used for malaria diagnosis in field settings with similar sensitivity and specificity to SHERLOCK [34]. LAMP shows promise as a field-deployable molecular diagnostic, but its use for bespoke applications has been hampered by the complexity of target selection and primer design. CRISPR-based diagnostic approaches like SHERLOCK are an emerging technology that can be rapidly adapted in response to malaria’s evolving epidemiology [35].

Species discrimination was excellent across Plasmodium spp. SHERLOCK assays, with the exception of the P. vivax SHERLOCK assay that demonstrated cross-reactivity with P. knowlesi. The P. vivax spacer and the analogous region on P. knowlesi differ by four nucleotides, so this cross-reactivity was unexpected. One explanation is that these nucleotides are towards the 3’ end of the crRNA spacer (positions 20, 26, 27 in the 28), which have been shown to have a smaller influence on crRNA binding efficiency [9]. Another explanation is unappreciated homology between P. vivax and P. knowlesi spacer binding sites in the setting of incomplete understanding of P. knowlesi’s genetic diversity. These findings highlight the importance of using high-quality genomic data when designing target sequences for CRISPR-based diagnostics and consideration of sequence variability within targets. Future SHERLOCK assays will be strengthened by efforts to improve our understanding of parasite genomic diversity [36,37].

Our novel SNV detection SHERLOCK assay for the dhps 581G variant in P. falciparum represents one of the first uses of SHERLOCK to detect SNVs in clinical isolates outside of its original description [9,10]. We chose to develop a SHERLOCK SNV detection assay for Plasmodium dhps variants due to their public health importance in the prevention of malaria during pregnancy. Variants in the dhps gene can confer resistance to sulfadoxine, which is used in combination with pyrimethamine (SP) as the primary antimalarial drug for intermittent preventive treatment in pregnancy (IPTp) to prevent malaria in pregnancy throughout much of sub-Saharan Africa [38]. Our dhps SHERLOCK assays demonstrated parasite-density dependent sensitivity and perfect specificity when compared to amplicon-based deep sequencing. When applied to a wide range of parasite inputs, the assay only produced false-negative results in samples with low parasite densities (6/7 samples with ≤319 parasites/µL sample input). While the SNV detection assay is concentration dependent, it performed well at parasite densities typically associated with clinically significant malaria [39]. In future, mixed infections involving both wild-type and 581G mutant strains could be identified by pairing the 581G-specific assay described here with a wild-type-specific assay in a multiplexed format. SHERLOCK’s SNV detection capabilities are a promising tool for malaria control programs in low-resource settings where sequencing facilities are not available to support surveillance. For example, high prevalence of resistance-associated dhps variants detected by SHERLOCK could trigger deployment of alternative drug regimens for IPTp in affected regions.

Our SHERLOCK assays are now one of two published CRISPR-based diagnostic modalities for Plasmodium detection; in a recently published manuscript, Lee et. al. describe a suite of highly sensitive and specific assays for P. falciparum, P. vivax, P. malariae, and P. ovale spp. [40]. These assays employ a detection approach most similar to the DNA endonuclease-targeted CRISPR trans reporter (DETECTR) methodology, which uses the DNA endonuclease Cas12 [41]. While our methods differ in this regard, both approaches highlight the potential uses for SHERLOCK and other CRISPR-based diagnostics for malaria diagnosis, research, and drug resistance surveillance.

The assays described by Lee et al have several advantages and disadvantages compared to our assays. First, the analytical sensitivity achieved by Lee et. al. is superior. The 95% lower LODs of their P. falciparum and P. vivax assays were 0-36 (0.23-1.0) and 1-2 (0.52-6.2) parasites/µL compared to our 95% lower LODs of 6-8 (5.3-11.6) and 18-8 (13.3-146.3), respectively. One explanation for this improved performance is that Lee et al. chose gene targets that are present in higher copy numbers: Pfr364 subtelomeric repeat DNA for P. falciparum (41 copies) and mitochondrial DNA for P. vivax (up to 20 copies) vs. 18s rRNA in our assays (~6 copies). While the use of 18s rRNA targets reduces assay sensitivity, it provides opportunities for streamlined, multiplexed assays that employ a single, shared RPA primer set targeting regions that are conserved across Plasmodium species and bespoke crRNAs for species identification. Second, Lee et al. describe streamlined approaches to nucleic acid extraction and reaction setup that are better suited for field use. These advances make it clear that some of the challenges we encountered with our Cas13a-based SHERLOCK approach can be overcome. Third, the clinical performance of the assays described by Lee et al. is not yet defined. They conducted validation experiments using a panel of simulated samples derived from cultured parasites and a small number of serum samples, whereas we validated our assays on dried blood spot samples collected in malaria endemic countries, including a large panel of 112 samples for our P. falciparum assay. This type of clinical validation is important because samples collected under field conditions is necessary to define real-world assay performance, both in terms of sample preparation/integrity and parasite genetic diversity. Genetic diversity of sites targeted by these assays can only be partly deduced from publicly available sequencing data, especially in the case of non-falciparum species like P. ovale and P. malariae that are not well represented in existing databases. Despite these differences, the performance of both sets of CRISPR-based diagnostic assays demonstrates that they can detect parasite concentrations well below what is expected in clinical malaria and supports future studies to adapt and validate these assays for use in research and clinical settings.

We chose LwCas13a-based detection over a Cas12a-based approach to take advantage of Cas13a’s minimal protospacer-adjacent motif (PAM) site nucleotide requirements compared to Cas12a. LwCas13a requires only H (not G) adjacent to the spacer region, which makes guide design and SNV detection for LwCas13a easier than for Cas12a, which has a PAM requirement of “TTTN” [41,42]. Additionally, multiplexing with SHERLOCK has been demonstrated using Cas13a isolated from multiple bacterial species, which have different collateral activities that can be used to activate different RNA reporters, enabling multiplexed assays [10]. These properties of Cas13a provide opportunities for further assay development, including translation of our malaria SHERLOCK assays into a single, multiplexed assay that enables species identification of multiple Plasmodium species and drug-resistance SNVs in a single reaction. We experienced success using SHERLOCK to detect Plasmodium spp. and drug-resistance variants; however, several limitations must be overcome for successful translation of SHERLOCK from the laboratory to the field. First, we could not achieve the sub-attomolar limits of detection or “one-pot” reaction conditions previously described for viral targets [10]. We also observed that our assays performed best using higher crRNA concentrations than those originally described [9]. Though this may reflect differences in crRNA synthesis or lot-to-lot variation in other reagents, we observed improved reaction performance with higher crRNA concentrations across multiple experiments.
Second, the cost of designing and validating a SHERLOCK assay is not trivial. In a reaction volume of 25 μL used for 96-well plates and using fluorescent output, the cost was roughly equivalent to PCR at over $2-00 of reagent costs per technical replicate, plus upfront costs of crRNA optimization and synthesis and the need for a fluorescence plate-reader. These costs can be reduced for assays brought to scale but are an important consideration during assay design. Finally, SHERLOCK requires multiple reagents, custom crRNAs, and Cas13a. Recent progress has been made to reduce its complexity and make these assays more easily accessible [43]. Indeed, the approach described by Lee et al. includes a streamlined workflow from sample collection to Cas12a-based detection; including an optimized nucleic acid extraction step, one-pot lyophilized reaction, reduced reaction time, and a handheld fluorometer and lateral-flow readout. Other groups have sought to replace RPA preamplification with LAMP, or eliminate it altogether in the case of one Cas13a-based SARS-CoV-2 diagnostic (https://doi.org/10.1101/2020.12.14.20247874) [44]. While these advances confirm rapid improvements in CRISPR-based assay performance and feasibility, implementation of SHERLOCK as a point-of-care molecular diagnostic will require further streamlining including the development of commercially-available mastermixes and the combination of nucleic acid extraction, Cas effector activation, and signal readout into a single device.

While these limitations must be overcome before immediate field applications, SHERLOCK is a promising technology with multiple potential uses in malaria diagnosis, research, and drug resistance surveillance. In particular, our SNV detection SHERLOCK assays demonstrate applications beyond infectious disease diagnosis and include genotyping pathogens at the nucleotide level. With further optimization, our SNV detection assays could facilitate drug resistance surveillance for malaria control programs without the need for PCR or sequencing. Additionally, our pilot application of SHERLOCK to detect *P. falciparum* in infected mosquitoes demonstrates potential beyond clinical diagnostics and other uses for research in low malaria transmission or near elimination settings. Continued development of new Cas effectors, streamlined workflows, and point-of-care read-outs will open new opportunities for CRISPR diagnostics in clinical, surveillance, and research applications. These novel malaria SHERLOCK assays confirm the promise of CRISPR-based diagnostics for diverse applications and in resource-limited settings (Fig. 6).

**Declaration of Competing Interest**

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**Author Contributions**

Clark Cunningham: Conceptualization, Methodology, Validation, Formal Analysis, Investigation, Visualization, Writing - Original Draft. Christopher Hennelly, Kyaw Thwai: Investigation. Jessica Lin, Ratawan Ubalee, Ross Boyce, Edgar Mulogo, Fernandine Phanzu, Albert Kalonji, Kashamuia Mwandagalirwa, Antoinette Tshefu. Nicholas

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**Fig. 6.** The dhps SHERLOCK assay detects *P. falciparum* parasites with (a) mutant (581G) but not (b) wild-type (A581) alleles. Parasite densities were determined by qPCR. N = 3 technical replicates, n = 1 biological replicate, ± SEM. Mutant (Mut) and WT gDNA standard inputs were 100,000 parasites/μL.
Hathaway: Software, Formal Analysis, Jonathan Juliano: Conceptualization, Supervision, Funding Acquisition, Jonathan Parr: Conceptualization, Supervision, Project Administration, Funding Acquisition, Visualization, Resources, Writing - Original Draft. All authors: Writing - Review and Editing.

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Supplementary materials

Supplementary material associated with this article can be found in the online version at doi:10.1016/j.ebiom.2021.103415.
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